

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 15, 2004, 16:35:53 ; Search time 3682 Seconds
(without alignments)

1671.567 Million cell updates/sec

Title: US-09-690-825-34

Perfect score: 778

Sequence: 1 MGAPLPPAWOPFLKDHRS.....EFETAKKVRRAIEQLAAMD 142

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delcp 6.0 , Delcxt 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlh
-Q=/cpn2.1/USPTO.spool/US09690825/runat.11082004.140951.13531/app.query.fasta_1.327
-DB=GenEmbl -OPMT=fastap -SUPFIX=rge -WINMATCH=0.1 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09690825 @CGN.1.1.3731 @runat.11082004.140951.13531 -NCPUS=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.*
1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_om.*
21: em_or.*
22: em_ov.*
23: em_pat.*
24: em_ph.*
25: em_pl.*
26: em_ro.*
27: em_sts.*
28: em_un.*

29: em_vi.*
30: em_htg_hum.*
31: em_htg_inv.*
32: em_htg_other.*
33: em_htg_mus.*
34: em_htg_pin.*
35: em_htg_rod.*
36: em_htg_man.*
37: em_htg_vrt.*
38: em_sy.*
39: em_htgo_hum.*
40: em_htgo_mus.*
41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	778	100.0	426	6	AR184473 Sequence
2	778	100.0	426	6	BD167854 Survivin
3	778	100.0	426	6	BD185366 Survivin
4	778	100.0	1619	6	AR093347 Sequence
5	778	100.0	1619	6	BD273550 Antisense
6	778	100.0	1619	6	AR181635 Sequence
7	778	100.0	1619	6	AX775129 Sequence
8	778	100.0	1619	6	AX779941 Sequence
9	778	100.0	1629	9	AF077350 Homo sapi
10	778	100.0	1643	9	BC034148 Homo sapi
11	778	100.0	1653	9	BC008718 Homo sapi
12	775	99.6	1630	4	AB095108 Canis fam
13	756.5	97.2	600	9	AB028869 Homo sapi
14	748	96.1	1165	6	AR097642 Sequence
15	748	96.1	1165	6	AR154245 Sequence
16	721	92.7	740	6	AF270355 Sequence
17	718	92.3	794	4	AF195781 Sus scrofa
18	663.5	85.3	463	6	AX778483 Sequence
19	660	84.8	903	10	AF276775 Rattus no
20	660	84.8	924	10	AF077349 Mus muscu
21	660	84.8	955	6	AR181548 Sequence
22	660	84.8	955	10	AB013819 Mus muscu
23	642	82.5	399	6	AX886452 Sequence
24	642	82.5	399	6	BD026062 Sequence
25	618	79.4	1011	9	HUMMNASEQ L26245 Human efec
26	556	71.5	3352	10	BC004702 Mus muscu
27	531.5	68.3	1539	9	BC000784 Homo sapi
28	486	62.5	503	5	AF322051 Gallus ga
29	459.5	59.1	555	5	AF377323 Gallus ga
30	456	58.6	772	5	AY174765 Xenopus l
31	389	50.0	701	5	AY057057 Danio rer
32	389	50.0	1239	5	BC055739 Danio rer
33	382	49.1	14796	6	AR157507 Sequence
34	382	49.1	14796	6	AR181541 Sequence
35	382	49.1	14796	6	AX333491 Sequence
36	382	49.1	14796	6	AX334154 Sequence
37	382	49.1	14796	6	AX336483 Sequence
38	382	49.1	14796	6	AX410775 Sequence
39	382	49.1	14796	6	BD192864 Survivin
40	382	49.1	14796	9	BD192864 Survivin
41	382	49.1	209751	9	AC087645 Homo sapi
42	363	46.7	489	5	AY057058 Danio rer
43	363	46.7	154840	2	AC032035 Homo sapi
44	361.5	46.5	228077	2	AC130552 Rattus no
45	361.5	46.5	240200	2	AC122075 Rattus no

ALIGNMENTS

RESULT 1

AR184473	AR184473	426 bp	DNA	linear	PAT 20-APR-2002
LOCUS	Sequence 2 from patent US 6346389.				
DEFINITION	AR184473				
ACCESSION	AR184473				
VERSION	AR184473.1	GI:20230438			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 426)				
AUTHORS	Altieri,D.C.				
TITLE	Method for selectively modulating the interactions between survivin and tubulin				
JOURNAL	Patent: US 6346389-A 2 12-FEB-2002;				
FEATURES	Location/Qualifiers				
source	1..426				
	/organism="unknown"				
	/mol_type="unassigned DNA"				
ORIGIN					
Alignment Scores:					
Pred. No.:	3,01e-77	Length:	426		
Score:	778.00	Matches:	142		
Percent Similarity:	100.00%	Conservative:	0		
Best Local Similarity:	100.00%	Mismatches:	0		
Query Match:	100.00%	Indels:	0		
DB:	6	Gaps:	0		
US-09-690-825-34 (1-142) x AR184473 (1-426)					
Qy	1 MetGlyAlaProThrLeuPProCoAlaTrpGlnProPheLeuLysAspHisArgIleSer	20			
Db	1 ATGGGTGCCCGGACGTTGCCCTGCCTGGCAGCCCTTTCTCAGGACCACCGCATCTCT	60			
Qy	21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu	40			
Db	61 ACATTCAAGAACTGGGCCCTTTCTTGGAGGGCTGGCCCTGCACCCCGAGCGGATGGCCGAG	120			
Qy	41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys	60			
Db	121 GCTGGCTTCATCCATGCCCATCTGAGACGACGCCAGACTTGGCCCGAGTGTTCCTCTGC	180			
Qy	61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluHisLysLysHis	80			
Db	181 TTCAAGGAGCTGAAGGCTGGGAGCCAGATGACGCCATAGAGGAACATAAAAGCAT	240			
Qy	81 SerSerGlyCysAlaPheLeuSerValLysGlnPheGluGluLeuThrLeuGlyGlu	100			
Db	241 TCGTCGGTTCGCTTCCTTCTGTCAAGACAGTTTGAAGATTATCCCTTTGTGAA	300			
Qy	101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys	120			
Db	301 TTTTTCGAACTGCACAGAGAAAGAGCCAAAGACAAATTTGAAAGGAAACCAACATAAG	360			
Qy	121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaLleGluGlnLeuAlaAla	140			
Db	361 AAGAAGAATTTGAGGAAACTGCGAAGAAAGTGGCCGTGCCATCGAGCAGCTGGCTGCC	420			
Qy	141 MetAsp	142			
Db	421 ATGGAT	426			
RESULT 2					
BD167854					
LOCUS	Survivin-like polypeptide and its DNA.	426 bp	DNA	linear	PAT 17-JAN-2003
DEFINITION	BD167854				
ACCESSION	BD167854				
VERSION	BD167854.1	GI:27873666			
KEYWORDS	WO 0233071-A/6				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				

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OM protein - protein search, using sw model

Run on: August 11, 2004, 14:14:00 ; Search time 16 Seconds
(without alignments)
853.700 Million cell updates/sec

Title: US-09-690-825-34
Perfect score: 778
Sequence: 1 MGAPLPPAWQFLKDHRS.....EPEETAKVRRRAIEQLAAMD 142
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	163	21.0	997	T43523	cutl7 protein - fi
2	160	20.6	4845	T31067	BIR repeat contain
3	157	20.2	308	T37474	apoptosis inhibito
4	155	19.9	1232	A55478	neuronal apoptosis
5	154	19.8	208	T03183	probable apoptosis
6	145.5	18.7	155	T37471	apoptosis inhibito
7	142	18.3	1447	T42628	neuronal apoptosis
8	136.5	17.5	275	A45679	inhibitor-of-apopt
9	136.5	17.5	298	JC7568	kidney inhibitor o
10	133.5	17.2	268	T10304	inhibitor of apopt
11	133.5	17.2	268	A53989	apoptosis-inhibiti
12	131	16.8	618	S68450	apoptosis inhibito
13	130	16.7	155	T30489	apoptosis inhibito
14	128.5	16.5	358	JC5964	apoptosis inhibito
15	125.5	16.1	497	S63544	apoptosis inhibito
16	121	15.6	604	S68452	apoptosis inhibito
17	118	15.2	496	S68452	apoptosis inhibito
18	118	15.2	497	S69545	apoptosis inhibito
19	106.5	13.7	150	T28409	ORF MSV248 probabl
20	106.5	13.7	954	S57108	apoptosis-inhibiti
21	99.5	12.8	275	T10310	hypothetical prote
22	96	11.1	329	T28403	ORF MSV242 probabl
23	85	10.9	329	T47419	hypothetical prote
24	83.5	10.7	385	T19201	hypothetical prote
25	83	10.7	434	A43252	probable transcrip
26	82	10.5	135	A38609	lectin, galactose-
27	80.5	10.3	1096	T48512	hypothetical prote
28	80	10.3	355	T22146	hypothetical prote
29	80	10.3	1390	S51364	sperm tail-specifi

ALIGNMENTS

RESULT 1

T43523
cutl7 protein - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 21-Jan-2000 #sequence-revision 21-Jan-2000 #text_change 02-Jun-2000
C:Accession: T43523; T41649; T41700
R:Morishita, J.; Matsusaka, T.; Yanagida, M.
Submitted to the EMBL Data Library, August 1999
A:Description: Fission yeast cutl7 is required for chromosome segregation.
A:Reference number: 222536
A:Accession: T43523
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-997 <MOR>
A:Cross-references: EMBL:AB031034; PIDN:BAAG3415.1
R:Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
Submitted to the EMBL Data Library, August 1998
A:Reference number: 222007
A:Accession: T41649
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-997 <HAR>
A:Cross-references: EMBL:AL031323; PIDN:CAA20434.1; GSPDB:GN00068; SPDB:SPCC962.02c
A:Experimental source: strain 972h-; cosmid c962
R:Medler, H.; Duesternoeft, A.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
Submitted to the EMBL Data Library, October 1999
A:Reference number: 222010
A:Accession: T41700
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 932-937 <WED>
A:Cross-references: EMBL:AL121859; PIDN:CAB58376.1; GSPDB:GN00068; SPDB:SPCP31B10.10c
C:Genetics:
A:Gene: cutl7; SPCC962.02c; SPDB:SPCP31B10.10c
A:Map position: 3L
A:Introns: 43/3

Query Match 21.0%; Score 163; DB 2; Length 997;
Best Local Similarity 41.6%; Pred.No. 3.le-06;
Matches 32; Conservative 9; Mismatches 32; Indels 4; Gaps 2;

QY	18	RISFT--KNPFFLE--GCATPFRMAGTHICTENEPDLAOCFFCKLEGWEPDDDP	73
DB	120	REQTFVQKWPFTYTRPDYHCEPSVMAASGFVYNTADAKAAHCLYCDINLHDWEPDDP	179
QY	74	IEEHKHSSGCAFLSVK	90
DB	180	YTEHKRRRADCVPFTWK	196

RESULT 2
T31067

BIR repeat containing ubiquitin-conjugating enzyme BRUCE - mouse
C:Species: Mus musculus (house mouse)
C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
C:Accession: T31067
R:Hauser, H.P.; Bardeff, M.; Pyrowolakis, G.; Jentsch, S.
J. Cell Biol. 141, 1415-1422, 1998
A>Title: A giant ubiquitin-conjugating enzyme related to IAP apoptosis inhibitors.
A:Reference number: 220963; MUID:98292517; PMID:19628897
A:Accession: T31067
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-4845 <HAU>
A:Cross-references: EMBL:Y17267; NID:g3319989; PIDN:CAA76720.1; PID:g3319990
A>Note: localized to the Golgi compartment and the vesicular system
C:Keywords: Membrane-associated protein

Query Match 20.6%; Score 160; DB 2; Length 4845;
Best Local Similarity 42.3%; Pred. No. 2.8e-05;
Matches 30; Conservative 10; Mismatches 31; Indels 0; Gaps 0;
QY 17 HRISTFKNWPF-LEGCACTPERMAEAGFHCPTENEPDLAOCFFCFKELEGWEPDDDDP 76
DB 263 NRRETFSTFVGVYRWYQDPMAQAGFYHQFASGDDDRAMCFCTCSVCLVCWEPTDEPWS 322
QY 77 HKHSHSGCAFL 87
DB 323 HERHSPNCPV 333

RESULT 3
T37474
apoptosis inhibitor homolog C50B8.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
C:Accession: T37474; T20098
R:Uren, A.G.
submitted to the EMBL Data Library, September 1996
A:Reference number: 221711
A:Accession: T37474
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-308 <URE>
A:Cross-references: EMBL:U72208; PIDN:AAD00182.1
R:Percy, C.
submitted to the EMBL Data Library, July 1996
A:Reference number: 219223
A:Accession: T20098
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-308 <WIL>
A:Cross-references: EMBL:Z77654; PIDN:CAB01130.1; GSPDB:GN00023; CBSP:C50B8.2
A:Experimental source: clone C50B8
C:Genetics:
A:Gene: C50B8.2
A:Map position: 5
A:Introns: 48/3; 143/1; 191/3

Query Match 20.2%; Score 157; DB 2; Length 308;
Best Local Similarity 30.1%; Pred. No. 3.1e-06;
Matches 37; Conservative 27; Mismatches 49; Indels 10; Gaps 3;
QY 16 DHRISTFKNWPF-LEGCACTPERMAEAGFHCPTENEPDLAOCFFCFKELEGWEPDDDDP 73
DB 168 DHRATFQNFIFDKRNVKYTSKLLAKAGWFSIANKDKTSKAPCPCLVELD-FDESDDP 226
QY 74 IEHKKHSGCAFLSVK------QFEELTGLBFLKLDREARNKIAKTNNKKKEFE 126
DB 227 WEEHQKFSASCDIFKLGKLBKWTNEALMIGARITIMQYKGVSWLIDELKENRIDE 286
QY 127 TAK 129
DB 287 IIK 289

RESULT 4
A55478
neuronal apoptosis inhibitory protein - human
N:Alternate names: NAIP
C:Species: Homo sapiens (man)
C>Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 02-Feb-2001
C:Accession: A55478
R:Roy, N.; Mahadevan, M.S.; McLean, M.; Shuttler, G.; Varaghi, Z.; Parahani, R.; Baird, S.
Cell 80, 167-178, 1995
A>Title: The gene for neuronal apoptosis inhibitory protein is partially deleted in indiv
A:Reference number: A55478; MUID:95112344; PMID:7813013
A:Accession: A55478
A:Molecule type: mRNA
A:Residues: 1-1232 <ROY>
A:Cross-references: GB:U19251
C:Genetics:
A:Gene: GDB:SMA@; SMA
A:Cross-references: GDB:120378; OMIM:600354; OMIM:253300
A:Map position: 5q12.2-5q13
C:Keywords: apoptosis; ATP; glycoprotein; nucleotide binding; P-loop; transmembrane prote
F:94-110/Domain: transmembrane #status predicted <TM1>
F:470-477/Region: nucleotide-binding motif A (P-loop)
F:479-496/Domain: transmembrane #status predicted <TM2>
F:476/Binding site: ATP (lys) #status predicted
F:618,632,823,923,1035/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 19.9%; Score 155; DB 2; Length 1232;
Best Local Similarity 40.5%; Pred. No. 1.9e-05;
Matches 34; Conservative 15; Mismatches 29; Indels 6; Gaps 3;
QY 15 KDHRISTFKNWPF-LEGCACTPERMAEAGFHCPTENEPDLAOCFFCFKELEGWEPDDDDP 73
DB 159 EBARLASFRNPFYVQG--ISPCVLSEAGFV--TGKQDTVQFCGGCGLGNWEEGDDP 213
QY 74 IEHKKHSGCAFLSVKQFELT 97
DB 214 WKEHAKWPFKCFERSKSSSEIT 237

RESULT 5
T03183
probable apoptosis inhibitor - Chilo iridescent virus
C:Species: Chilo iridescent virus
C>Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 02-Sep-2000
C:Accession: T03183
R:Bahr, U.; Tidona, C.A.; Darai, G.
Virus Genes 15, 235-245, 1997
A>Title: The DNA sequence of Chilo iridescent virus between the genome coordinates 0.101
A:Reference number: Z14834; MUID:98141693; PMID:9482589
A:Accession: T03183
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-208 <BAH>
A:Cross-references: EMBL:AF003534; NID:g2738385; PIDN:AAB94481.1; PID:g2738454
C:Superfamily: RING finger homology
F:159-202/Domain: RING finger homology <RNF>

Query Match 19.8%; Score 154; DB 2; Length 208;
Best Local Similarity 32.5%; Pred. No. 3.8e-06;
Matches 39; Conservative 23; Mismatches 38; Indels 20; Gaps 7;
QY 12 PELK-DHRISTFKNWPFLEGCACTPERMAEAGFHCPTENEPDLAOCFFCFKELEGWEPD 70
DB 33 PFASDERLNSQNFPI--QLLPSEKLSRAGFYL---NGDQVQCFYCDLKLKWKRS 87
QY 71 DDPIEEHKKHSS----GCAFLSVKQFQFELTGLBFLKLDREARNKIAKTNNKKKEFE 125
DB 88 DNPFEEHKKHKTQDLKINCLFV-----KSIFDFNFKVHSESCFQNFPI---TNNINQDL 138
RESULT 6

T37471
apoptosis inhibitor homolog T37471.3 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
C/Accession: T37471; T25380
R/Uren, A.G.
submitted to the EMBL Data Library, January 1997
A/Description: C. elegans IAP homologue.
A/Reference number: Z21708
A/Accession: T37471
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-155 <URE>
A/Cross-references: EMBL:U85911; PIDN: AAB94330.1
R/Lenhard, N.
submitted to the EMBL Data Library, June 1996
A/Reference number: Z20025
A/Accession: T25380
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-155 <WIL>
A/Cross-references: EMBL:Z74045; NID: e1062212; PIDN: CAA98553.1; GSPDB: GNO0023; CESP: T27F2
A/Experimental source: clone T27F2
C/Genetics:
A/Gene: T27F2.3
A/Map position: 5
A/Introns: 41/3

Query Match 18.7%; Score 145.5; DB 2; Length 155;
Best Local Similarity 37.1%; Pred. No. 1.5e-05;
Matches 36; Conservative 19; Mismatches 33; Indels 9; Gaps 6;
QY 13 FLKDRIHSTFKNWFLE--GCATPERMAEAGFIHCPTNEPDLAQCFFCFKELEGWEPD 70
Db 16 FYKD-RLMTFKNFEDRDPDAKTSQVAQAF-YC---TGFSQKCAFCNKELD-FDPE 69
QY 71 DDIIEHKKHSGCAFLSV-KQCFEELTLGEFLKIDR 106
Db 70 DDPWYHTRKDEPFCEVRICKLDDSELTINDAVRLSQ 106

RESULT 7
T42628
neuronal apoptosis inhibitory protein 2 - mouse
C/Species: Mus musculus (house mouse)
C/Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
R/Yaraghi, Z.; Diez, E.; Gros, P.; Mackenzie, A.
Mamm. Genome 10, 761-763, 1999
A/Title: CDNA cloning and the 5' genomic organization of Naip2, a candidate gene for murine
A/Reference number: Z22179; MUID: 99315342; PMID: 10384056
A/Accession: T42628
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-1447 <YAS>
A/Cross-references: EMBL:AF102871; NID: g3860228; PID: g3860229; PIDN: AAC73002.1
C/Genetics:
A/Gene: Naip2

Query Match 18.3%; Score 142; DB 2; Length 1447;
Best Local Similarity 37.3%; Pred. No. 0.00029;
Matches 31; Conservative 13; Mismatches 35; Indels 4; Gaps 2;
QY 15 KDRIHSTFKNWFLEGCATPERMAEAGFIHCPTNEPDLAQCFFCFKELEGWEPD 74
Db 159 EEARLESFDDPFY-AHGTSRVLGAAGFV---TKRDTVCFSGGGLGNWEGDDPW 214
QY 75 EEHKKHSGCAFLSVKQFEELT 97
Db 215 KGHAKWFPKCEFLQSKSPEEIT 237

RESULT 8

A45679
inhibitor-of-apoptosis polypeptide (IAP) - Cydia pomonella granulosis virus CpGV
C/Species: Cydia pomonella granulosis virus CpGV
C/Date: 21-Sep-1993 #sequence_revision 25-Apr-1997 #text_change 15-Sep-2000
C/Accession: A45679
R/Crook, N.E.; Clem, R.J.; Miller, L.K.
J. Virol. 67, 2168-2174, 1993
A/Title: An apoptosis-inhibiting baculovirus gene with a zinc finger-like motif.
A/Reference number: A45679; MUID: 93188168; PMID: 8445726
A/Accession: A45679
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-275 <CRO>
A/Cross-references: GB: L05494; NID: g289583; PIDN: AAA43835.1; PID: g289584
A/Note: sequence extracted from NCBI backbone (NCBIN: 127014, NCBI: 127015)
C/Superfamily: viral apoptosis inhibitor IAP; RING finger homology

Query Match 17.5%; Score 136.5; DB 2; Length 275;
Best Local Similarity 36.4%; Pred. No. 0.00016;
Matches 28; Conservative 14; Mismatches 24; Indels 11; Gaps 3;
QY 18 RISTFKNWFLEGCAC---TPERMAEAGFIHCPTNEPDLAQCFFCFKELEGWEPD 74
Db 111 RVKSFHNWP-----RCMKQRPQVADAGFFY---TGYGDNTKCFYCDGGLKWDPEDPVP 162
QY 75 EEHKKHSGCAFLSVKX 91
Db 163 EQVRFDRCAIVQLVK 179

RESULT 9
JC7568
kidney inhibitor of apoptosis protein - human
C/Species: Homo sapiens (man)
C/Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
C/Accession: JC7568
R/Lin, J.H.; Deng, G.; Huang, Q.; Morser, J.
Biochem. Biophys. Res. Commun. 279, 820-831, 2000
A/Title: KIAIP, a novel member of the inhibitor of apoptosis protein family.
A/Reference number: JC7568; MUID: 21092523; PMID: 11162435
A/Contents: Fetal kidney
A/Accession: JC7568
A/Molecule type: mRNA
A/Residues: 1-298 <LIN>
C/Comment: This protein, a new member of the inhibitor of apoptosis protein family, plays

C/Genetics:
A/Gene: kiap
A/Map position: 20q13.3
C/Keywords: apoptosis
Query Match 17.5%; Score 136.5; DB 2; Length 298;
Best Local Similarity 36.6%; Pred. No. 0.00018;
Matches 27; Conservative 9; Mismatches 29; Indels 5; Gaps 2;
QY 18 RISTFKNWFLEGCACTPERMAEAGFIHCPTNEPDLAQCFFCFKELEGWEPD 77
Db 90 RLASFYDWPILT--AEVPELLAAGFFH---TGQDKVRQCFYCGGLQSKRGDDPWTEH 144
QY 78 KKHSSGCAFL 87
Db 145 AKWFPSQFL 154

RESULT 10
TI0304
inhibitor of apoptosis protein 3 - Orgyia pseudotsugata nuclear polyhedrosis virus
C/Species: Orgyia pseudotsugata nuclear polyhedrosis virus, OpMNPV
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Sep-2000
C/Accession: TI0304
R/Ahrens, C.A.; Russell, R.R.; Funk, C.J.; Evans, J.; Harwood, S.; Rohrmann, G.F.
Virology 229, 381-399, 1997
A/Title: The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis

A:Reference number: Z17011; MUID:97271300; PMID:9126251

A:Accession: T10304

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-268 <AUR>

A:Cross-references: EMBL:U75930; NID:g2934903; PIDN:AAC59034.1; PID:g1911281

C:Superfamily: viral apoptosis inhibitor IAP; RING finger homology

F:217-261/Domain: RING finger homology <RRN>

Query Match 17.2%; Score 133.5; DB 2; Length 268;

Best Local Similarity 36.5%; Pred. No. 0.00029;

Matches 27; Conservative 12; Mismatches 30; Indels 5; Gaps 2;

QY 18 RISTFKWPFLEGGCACTPERMAEAGFIHCPTENEPDLAQCFKKELEGWEPDDPIEEH 77

DB 114 RLRTFAEWP--RGLKQRPPELAAGFFY--TGQDKTRCFCCDGGGLKWEPDDAPWQCH 168

QY 78 KKHSSGCAFLSVKK 91

DB 169 ARWYDRCBYVLVK 182

RESULT 11

A53989

apoptosis-inhibiting protein - Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus

C:Species: Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus, OpMNPV

C:Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 15-Sep-2000

C:Accession: A53989

R:Binbaum, M.J.; Clien, R.J.; Miller, L.K.

A:Title: An apoptosis-inhibiting gene from a nuclear polyhedrosis virus encoding a polyP

A:Reference number: A53989; MUID:94187094; PMID:8139034

A:Accession: A53989

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-268 <BTR>

A:Cross-references: NID:g456111; PIDN:AAB02610.1; PID:g456114

A:Note: authors translated the codon TGG for residue 28 as Tyr, GAC for residue 50 as As

C:Superfamily: viral apoptosis inhibitor IAP; RING finger homology

F:217-261/Domain: RING finger homology <RRN>

Query Match 17.2%; Score 133.5; DB 2; Length 268;

Best Local Similarity 36.5%; Pred. No. 0.00029;

Matches 27; Conservative 12; Mismatches 30; Indels 5; Gaps 2;

QY 18 RISTFKWPFLEGGCACTPERMAEAGFIHCPTENEPDLAQCFKKELEGWEPDDPIEEH 77

DB 114 RLRTFAEWP--RGLKQRPPELAAGFFY--TGQDKTRCFCCDGGGLKWEPDDAPWQCH 168

QY 78 KKHSSGCAFLSVKK 91

DB 169 ARWYDRCBYVLVK 182

RESULT 12

S68450

apoptosis inhibitor hiap-2 - human

C:Species: Homo sapiens (man)

C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 21-Jul-2000

C:Accession: S68450

R:Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farahani,

Nature 379, 349-353, 1996

A:Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP

A:Reference number: A58182; MUID:96149249; PMID:8552191

A:Accession: S68450

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-618 <LIS>

A:Cross-references: EMBL:U45679; NID:g1184317; PIDN:AAC50372.1; PID:g1184318

C:Function:

A:Description: apoptotic suppressor

C:Superfamily: RING finger homology

C:Keywords: apoptosis; zinc finger

F:567-611/Domain: RING finger homology <RNG>

Query Match 16.8%; Score 131; DB 2; Length 618;

Best Local Similarity 34.1%; Pred. No. 0.0011;

Matches 29; Conservative 12; Mismatches 34; Indels 10; Gaps 3;

QY 5 TLPPAWQFLKDRISTFKWPF--FLEGCACCTPERMAEAGFIHCPTENEPDLAQCFK 62

DB 174 TNPYSYAMSTEARFLTYHWPFLTEL-----SPSLARAGFYI---GPGDRVACFACGG 225

QY 63 ELEGWEPDDPIEBKHKHSSGCAFL 87

DB 226 KLSNWEPKDAMSEHRRHFPNCPFL 250

RESULT 13

T30489

apoptosis inhibitor - Lymantria dispar nuclear polyhedrosis virus

C:Species: Lymantria dispar nuclear polyhedrosis virus, LdMNPV

C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999

C:Accession: T30489

R:Kuzio, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; Rohm

Virology 253, 17-34, 1999

A:Title: Sequence and analysis of the genome of a baculovirus pathogenic for Lymantria di

A:Reference number: Z20836; MUID:99124785; PMID:9887315

A:Accession: T30489

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-155 <KUZ>

A:Cross-references: EMBL:AF081810; PIDN:AAC70325.1

Query Match 16.7%; Score 130; DB 2; Length 155;

Best Local Similarity 25.0%; Pred. No. 0.00033;

Matches 31; Conservative 29; Mismatches 44; Indels 20; Gaps 5;

QY 18 RISTFKWPFLEGGCACTPERMAEAGFIHCPTENEPDLAQCFKKELEGWEPDDPIEEH 77

DB 7 RLASPRNWSAVD--APAPAEIAHAGF-YC--ANRQDFVKCAICHIEIGNWSIGSDMSDH 61

QY 78 KKHSSGCAFLSVKKQFELTGLERAKNKIAKTNKKKPEPETAKKVRRATEQ 137

DB 62 KYSIACRFVC-----ELIK-----RPVSFVERDDDDDEDSAEFARGGEL 106

QY 138 LAAM 141

DB 107 LCSV 110

RESULT 14

JCS964

apoptosis inhibitor - pig

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 02-Sep-2000

C:Accession: JCS964

R:Stellik, C.; de Martin, R.; Binder, B.R.; Lipp, J.

Biochem. Biophys. Res. Commun. 243, 827-832, 1998

A:Title: Cytokine induced expression of porcine inhibitor of apoptosis protein (Iap) fami

A:Reference number: JCS964; MUID:98162622; PMID:9501011

A:Accession: JCS964

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-358 <STE>

A:Cross-references: GB:U99142; NID:g2957174; PIDN:AAC39171.1; PID:g2957175

C:Superfamily: RING finger homology

F:307-351/Domain: RING finger homology <RRN>

Query Match 16.5%; Score 128.5; DB 2; Length 358;

Best Local Similarity 38.8%; Pred. No. 0.001;

Matches 31; Conservative 10; Mismatches 28; Indels 11; Gaps 4;

QY 15 KDRISTFKWPF--FLEGCACCTPERMAEAGFIHCPTENEPDLAQCFKKELEGWEPDD 72

DB 5 KD-RLITQMWPLTEL-----SPADLAKAGFYI---GPGDRVACFACGGKLSNWEPKDD 55

Qy	73	PIEHHKHS	GCAPL	SVKKQ	92
		:	:	:	
		:	:	:	
		:	:	:	
Db	56	AMTEHLR	HFNCPL	GNQLQ	75

RESULT 15

S69544

apoptosis inhibitor IAP homolog - human

C/Species: Homo sapiens (man)

C/Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 17-Nov-2000

C/Accession: S69544; S68451

E/Duckett, C.S.; Nava, V.E.; Gedrich, R.W.; Clem, R.J.; van Dongen, J.L.; Gilfillan, M.C.

EMBO J. 15, 2685-2694, 1996

A/Title: A conserved family

A/Reference number: S69544; PMID:8654366

A/Reference number: S69544; PMID:8654366

A/Title: A conserved family of cellular genes related to the baculovirus iap gene and en

RESULT 15
S69544
apoptosis inhibitor IAP homolog - human
C/Species: Homo sapiens (man)
C/Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 17-Nov-2000
C/Accession: S69544; S68451
E/Duckett, C.S.; Nava, V.E.; Gedrich, R.W.; Clem, R.J.; van Dongen, J.L.; Gilfillan, M.C.
EMBO J. 15, 2685-2694, 1996
A/Title: A conserved family
A/Reference number: S69544; MUID:96256286; PMID:8654366
A/Reference number: S69544; MUID:96256286; PMID:8654366

apoptosis inhibitor IAP homolog - human
 C/Species: Homo sapiens (man)
 C/Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 17-Nov-2000
 C/Accession: S69544; S69451
 E/Duckett, C.S.; Nava, V.E.; Gedrich, R.W.; Clem, R.J.; van Dongen, J.L.; Gilfillan, M.O.
 EMBO J. 15, 2685-2694, 1996
 A>Title: A conserved family
 A/Reference number: S69544; MUID:96256286; PMID:8654366
 A/Reference number: S69544; MUID:96256286; PMID:8654366

Query Match	16.1%	Score 125.5;	DB 2;	Length 497;
Best Local Similarity	33.3%;	Pred. No. 0.0026;		
Matches	25;	Conservative	14;	Mismatches 31;
				Indels 5;
				Gaps 2;

```

Qy 13 FLKDHRISTFKWPFLEGCACCTPERMAEAGFIHCPTENEPDIAQCFFCFKELEGWEPDD 72
    :::::
Db 161 YSEARLKSQWNP--DYAHITTPRELASAGLY---TGIGDOVQCFCGGGLKWEPCDR 215

```

OV 73 PIEHKKHSSGCAFL 87

Db 216 AWSEHRRRHEPNCFFV 230

Search completed: August 11, 2004, 14:17:35
Job time : 17 secs

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PENDING

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 11, 2004, 14:10:30 ; Search time 14 Seconds
(without alignments)
528.140 Million cell updates/sec

Title: US-09-690-825-34

Perfect score: 778

Sequence: 1 MGAPTLPPAWQPFKDRHS.....EFETAKKVRRAIEQLAAMD 142

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	778	100.0	142	1 BIR5_HUMAN	O15392 homo sapien
2	660	84.8	140	1 BIR5_MOUSE	O15392 homo sapien
3	660	84.8	142	1 BIR5_RAT	O15392 homo sapien
4	163	21.0	997	1 BIR1_SCHPO	O9jby7 rattus norv
5	160	20.6	4829	1 BIR6_HUMAN	O14064 schizosacch
6	155	19.9	1403	1 BIR2_HUMAN	O9nr09 homo sapien
7	154	19.8	208	1 ZFP_IRV6	Q13075 homo sapien
8	145	18.6	1403	1 BIR7_MOUSE	P47732 chilo iride
9	143	18.4	1402	1 BIR8_MOUSE	O9jib6 mus musculu
10	143	18.4	1403	1 BIR8_MOUSE	O9jib3 mus musculu
11	143	18.4	1403	1 BIR8_MOUSE	O9qk5 mus musculu
12	142	18.3	1447	1 BIR8_MOUSE	O9r016 mus musculu
13	136.5	17.5	275	1 IAP_GVCP	O9qk4 mus musculu
14	136.5	17.5	298	1 BIR7_HUMAN	P41436 cydia pomon
15	133.5	17.2	268	1 IAP3_NPVOP	O96ca5 homo sapien
16	133.5	17.2	496	1 BIR4_MOUSE	P41437 orgyia pseu
17	133	17.1	496	1 BIR4_RAT	O60989 mus musculu
18	131	16.8	618	1 BIR2_HUMAN	O9r016 rattus norv
19	130	16.7	236	1 BIR8_HUMAN	O13490 homo sapien
20	129.5	16.6	612	1 BIR2_MOUSE	O96009 homo sapien
21	129	16.6	236	1 BIR8_PANTR	O62210 homo sapien
22	128.5	16.5	358	1 PIAP_PIG	O95t72 pan troglod
23	125.5	16.1	497	1 BIR4_HUMAN	O62640 sus scrofa
24	125	16.1	236	1 BIR8_GORGO	P98170 homo sapien
25	125	16.1	600	1 BIR3_MOUSE	O95w71 gorilla gor
26	122	15.7	604	1 BIR3_HUMAN	O08963 mus musculu
27	119.5	15.4	438	1 IAP1_DROME	Q13489 homo sapien
28	118.5	15.2	611	1 BIR_CHECK	Q24306 drosophila
29	118	15.2	498	1 IAP2_DROME	O90660 gallus gall
30	106.5	13.7	954	1 BIR1_YEAST	O24307 drosophila
31	99.5	12.8	275	1 IAP1_NPVOP	P47134 saccharomyc
32	83	10.7	434	1 ADA2_YEAST	O10296 orgyia pseu
33	82	10.5	135	1 LECG_BITAR	O92336 saccharomyc
					O9psn0 bitis ariet

34	82	10.5	135	1 LECG_CROAT	P21963 crotalus at
35	81.5	10.5	286	1 IAP1_NPVAC	P41435 autographa
36	80	10.3	213	1 R29_MOUSE	P97762 mus musculu
37	80	10.3	1391	1 M2F2_DROHY	Q08696 drosophila
38	79	10.2	221	1 R29_HUMAN	Q62a86 homo sapien
39	79	10.2	226	1 YB34_METUA	Q58534 methanococc
40	78	10.0	1052	1 BULB_MOUSE	Q92180 mus musculu
41	77.5	10.0	454	1 TIG_BORBU	O51555 borrelia bu
42	77.5	10.0	489	1 DMW2_MOUSE	P23804 mus musculu
43	76.5	9.8	361	1 CB45_MOUSE	Q61112 mus musculu
44	76	9.8	1818	1 HMW2_MYCPN	P75471 mycoplasma
45	75.5	9.7	180	1 GLUC_RAT	P06883 rattus norv

ALIGNMENTS

RESULT 1				
BIR5_HUMAN				
ID	BIR5_HUMAN	STANDARD;	PRT;	142 AA.
AC	O15392; Q9P2W8;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Baculoviral IAP repeat-containing protein 5 (Apoptosis inhibitor			
DE	survivin) (Apoptosis inhibitor 4).			
GN	BIRC5 OR API4 OR IAP4.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM ALPHA).			
RX	MEDLINE=97398388; PubMed=9256286;			
RA	Ambrosini G., Adida C., Altieri D.C.;			
RT	"A novel anti-apoptosis gene, survivin, expressed in cancer and			
RT	lymphoma."			
RL	Nat. Med. 3:917-921 (1997).			
RL	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM ALPHA).			
RC	TISSUE=Pancratic carcinoma;			
RA	Uren A.G., Vaux D.L.;			
RT	"Mammalian inhibitor of apoptosis (IAP) homolog."			
RL	Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM BETA).			
RA	Kageyama H., Islam A., Takayasu H., Nakagawara A.;			
RT	"An isoform of survivin (survivin-beta) which has 23 amino acids			
RT	insertion into the BIR domain."			
RL	Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A. (ISOFORM ALPHA).			
RC	TISSUE=Lung, and Muscle;			
RX	MEDLINE=22386257; PubMed=12477932;			
RA	Strausberg R.L., Feigold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,			
RA	Schneerch A., Schein J.E., Jones S.J.M., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length			
RT	human and mouse cDNA sequences."			

```

RL  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN  [5]
RP  FUNCTION.
RX  MEDLINE=9075336; PubMed=9859933;
RA  Li F., Ambrosini G., Chu E.Y., Plescia J., Tognin S., Marchisio P.C.,
RA  Altieri D.C.;
RT  "Control of apoptosis and mitotic spindle checkpoint by survivin.";
RL  Nature 396:580-584 (1998).
RN  [6]
RP  X-RAY CRYSTALLOGRAPHY (2.71 ANGSTROMS) OF ISOFORM ALPHA.
RX  MEDLINE=20403315; PubMed=10949039;
RA  Chantalat L., Skoufias D.A., Klemm J.P., Jung B., Dideberg O.,
RA  Margolis R.L.;
RT  "Crystal structure of human survivin reveals a bow tie-shaped dimer
RT  with two unusual alpha-helical extensions.";
RL  Mol. Cell 6:183-189 (2000).
RN  [7]
RP  X-RAY CRYSTALLOGRAPHY (2.58 ANGSTROMS) OF ISOFORM ALPHA.
RX  MEDLINE=20336902; PubMed=10876248;
RA  Verdecia M.A., Huang H., Dutil E., Kaiser D.A., Hunter T., Noel J.P.;
RT  "Structure of the human anti-apoptotic protein survivin reveals a
RT  dimeric arrangement.";
RL  Nat. Struct. Biol. 7:602-608 (2000).
RN  [8]
RP  PHOSPHORYLATION OF THR-34.
RX  MEDLINE=20542086; PubMed=11069302;
RA  O'Connor D.S., Groesman D., Plescia J., Li F., Zhang H., Villa A.,
RA  Tognin S., Marchisio P.C., Altieri D.C.;
RT  "Regulation of apoptosis at cell division by p34cdc2 phosphorylation
RT  of survivin.";
RL  Proc. Natl. Acad. Sci. U.S.A. 97:13103-13107 (2000).
CC  -!- FUNCTION: May play a role in neoplasia. May counteract a default
CC  induction of apoptosis in G2/M phase. Interacts with tubulin.
CC  Inhibitor of caspase-3 and caspase-7.
CC  -!- SUBUNIT: Homodimer.
CC  -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC  -!- ALTERNATIVE PRODUCTS:
CC  Event=Alternative splicing; Named isoforms=2;
CC  Name=Alpha;
CC  IsoId=O15392-1; Sequence=Displayed;
CC  Name=Beta;
CC  IsoId=O15392-2; Sequence=VSP_002454;
CC  -!- TISSUE SPECIFICITY: Expressed only in fetal kidney and liver, and
CC  to lesser extent, lung and brain. Abundantly expressed in
CC  adenocarcinoma (lung, pancreas, colon, breast, and prostate) and
CC  in high-grade lymphomas.
CC  -!- SIMILARITY: Contains 1 BIR repeat.
CC  -!- SIMILARITY: Belongs to the IAP family.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.ebi.ac.uk/ebis/sib.ch/announcements/
CC  or send an email to license@sib.ch).
CC  -----
DR  EMBL; U75285; AAC51660.1; -
DR  EMBL; AF077350; AAD34226.1; -
DR  EMBL; AB028869; BAA93676.1; -
DR  EMBL; BC008718; AAH08718.1; -
DR  EMBL; BC034148; AAH34148.1; -
DR  FDB; 1231; 03-JAN-01.
DR  FDB; 1F3H; 16-MAY-01.
DR  Genew; HGNC:593; BIRC5.
DR  MIM; 603352; -
DR  GO; GO:0005876; C:spindle microtubule; TAS.
DR  GO; GO:0008189; P:apoptosis inhibitor activity; TAS.
DR  GO; GO:0006916; P:anti-apoptosis; TAS.
DR  GO; GO:0000086; P:G2/M transition of mitotic cell cycle; TAS.
DR  InterPro; IPR001370; BIR.
DR  Pfam; PF00653; BIR; 1.
DR  SMART; SM00238; BIR; 1.

```

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DR  PROSITE; PS01282; BIR_REPEAT_1; FALSE_NEG.
DR  PROSITE; PS0143; BIR_REPEAT_2; 1
KW  Apoptosis; Thiol protease inhibitor; Alternative splicing;
KW  Metal-binding; Zinc; Phosphorylation; 3D-structure.
FT  REPEAT 15 87
FT  METAL 57 57
FT  METAL 60 60
FT  METAL 77 77
FT  METAL 84 84
FT  MOD_RES 34 34
FT  VARSPLIC 74 74
FT  MUTAGEN 84 84
FT  HELIX 8 13
FT  HELIX 15 20
FT  TURN 21 21
FT  TURN 29 30
FT  HELIX 35 40
FT  TURN 41 42
FT  STRAND 43 45
FT  STRAND 55 57
FT  TURN 58 60
FT  STRAND 63 64
FT  TURN 69 70
FT  HELIX 73 80
FT  TURN 82 83
FT  HELIX 85 87
FT  TURN 88 88
FT  HELIX 93 95
FT  STRAND 97 97
FT  HELIX 98 139
SQ  SEQUENCE 142 AA; 16389 MW; 9E7CADCDF2822286 CRC64;
Query Match 100.0%; Score 778; DB 1; Length 142;
Best Local Similarity 100.0%; Pred. No. 4.6e-61;
Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGAPTLPPAWQFLKDHRISTFKNWPFLGGCACTPERMAEAGFIHCPTEPDLAQCFFC 60
Db 1 MGAPTLPPAWQFLKDHRISTFKNWPFLGGCACTPERMAEAGFIHCPTEPDLAQCFFC 60
QY 61 FKELEGWEDDDPIEHHKGGSGCAFLSVKKQFELTIGEFKLDREKAKKIATETNNK 120
Db 61 FKELEGWEDDDPIEHHKGGSGCAFLSVKKQFELTIGEFKLDREKAKKIATETNNK 120
QY 121 KKEFEETAKKVRRAIEQLAAMD 142
Db 121 KKEFEETAKKVRRAIEQLAAMD 142
RESULT 2
BIRS_MOUSE STANDARD; PRT; 140 AA.
ID BIRS_MOUSE STANDARD; PRT; 140 AA.
AC O70201; Q923F7; Q9WU53; Q9WU54;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Baculoviral IAP repeat-containing protein 5 (Apoptosis inhibitor
DE survivin) (Apoptosis inhibitor 4) (TIAP).
GN BIRC5 OR API4 OR IAP4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Uren A.G., Vaux D.L.;
RA "Mammalian inhibitor of apoptosis (IAP) homolog.";
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Embryo;

```


RA Kobayashi K., Otaki M., Ogasawara T., Tokuhisa T.;
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
 RX MEDLINE=20129603; PubMed=10666222;
 RA Conway E.M., Pollifey S., Cornelissen J., DeGaere I.,
 RA Seiner-Mosonyi M., Ong K., Baens M., Collien D., Schuh A.C.;
 RT "three differentially expressed survivin cDNA variants encode
 RL proteins with distinct antiapoptotic functions.";
 RL Biol 95:1435-1442(2000).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McWan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallalao D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RL human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 7-118, AND PHOSPHORYLATION
 OF THR-34.
 RX MEDLINE=20403314; PubMed=10949038;
 RA Muchmore S.W., Chen J., Jakob C., Zakula D., Matayoshi E.D., Wu W.,
 RA Zhang H., Li F., Ng S.C., Altieri D.C.;
 RT "Crystal structure and mutagenic analysis of the
 RL inhibitor-of-apoptosis protein survivin.";
 RL Mol. Cell 6:173-182(2000).
 CC -1- FUNCTION: May play a role in neoplasia. May counteract a default
 CC induction of apoptosis in G2/M phase. Interacts with tubulin.
 CC Inhibitor of caspase-3 and caspase-7 (By similarity).
 CC -1- SUBUNIT: Homodimer; zinc-dependent.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=3;
 CC Name=1; Synonyms=Survivin 140;
 CC IsoId=O70201-1; Sequence=Displayed;
 CC Name=2; Synonyms=Survivin 121;
 CC IsoId=O70201-2; Sequence=VSP_002457;
 CC Name=3; Synonyms=Survivin 40;
 CC IsoId=O70201-3; Sequence=VSP_002455, VSP_002456;
 CC -1- SIMILARITY: Contains 1 BIR repeat.
 CC -1- SIMILARITY: Belongs to the IAP family.
 CC -----
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 CC -----
 CC EMBL; AF077349; AA034225.1; -
 CC EMBL; AB013819; BA228266.1; -
 CC EMBL; AF115517; AA026199.1; -
 CC EMBL; AF115517; AA026200.1; -
 CC EMBL; AF115517; AA026201.1; -
 CC EMBL; BC004702; AA04702.1; -
 CC PDB; 1M4M; 25-SEP-02.

DR MGD; MGI:1203517; Birc5.
 DR GO; GO:0005737; C:cytoplasm; IDA.
 DR GO; GO:0008189; F:apoptosis inhibitor activity; IMP.
 DR GO; GO:0006916; P:anti-apoptosis; IMP.
 DR InterPro; IPR001370; BIR.
 DR Pfam; PF00653; BIR; 1.
 DR SMART; SM00238; BIR; 1.
 DR PROSITE; PS01282; BIR_REPEAT_1; FALSE_NEG.
 DR PROSITE; PS0143; BIR_REPEAT_2; 1.
 DR Apoptosis; Thiol protease inhibitor; Alternative splicing;
 KW Phosphorylation; Metal-binding; Zinc; 3D-structure.
 FT REPEAT 15 87
 FT MOD_RES 34 34 PHOSPHORYLATION (BY CDC2).
 FT METAL 57 57 ZINC 1.
 FT METAL 60 60 ZINC 1.
 FT METAL 76 76 ZINC 1.
 FT METAL 77 77 ZINC 1.
 FT METAL 80 80 ZINC 2.
 FT METAL 84 84 ZINC 1.
 FT VARSPLIC 38 40 MAE -> RGA (in isoform 3).
 FT VARSPLIC 41 140 /FTid=VSP_002455.
 FT VARSPLIC 114 140 Missing (in isoform 3).
 FT VARSPLIC 114 140 AKETNNKQKEFEETAKTTQSIQLAA -> VCMENKD
 FT (in isoform 2).
 FT /FTid=VSP_002457.
 SQ SEQUENCE 140 AA; 16297 MW; 26F5ABF501A5D83C CRC64;
 Query Match 84.8%; Score 660; DB 1; Length 140;
 Best Local Similarity 84.3%; Pred. No. 8.3e-51;
 Matches 118; Conservative 12; Mismatches 10; Indels 0; Gaps 0;
 QY 1 MGAPLPPAWQFLLKDHRISTFKWPFLEGGCACTPERMAEAGFIHCPTENEPDLAQCFFC 60
 DB 1 MGAPALPQWLYLKNYRIATFKWPFLEDCACTPERMAEAGFIHCPTENEPDLAQCFFC 60
 QY 61 FKELEGWPDDEPIEHHKXSGCAFLSVKKQFBEITLGEFLKLDRAKAKIATNNK 120
 DB 61 FKELEGWPDDEPIEHHKXSGCAFLSVKKQFBEITLGEFLKLDRAKAKIATNNK 120
 QY 121 KKEFEETAKVRRATEQLAA 140
 DB 121 KKEFEETAKTTQSIQLAA 140
 RESULT 3
 BIR5 RAT STANDARD; PRT; 142 AA.
 ID Q9JH77;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Baculoviral IAP repeat-containing protein 5 (Apoptosis inhibitor
 DE survivin).
 GN BIRC5.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RA Chen D., Cao G., Chen J.;
 RT "Molecular cloning and characterization of rat survivin.";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: May play a role in neoplasia. May counteract a default
 CC induction of apoptosis in G2/M phase. Interacts with tubulin.
 CC Inhibitor of caspase-3 and caspase-7 (By similarity).
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Contains 1 BIR repeat.
 CC -1- SIMILARITY: Belongs to the IAP family.

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CC -----
 CC EMBL; AF276775; AAF82586.1; --
 CC HSSP; Q15392; 1E31.
 CC InterPro; IPR001370; BIR.
 CC Pfam; PF00653; BIR; 1.
 CC SMART; SM00238; BIR; 1.
 CC PROSITE; PS01282; BIR_REPEAT_1; FALSE_NEG.
 CC PROSITE; PS01443; BIR_REPEAT_2; 1.
 CC Apoptosis; Thiol protease inhibitor; Metal-binding; Zinc;
 KW Phosphorylation.
 FT REPEAT 15 87 BIR.
 FT METAL 57 57 ZINC (BY SIMILARITY).
 FT METAL 60 60 ZINC (BY SIMILARITY).
 FT METAL 77 77 ZINC (BY SIMILARITY).
 FT METAL 84 84 ZINC (BY SIMILARITY).
 FT MOD_RES 34 34 PHOSPHORYLATION (BY CDC2)
 FT (BY SIMILARITY).
 SQ SEQUENCE 142 AA; 16692 MW; 99BCFAE15B4D0CAC CRC64;

Query Match 84.8%; Score 660; DB 1; Length 142;
 Best Local Similarity 83.0%; Pred.No. 8.4e-51;
 Matches 117; Conservative 13; Mismatches 11; Indels 0; Gaps 0;
 QY 1 MGAPILPAAQVFLKXDRISTFKWPFLEGGACTPERMAEAGFHCPTENEPDLAQCFFC 60
 DB 1 MGATALLPPIQWYLYKXDRIFYKWPFLDSCIPERMAEAGFHCPTENEPDLAQCFFC 60
 QY 61 FVELGSGPDDPIIEHKHSGGAFVSKVQFELTGEFLKLDRAKAKIAKFNK 120
 DB 61 FVELGSGPDDPIIEHRSKSGGAFVSKVQFELTGEFLKLDRAKAKIAKFNK 120
 QY 121 KKEFEETAKVRAIEQAAM 141
 DB 121 KKEFEETRTVRSIEQAAL 141

RESULT 4
 BIR1 SCHPO
 AC Q14054; Q9USG4; STANDARD; PRT; 997 AA.
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DE BIR1 protein (Chromosome segregation protein cut17).
 GN BIR1 OR CUT17 OR PBH1 OR SPCC962.02C OR SPCC31B10.10C.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales;
 OC Schizosaccharomycetaceae;
 OC NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A., FUNCTION, AND SUBCELLULAR LOCATION.
 RX MEDLINE=21439264; PubMed=11554922;
 RA Morishita J., Matsusaka T., Goshima G., Nakamura T., Tatebe H.,
 RA Yanagida M.,
 RT "Bir1/Cut17 moving from chromosome to spindle upon the loss of
 RT cohesion is required for condensation, spindle elongation and
 RT repair".
 RL Genes Cells 6:743-763 (2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
 RA Gentles S., Goble A., Hanlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
 RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas R., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerretti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shipakowski G.V., Ussery D., Barrell B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomyces pombe".
 RL Nature 415:871-880 (2002).
 RN [3]
 RN CHARACTERIZATION.
 RP MEDLINE=99398681; PubMed=10468581;
 RX Uren A.G., Beilharz T., O'Connell M.J., Bugg S.J., van Driel R.,
 RA Vaux D.L., Litgow T.;
 RT "Role for yeast inhibitor of apoptosis (IAP)-like proteins in cell
 RT division".
 RL Proc. Natl. Acad. Sci. U.S.A. 96:10170-10175 (1999).
 RN [4]
 RN CHARACTERIZATION.
 RP MEDLINE=21850422; PubMed=11861551;
 RX Rajagopalan S., Balasubramanian M.K.;
 RA "Schizosaccharomyces pombe Birp, a nuclear protein that localizes to
 RT kinetochores and the spindle midzone, is essential for chromosome
 RT condensation and spindle elongation during mitosis".
 RL Genetics 160:445-456 (2002).
 RN [5]
 RN FUNCTION.
 RX MEDLINE=20035862; PubMed=10571085;
 RA Rajagopalan S., Balasubramanian M.K.;
 RT "S. pombe Phip: an inhibitor of apoptosis domain containing protein
 RT is essential for chromosome segregation".
 RL FEBS Lett. 460:187-190 (1999).
 CC -!- FUNCTION: Seems to act in the pleiotropic control of cell
 CC division. Has a role in chromosome segregation by recruiting
 CC condensin and ark1 kinase to appropriate sites as the cell
 CC progresses through mitosis.
 CC -!- SUBCELLULAR LOCATION: Nuclear. Interacts with the outer
 CC centromeric regions of the chromosomes during interphase. After
 CC chromatid separation moves to the middle of the spindle.
 CC -!- SIMILARITY: Contains 2 BIR repeats.
 CC -----
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CC EMBL; AB031034; BAA83415.1; --
 CC EMBL; AL031323; CAA20434.1; --
 CC EMBL; AL121859; CAB58376.1; --
 CC PIR; T43523; T43523.
 CC HSSP; Q13490; 1QBH.
 CC GeneDB_Spombe; SPCC962.02C;
 CC InterPro; IPR001370; BIR.
 CC Pfam; PF00653; BIR; 2.
 CC SMART; SM0238; BIR; 2.
 CC PROSITE; PS01282; BIR_REPEAT_1; FALSE_NEG.

[illegible]

PC TISSUE=Brain;
RX MEDLINE=98163755; PubMed=9503025;
RA Chen Q., Baird S.D., Mahadevan M., Besner-Johnston A., Farahani R.,
Xuan J.-Y., Kang X., Lefebvre C., Ikeda J.-E., Korneluk R.G.,
Mackenzie A.E.;
RA "Sequence of a 131-kb region of 5q13.1 containing the spinal muscular
atrophy candidate genes SMN and NAIP";
RL Genomics 48:121-127(1998).
RN [3].
RP SEQUENCE OF 386-623 FROM N.A.
RA der Steege G., Draaijers T.G., Grootsholten P.M., Osinga J.,
RA Anzevino R., Velsona I., Brahe C., Scheffer H., van Ommen G.J.B.,
RA Buys C.H.C.M.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
RN [4].
RP SEQUENCE OF 222-1403 FROM N.A.
RA Jones K., Graves T., McPherson J.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [5].
RP FUNCTION.
RC TISSUE=Liver;
RX MEDLINE=96149249; PubMed=8552191;
RA Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Cherton-Horvat G.,
RA Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;
RT "Suppression of apoptosis in mammalian cells by NAIP and a related
family of IAP genes";
RL Nature 379:349-353(1996).
CC -!- FUNCTION: Prevents motor-neuron apoptosis induced by a variety of
signals.
CC -!- TISSUE SPECIFICITY: Expressed in motor neurons, but not in sensory
neurons. Found in liver and placenta, and to a lesser extent in
spinal cord.
CC -!- DISEASE: Mutated or deleted forms of NAIP have been found in
individuals with spinal muscular atrophy type I (SMA1)
[MIM:253300]. SMA are fatal autosomal recessive disorders
subclassified as type I (Werdnig-Hoffmann disease), type II
(intermediate form), and type III (Wohlfart-Kugelberg-Welander
disease) based upon the age of onset and clinical severity. These
neurodegenerative disorders are characterized by degeneration of
lower motor neurons, leading to progressive paralysis muscular
atrophy. Concerns 1 in 6000 newborns.
CC -!- SIMILARITY: Contains 3 BIR repeats.
CC -!- SIMILARITY: Contains 1 NACHT domain.
CC
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CC
CC EMBL; U19251; AAC52045.1; -.
CC EMBL; U80017; AAC52047.1; -.
CC EMBL; U21913; AAA64504.1; -.
CC EMBL; AC005031; AAC62261.1; -.
CC HSPF; Q13490.1; QH.
CC Genew; HGNC:7634; BIRC1.
CC MIM; 600355; -.
CC MIM; 253300; -.
CC GO; GO:0008189; F:apoptosis inhibitor activity; TAS.
CC GO; GO:0006916; P:anti-apoptosis; TAS.
CC GO; GO:0007399; P:neurogenesis; TAS.
CC InterPro; IPR003593; AAA_ATPase.
CC InterPro; IPR001370; BIR.
CC InterPro; IPR007111; NACHT_NTPase.
CC Pfam; PF00653; BIR; 3.
CC Pfam; PF05729; NACHT; 1.
CC SMART; SM00382; AAA; 1.
CC SMART; SM00238; BIR; 3.
CC PROSITE; PS01282; BIR_REPEAT_1; 3.
CC PROSITE; PS01443; BIR_REPEAT_2; 3.
CC PROSITE; PS50837; NACHT; 1.

KW Apoptosis; Repeat. 127 BIR 1.
FT REPEAT 60 BIR 2.
FT REPEAT 159 227 BIR 3.
FT REPEAT 278 345 NACHT.
FT DOMAIN 464 758
FT CONFLICT 222 223 PK -> YR (IN REF. 4).
FT CONFLICT 386 387 VP -> ST (IN REF. 3).
FT CONFLICT 535 535 M -> V (IN REF. 3).
FT CONFLICT 553 553 Y -> H (IN REF. 3).
FT CONFLICT 1228 1231 MISSING (IN REF. 4).
SQ SEQUENCE 1403 AA; 159613 MW; 566304C154DA5E64 CRC64;

Query Match 19.9%; Score 155; DB 1; Length 1403;
Best Local Similarity 40.5%; Pred. No. 8.8e-06;
Matches 34; Conservative 15; Mismatches 29; Indels 6; Gaps 3;

QY 15 KDHRISTKRWPF-LEGACATPERMABAGFTHCTENEPDLAQCFKCELEGWEPDDDP 73
Db 159 EARLASFRNWFVVG--ISPCVLSAAGVF---TGKQDTVQCFCGCGCLGNWEEGDDP 213
QY 74 IEHKKHSSGCAFLSVKQFBEIT 97
Db 214 WKHAKWPKCEFLRSKKSSEIT 237

RESULT 7
ZFP_IRV6 STANDARD; PRT; 208 AA.
AC P47732; O85770;
DT 01-FEB-1996 (Rel. 33; Created)
DT 10-OCT-2003 (Rel. 42; Last sequence update)
DT 10-OCT-2003 (Rel. 42; Last annotation update)
DE Zinc finger protein.
OS Chilo iridescent virus (CIV) (Insect iridescent virus type 6).
OC Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Iridovirus.
OX NCBI_TaxID:10488;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92196996; PubMed=1549908;
RA Handermann M., Schmitz P., Roosen-Wolff A.P., Raab K.,
RA Sontag K.C., Darai G.;
RT "Identification and mapping of origins of DNA replication within the
DNA sequences of the genome of insect iridescent virus type 6";
RL Virus Genes 6:19-32(1992).
RN [2]
RP REVISIONS TO C-TERMINUS.
RA Jakob N.J., Mueller K., Bahr U., Darai G.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 BIR repeat.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC
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CC
CC EMBL; AF303741; AAB94481.1; -.
CC HSPF; Q15392; IE31.
CC InterPro; IPR001370; BIR.
CC InterPro; IPR001841; Znf_ring.
CC Pfam; PF00653; BIR; 1.
CC Pfam; PF00097; zf-C3HC4; 1.
CC SMART; SM00238; BIR; 1.
CC SMART; SM00184; RING; 1.
CC PROSITE; PS01282; BIR_REPEAT_1; FALSE_NEG.
CC PROSITE; PS01443; BIR_REPEAT_2; 1.
CC PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
CC PROSITE; PS00089; ZF_RING_2; 1.
KW Zinc-finger; Repeat.
FT REPEAT 37 108 BIR.

```

PT DOMAIN      134      151      3 X 6 AA TANDEM REPEATS.
FT REPEAT      134      139      1.
FT REPEAT      140      145      2.
FT REPEAT      146      151      3.
FT ZN FING      163      197      RING-TYPE.
SQ SEQUENCE    208 AA; 24142 MW; 41A3E2FC18833390 CRC64;

Query Match      19.8%; Score 154; DB 1; Length 208;
Best Local Similarity 32.5%; Pred. No. 1.4e-06;
Matches 39; Conservative 23; Mismatches 38; Indels 20; Gaps 7;

QY 12 PFLK-DHRISTFKNWPFLEGCACCTPERMAEAGFIHCPTENEPDLAQCFFCFKELEGEWPD 70
DB 33 PFASYDERLNSFNQWFI--QLLSKQSLSPAGFIYL--NIGDQVOCFYCDLKLKWKRS 87
QY 71 DDPIEHKHS-----GCAPLSVKKQFEBLTIGCFKLDRERA-RNKIAKETNNKKKEPE 125
DB 88 DNPFEHKKHTDCLKNCLFV-----KGIEDFNFKHNSHSCFNPI---TNNINQDLID 138

RESULT 8
BIRF_MOUSE
ID BIRF_MOUSE STANDARD; PRT; 1403 AA.
AC Q9JIB6; O09121; O09122; P81704;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 1f (Neuronal apoptosis
DE inhibitory protein 6).
GN BIRC1F OR NAIP-OR-RS4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20414747; PubMed=10958627;
RA Endrizzi M.G., Hadinoto V., Gowney J.D., Miller W., Dietrich W.F.;
RT "Genomic sequence analysis of the mouse Naip gene array.";
RL Genome Res. 10:1095-1102(2000).
RN [2]
RP SEQUENCE OF 82-168 FROM N.A.
RC STRAIN=129/SVJ;
RX MEDLINE=97131520; PubMed=8975718;
RA Scharf J.M., Damron D., Frisella A., Bruno S., Beggs A.H.,
RA Kunkel L.M., Dietrich W.F.;
RT "The mouse region syntenic for human spinal muscular atrophy lies
RT within the Lgln critical interval and contains multiple copies of Naip
RL exon 5.", 38:405-417(1996).
CC
CC -!- FUNCTION: Prevents motor-neuron apoptosis induced by a variety of
CC signals.
CC -!- SIMILARITY: Contains 3 BIR repeats.
CC -!- SIMILARITY: Contains 1 NACHT domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF242431; AAF82751.1; -.
CC HSPB; U66327; AAC52975.1; -.
CC HSPB; Q13490; 1QBR.
CC MGD; MGI:1298222; Birc1f.
CC InterPro; IPR001370; BIR.
CC InterPro; IPR007111; NACHT_NTPase.
CC Pfam; PF00653; BIR; 3.
CC SMART; SM00238; BIR; 3.
CC PROSITE; PS01282; BIR_REPEAT_1; 2.
CC PROSITE; PS0143; BIR_REPEAT_2; 3.
CC PROSITE; PS00837; NACHT; 1.
CC Apoptosis; Repeat; Multigene family.
CC REPEAT 60 127 BIR 1.
CC REPEAT 159 227 BIR 2.
CC REPEAT 278 345 BIR 3.
CC Pfam; PF00653; BIR; 3.
CC SMART; SM00238; NACHT; 1.
CC PROSITE; PS01282; BIR_REPEAT_1; 2.

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DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR PROSITE; PS00837; NACHT; 1.
KW Apoptosis; Repeat; Multigene family.
FT REPEAT 60 127 BIR 1.
FT REPEAT 159 227 BIR 2.
FT REPEAT 278 345 BIR 3.
FT DOMAIN 464 759 NACHT.
SQ SEQUENCE 1403 AA; 159823 MW; 9D4912503358C4E9 CRC64;

Query Match      18.6%; Score 145; DB 1; Length 1403;
Best Local Similarity 36.6%; Pred. No. 6.5e-05;
Matches 30; Conservative 13; Mismatches 35; Indels 4; Gaps 2;

QY 15 KDHRISTFKNWPFLEGCACCTPERMAEAGFIHCPTENEPDLAQCFFCFKELEGEWPD 74
DB 159 BEARLESPEDEWFFV-AHGTSPRLASAGFVF---TGKRDIVQCFSCGSLGNWEEGDDPW 214
QY 75 BEHKHSSGCAFLSVKKQFEL 96
DB 215 KEHAKWPKCEFLQSKSSEI 236

RESULT 9
BIRF_MOUSE
ID BIRF_MOUSE STANDARD; PRT; 1402 AA.
AC Q9JIB3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 1g (Neuronal apoptosis
DE inhibitory protein 7).
GN BIRC1G OR NAIP7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20414747; PubMed=10958627;
RA Endrizzi M.G., Hadinoto V., Gowney J.D., Miller W., Dietrich W.F.;
RT "Genomic sequence analysis of the mouse Naip gene array.";
RL Genome Res. 10:1095-1102(2000).
CC -!- FUNCTION: Prevents motor-neuron apoptosis induced by a variety of
CC signals.
CC -!- SIMILARITY: Contains 3 BIR repeats.
CC -!- SIMILARITY: Contains 1 NACHT domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF242433; AAF82749.1; -.
CC HSPB; Q13490; 1QBR.
CC MGD; MGI:1858256; Birc1g.
CC InterPro; IPR001370; BIR.
CC InterPro; IPR007111; NACHT_NTPase.
CC Pfam; PF00653; BIR; 3.
CC Pfam; PF05729; NACHT; 1.
CC SMART; SM00238; BIR; 3.
CC PROSITE; PS01282; BIR_REPEAT_1; 2.
CC PROSITE; PS0143; BIR_REPEAT_2; 3.
CC PROSITE; PS00837; NACHT; 1.
CC Apoptosis; Repeat; Multigene family.
CC REPEAT 60 127 BIR 1.
CC REPEAT 159 227 BIR 2.
CC REPEAT 278 345 BIR 3.
CC Pfam; PF00653; BIR; 3.
CC SMART; SM00238; NACHT; 1.
CC PROSITE; PS01282; BIR_REPEAT_1; 2.

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Query Match      18.4%; Score 143; DB 1; Length 1402;
Best Local Similarity 36.6%; Pred. No. 9.7e-05;
Matches 30; Conservative 13; Mismatches 35; Indels 4; Gaps 2;

QY      15 KDHRISTFKWPLEGCACTPERMAFAGIHCTENEPDLAQCFKCEGKEPDDDDPI 74
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DDB     159 EEAKLESFEDWPPY-AHGTSFPRVLSAAGFV---TGKRDVTQCFSGCSLGNWEGDDPW 214
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      75 EHKHKSSGCAFLSVKKQFEEL 96
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      215 KEHAKWPKCEFLQSKSSEI 236
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 10
BIRA_MOUSE
ID      BIRA_MOUSE      STANDARD;      PRT; 1403 AA.
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      15-MAR-2004 (Rel. 43, Last annotation update)
DE      Baculoviral IAP repeat-containing protein 1a (Neuronal apoptosis
GN      inhibitory protein 1).
GN      BIRC1A OR NAIP1 OR NAIP.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Scuriongnathi; Muridae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RN      SEQUENCE FROM N.A.
RA      MEDLINE=98360097; PubMed=9693038;
RA      Varachi Z., Korneluk R.G., Mackenzie A.E.;
RT      "Cloning and characterization of the multiple murine homologues of
RT      NAIP (neuronal apoptosis inhibitory protein).";
RL      Genomics 51:107-113(1998).
RN      [2]
RN      SEQUENCE FROM N.A.
RA      MEDLINE=99431676; PubMed=10501978;
RA      Huang S., Scharf J.M., Gowney J.D., Endrizzi M.G., Dietrich W.F.;
RT      "The mouse Naip gene cluster on Chromosome 13 encodes several distinct
RT      functional transcripts.";
RL      Mamm. Genome 10:1032-1035(1999).
RN      [3]
RN      SEQUENCE FROM N.A.
RA      MEDLINE=20414747; PubMed=10958627;
RA      Endrizzi M.G., Hadinto V., Gowney J.D., Miller W., Dietrich W.F.;
RT      "Genomic sequence analysis of the mouse Naip gene array.";
RL      Genome Res. 10:1095-1102(2000).
CC      -!- FUNCTION: 10 prevents motor-neuron apoptosis induced by a variety of
CC      signals.
CC      -!- SIMILARITY: Contains 3 BIR repeats.
CC      -!- SIMILARITY: Contains 1 NACHT domain.
CC      -!- SIMILARITY: Contains 1 NACHT domain.
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC      entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL; AF007769; AAB69223.1; -
CC      EMBL; AF135491; AAD56763.1; -
CC      EMBL; AF242432; AAF82752.1; -
CC      HSP; Q13490; IQBH.
CC      MGD; MGI:1298223; Birc1a.
CC      InterPro; IPR003593; AAA_Atpase.
CC      InterPro; IPR001370; BIR.
CC      InterPro; IPR007111; NACHT_NTPase.
CC      Pfam; PF00853; BIR; 3.
CC      Pfam; PF05729; NACHT; 1.
CC      SMART; SM00382; AAA; 1.
CC      SMART; SM00238; BIR; 3.
CC      PROSITE; PS01282; BIR_REPEAT_1; 1.

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PROSITE; PS50143; BIR_REPEAT_2; 3.
PROSITE; PS50837; NACHT; 1.
Apoptosis; Repeat; Multigene family.
REPEAT 60 127 BIR 1.
REPEAT 159 227 BIR 2.
REPEAT 278 345 BIR 3.
DOMAIN 464 758 NACHT.
CONFLICT 343 343 I -> V (IN REF. 2).
CONFLICT 359 359 L -> Q (IN REF. 2).
CONFLICT 624 624 E -> K (IN REF. 2).
CONFLICT 1092 1092 D -> E (IN REF. 3).
CONFLICT 1116 1116 D -> N (IN REF. 3).
CONFLICT 1123 1123 G -> R (IN REF. 3).
CONFLICT 1129 1129 L -> H (IN REF. 1).
CONFLICT 1140 1140 T -> M (IN REF. 1).
CONFLICT 1269 1269 A -> V (IN REF. 3).
SEQUENCE 1403 AA; 158692 MW; B31630259595EE67 CRC64;

Query Match 18.4%; Score 143; DB 1; Length 1403;
Best Local Similarity 36.6%; Pred.No. 9.7e-05;
Matches 30; Conservative 13; Mismatches 35; Indels 4; Gaps 2;

QY 15 KHRISTFKNWPFLECCACTPRMAEAGFIHCPTENEDLAQCFCFKELEGWEPDDPI 74
Db 159 EARLSEFEDWPFY-AHGTSPEVLGAAGFVF---TGKRDITVQCFCGSGSLGNWEEGDDPW 214

QY 75 EEHKHSSGCAFLSVKKQPEEL 96
Db 215 KEHAKWFPKCEFLQSKSSEI 236

RESULT 11
BIRE_MOUSE
ID BIRE_MOUSE STANDARD; PRT: 1403 AA.
AC Q9R0I6; Q09121; Q09122; P81703; Q9R029;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 1e (Neuronal apoptosis
inhibitory protein 5).
BIRC15 OR NAIP5 OR NAIP-RS3.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
RP MEDLINE=99431676; PubMed=10501978;
RX Huang S., Scharf J.M., Growney J.D., Endrizzi M.G., Dietrich W.F.;
RA "The mouse Naip gene cluster on Chromosome 13 encodes several distinct
functional transcripts.";
RL Mamm. Genome 10:1032-1035(1999).
[2]
SEQUENCE FROM N.A.
RP STRAIN=129/SV;
RC MEDLINE=99417674; PubMed=10486205;
RX Endrizzi M., Huang S., Scharf J.M., Kelter A.R., Wirth B.,
RA Kunkel L.M., Miller W., Dietrich W.F.;
RT "Comparative sequence analysis of the mouse and human Lgn1/SMA
interval.";
RL Genomics 60:137-151(1999).
[3]
SEQUENCE OF 82-168 FROM N.A.
RP STRAIN=129/SVJ;
RC MEDLINE=97131520; PubMed=8975718;
RX Scharf J.M., Damron D., Frisella A., Bruno S., Beggs A.H.,
RA Kunkel L.M., Dietrich W.F.;
RT "The mouse region syntenic for human spinal muscular atrophy lies
within the Lgn1 critical interval and contains multiple copies of Naip
exon 5.";
RL Genomics 38:405-417(1996).
CC -!- FUNCTION: Prevents motor-neuron apoptosis induced by a variety of
signals.

```


HSP; Q13490; IQBH.
InterPro; IPR001370; BIR.
InterPro; IPR001841; Znf_ring.
Pfam; PF00653; BIR; 2.
SMART; SM00238; BIR; 2.
SMART; SM00184; RING; 1.
PROSITE; PS01282; BIR_REPEAT_1; 2.
PROSITE; PS00143; BIR_REPEAT_2; 2.
PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
PROSITE; PS00089; ZF_RING_2; 1.
Apoptosis; Zinc-finger; Repeat.
REPEAT 7
REPEAT 108 175 BIR 1.
REPEAT 228 263 BIR 2.
ZN_FING RING-TYPE.
SEQUENCE 275 AA; 31290 MW; 84605448869CAD60 CRC64;

Query Match 17.5%; Score 136.5; DB 1; Length 275;
Best Local Similarity 36.4%; Pred. No. 6.1e-05;
Matches 28; Conservative 14; Mismatches 24; Indels 11; Gaps

OY 18 RISIPKWPFFLEGCAC-----TTERMAERGFHCPTENEPDLAQCFPCFKELSGWPPDDPI 74
| : | | | | | : | | | | | : | | | | | : | | | | |
DB 111 RVKSFHPNP-----RCMKQREQOMADAGFFY---TGVDNTKCFYCDGLXDNRPEDVPV 163
| : | | | | | : | | | | | : | | | | | : | | | | |
OY 75 EEHKHSSGCCAPLSVKK 91
| : | | | | | : | | | | | : | | | | | : | | | | |
DB 163 EQHVWFDRCAIVQLVK 179
| : | | | | | : | | | | | : | | | | | : | | | | |

RESULT 14
BIR7 HUMAN
ID BIR7 HUMAN STANDARD; PRT; 298 AA.
AC O96CÅS; OSBQVO; Q9H2A8; Q9HAP7;
DT 28-FEB-2003 (Rel. 41, Created)
DI 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Baculoviral IAP repeat-containing protein 7 (Kidney inhibitor of
apoptosis protein) (KIAP) (Melanoma inhibitor of apoptosis protein)
DE (M-IAP) (Livin).
DE BIRC7 OR KIAP OR MLTAP OR LIVIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Fetal kidney;
RX MEDLINE=21092523; PubMed=11162435;
RA Lin J.-H., Deng G., Huang Q., Morser J.;
RT "KIAP, a novel member of the inhibitor of apoptosis protein family.";
RL Biochem. Biophys. Res. Commun. 279:820-831(2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Melanoma;
RX MEDLINE=21230343; PubMed=11322947;
RA Ashab Y., Allan A., Pollack A., Panet A., Yehuda D.B.;
RT "Two splicing variants of a new inhibitor of apoptosis gene with
different biological properties and tissue distribution pattern.";
RL FEBS Lett. 495:56-60(2001).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Kidney;
RX PubMed=11024045;
RA Kasof G.M., Gomes B.C.;
RT "Livin, a novel inhibitor of apoptosis protein family member.";
RL J. Biol. Chem. 276:3238-3246(2001).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RX MEDLINE=21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Beard K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgman A.M., Brown A.J.,
RA

RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.R., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Lehesvaisto M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConachie L.J., McLay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkhen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulton J.E.,
RA Swann R.M., Scymore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RT Nature 414:865-871(2001).
RL [5]
RN SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Skin;
RP MEDLINE=22388257; PubMed=12477932;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T.I., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Srapletenko M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villallon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buttigieg Y.S.N., Krzywinski M.I., Skalska U., Smalus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RP FUNCTION, AND MUTAGENESIS OF GLU-87; GLU-88; CYS-124; ASP-120 AND
RP ASF-138.
RX MEDLINE=20538921; PubMed=11084335;
RA Vucic D., Stennicke H.R., Pisabarro M.T., Salvesen G.S., Dixit V.M.;
RT "ML-TAP, a novel inhibitor of apoptosis that is preferentially
RT expressed in human melanomas.";
RL Curr. Biol. 10:1359-1366(2000).
RN [7]
RN INTERACTION WITH SMAC.
RX MEDLINE=21922807; PubMed=11801603;
RA Vucic D., Deshayes K., Ackerly K., Pisabarro M.T., Kadkodayan S.,
RA Fairbrother W.J., Dixit V.M.;
RT "SMAC negatively regulates the anti-apoptotic activity of melanoma
RT inhibitor of apoptosis (ML-TAP).";
RL J. Biol. Chem. 277:12275-12279(2002).
RN [8]
RN ACTIVATION OF MAP KINASES.
RX MEDLINE=21853687; PubMed=11865055;
RA Sanna M.G., da Silva Correia J., Ducey O., Lee J., Nomoto K.,
RA Schrantz N., Devereaux Q.L., Ulevitch R.J.;
RT "TAP suppression of apoptosis involves distinct mechanisms: the
RT TAK1/IKK1 signaling cascade and caspase inhibition.";
RL Mol. Cell. Biol. 22:1754-1766(2002).
CC -!- FUNCTION: Protects against apoptosis induced by TNF or by chemical
CC agents such as adriamycin, etoposide or staurosporine. Suppression

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FFCYGGLQSKRGDDPWEHAKWFP -> MFLPMDYFEAP
WRLHSSPPRCPRALQGRGRRGNDPRGSKGLKQTVGAL
NPNHLWGIC (in isoform 3).
/FTid=VSP_002458.
Missing (in isoform 1).
/FTid=VSP_002459.
EE->AA: NO CHANGE IN SMAC INTERACTION AND
ANTI-APOPTOTIC ACTIVITY.
D->A: ABOLISHES INHIBITION OF CASPASES,
SMAC BINDING AND ANTI-APOPTOTIC ACTIVITY.
C->A: ABOLISHES INHIBITION OF CASPASES
AND ANTI-APOPTOTIC ACTIVITY.

Query Match 17.5%; Score 136.5; DB 1; Length 298;
Best Local Similarity 38.6%; Pred. No. 6.7e-05;
Matches 27; Conservative 9; Mismatches 29; Indels 5; Gaps 2;

QY 18 RISTFKWPFLEGGCACTPERMAEAGFIHCPTENEPDLAQCFCKELEGWEPDDDDPIEEH 77
Db 90 RLASFYDWPLT--AEVPELLAAGFFH---TGHQDKVRFCFCYGLQSWRGDDPWTEH 144
QY 78 KKHSSGCAFL 87
Db 145 AKWPPSCQFL 154

RESULT 15
IAP3_NPVOF
ID IAP3_NPVOF STANDARD; PRT; 268 AA.
AC P41437;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Apoptosis inhibitor 3 (IAP-3).
GN IAP3 OR IAP.
OS Orygia pseudotsugata multicapsid polyhedrosis virus (OpMPNV).
OC Viruses; dsDNA viruses, no RNA stage, Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=164623;
RN [1]_TaxID=164623;
RP SEQUENCE FROM N.A.
RX MEDLINE=94187094; PubMed=8139034;
RA Birnbaum M.J., Clem R.J., Miller L.K.;
RT "An apoptosis-inhibiting gene from a nuclear polyhedrosis virus
RT encoding a polypeptide with Cys/His sequence motifs.";
RL J. Virol. 68:2521-2528(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97271300; PubMed=9126251;
RA Ahrens C.H., Russell R.R., Funk C.J., Evans J., Harwood S.,
RA Rohrmann G.F.;
RT "The sequence of the Orygia pseudotsugata multinucleocapsid nuclear
RT polyhedrosis virus genome.";
RL Virology 229:381-395(1997).
CC -!- FUNCTION: ACTS BY BLOCKING CELLULAR APOPTOSIS RATHER THAN BY
CC PREVENTING VIRAL STIMULATION OF APOPTOSIS.
CC -!- SIMILARITY: Contains 2 BIR repeats.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L22564; AB02610.1; -
DR EMBL; U75930; AAC59034.1; -
DR PIR; A53989; A53989.
DR HSSP; Q13490; 1QBH.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_ring.
```

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DR Pfam; PF00653; BIR; 2.
DR Pfam; PF00097; ZF-C3HC4; 1.
DR SMART; SM00238; BIR; 2.
DR SMART; SM00184; BIR; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS01443; BIR_REPEAT_2; 2.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS00089; ZF_RING_2; 1.
KW Apoptosis; Zinc-finger; Repeat.
FT REPEAT 18 84 BIR 1.
FT REPEAT 111 178 BIR 2.
FT ZN_FING 221 256 RING-TYPE
FT SEQUENCE 268 AA; 30076 MW; DF89175FDE85A708 CRC64;

Query Match 17.2%; Score 133.5; DB 1; Length 269;
Best Local Similarity 36.5%; Pred. No. 0.00011;
Matches 27; Conservative 12; Mismatches 30; Indels 5; Gaps 2;

QY 18 RISTFKWPFLEGGCACTPERMAEAGFIHCPTENEPDLAQCFCKELEGWEPDDDDPIEEH 77
Db 114 RLRTFAEWP--RGLQRPEELAEAGFFY---TGQGDKTRCFCCDGLKDWEPDDAPWQOH 168
QY 78 KKHSSGCAFLSVKK 91
Db 169 ARWYDRCEYVLLVK 182
```

Search completed: August 11, 2004, 14:16:18
Job time : 15 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 11, 2004, 14:13:25 ; Search time 39 Seconds
(without alignments)
1148.810 Million cell updates/sec

Title: US-09-690-825-34

Perfect score: 778

Sequence: 1 MGAPLPPAWOPFLKDHRS.....EFETAKVRAIEQLAAMD 142

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_25.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirs.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	775	99.6	142	6	Q81009 canis famil
2	718	92.3	142	6	Q9GIN5 sus scrofa
3	556	71.5	121	11	Q923F7 Q923f7 mus musculu
4	486	62.5	142	13	Q9DDK0 Q9ddk0 gallus gall
5	456	58.6	157	13	Q804H7 xenopus lae
6	444	57.1	135	13	Q90ZN0 gallus gall
7	389	50.0	142	13	Q90WU9 Q90w9 brachydanio
8	361	46.4	128	13	Q90WU8 Q90w8 brachydanio
9	356.5	45.8	160	13	Q8JG75 xenopus lae
10	356.5	45.8	160	13	Q8JGN5 xenopus lae
11	351.5	45.2	160	13	Q8AXI6 Q8axi6 xenopus lae
12	246.5	31.7	153	5	Q9VSM2 Q9vem2 drosophila
13	160	20.6	524	11	Q8BNX0 Q8bnx0 mus musculu
14	160	20.6	865	11	Q8BR72 Q8br72 mus musculu
15	160	20.6	4845	11	Q8R738 Q8r738 mus musculu
16	158	20.3	1151	5	Q8MS47 Q8ms47 drosophila

17	158	20.3	4876	5	Q8MUM9
18	158	20.3	4904	5	Q9VH01
19	157	20.2	308	5	Q18727
20	155.5	20.0	281	12	Q9VNL8
21	149	19.2	288	12	Q9IF18
22	148	19.0	288	12	Q9E232
23	146.5	18.8	405	13	Q8UWH2
24	146.5	18.8	415	13	Q7SXU1
25	145.5	18.7	155	5	Q22837
26	145	18.6	346	5	Q8IS31
27	145	18.6	1403	11	Q8CH68
28	145	18.6	1403	11	Q8CH64
29	143	18.4	346	5	Q968F8
30	143	18.4	597	11	Q9R015
31	143	18.4	1402	11	Q8CH65
32	143	18.4	1402	11	Q8CGT4
33	143	18.4	1402	11	Q8CGT3
34	143	18.4	1403	11	Q8CH70
35	143	18.4	1403	11	Q8CGT2
36	142	18.3	283	12	Q80LK9
37	142	18.3	1271	11	Q8CH71
38	142	18.3	1432	11	Q8CGS9
39	142	18.3	1446	11	Q8CG17
40	142	18.3	1447	11	Q8CH66
41	142	18.3	1447	11	Q8CGT1
42	142	18.3	1447	11	Q8CGT0
43	142	18.3	1447	11	Q8CGS8
44	142	18.3	1447	11	Q8CGS7
45	140.5	18.1	249	5	Q8SVK6

ALIGNMENTS

RESULT 1

Q81009 PRELIMINARY; PRT; 142 AA.
 AC Q81009;
 DT 01-MAR-2003 (TRENBLrel. 23, Created)
 DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE Survivin.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCEL_faxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Inoue C., Yamazaki J., Kano R., Hasegawa A.;
 RT "Canis familiaris mRNA for survivin-protein, complete cds."
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB095108; BAC22748.2;
 DR GO; GO:0005622; C:intracellular; IEA.
 DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
 DR GO; GO:0006916; P:anti-apoptosis; IEA.
 DR InterPro; IPR001370; BIR.
 DR Pfam; PF00653; BIR; 1.
 DR SMART; SM00238; BIR; 1.
 DR PROSITE; PS50143; BIR; REPEAT 2; 1.
 DR SEQUENCE 142 AA; 16375 MW; E960DC9DE6D36792 CRC64;

Query Match 99.6%; Score 775; DB 6; Length 142;

Best Local Similarity 99.3%; Pred. No. 1.5e-64;

Matches 141; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGAPLPPAWOPFLKDHRSIFTKWPFLEGGACCTPERMAEAGTHCPTENEPDLAQCFPC 60

Db 1 MGAPLPPAWOPFLKDHRSIFTKWPFLEGGACCTPERMAEAGTHCPTENEPDLAQCFPC 60

Qy 61 PKELEGWPDPTIEEHKHSGCCAFLSVKKQFELTIGELKLDREPAKNAKETNNK 120

Db 61 PKELEGWPDPTIEEHKHSGCCAFLSVKKQFELTIGELKLDREPAKNAKETNNK 120

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QY 121 KKEFEETAKVRRATEIQLAAMD 142
Db 121 KKEFEETAKVRRATEIQLAAMD 142

RESULT 2
Q9GLNS
ID Q9GLNS PRELIMINARY; PRT; 142 AA.
AC Q9GLNS;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Apoptosis inhibitor survivin.
OS Scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=21328903; PubMed=11435714;
RA Cirera S., Fredholm M.;
RT "Isolation and mapping the pig homologs survivin (BIRC5) and effector
RL cell protease receptor 1 (APR1) genes.";
DR EMBL; AF195781; AAG17540.1; -.
DR HSSP; O15392; IE31.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 1.
DR SMART; SM00238; BIR; 1.
DR PROSITE; PS0143; BIR_REPEAT_2; 1.
SQ SEQUENCE 142 AA; 16297 MW; 56BA753BES1F4F2C CRC64;

Query Match 92.3%; Score 718; DB 6; Length 142;
Best Local Similarity 92.3%; Pred. No. 3e-59; Indels 0; Gaps 0;
Matches 131; Conservative 5; Mismatches 6;

QY 1 MSAPSLPAWQPLKDHRISTFKNWPFLGCACTPERMAAGFHCPTNEPDLAQCFK 60
Db 1 MSAPSLPAWQPLKDHRISTFKNWPFLGCACTPERMAAGFHCPTNEPDLAQCFK 60

QY 61 FKELEGWEPDDPIEHHKHSGCCAFSLVKQFELTLGFLKLDREKAKNIKAKETNNK 120
Db 61 FKELEGWEPDDPIEHHKHSGCCAFSLVKQFELTLGFLKLDREKAKNIKAKETNNK 120

QY 121 KKEFEETAKVRRATEIQLAAMD 142
Db 121 KKEFEETAKVRRATEIQLAASE 142

RESULT 3
Q923F7
ID Q923F7 PRELIMINARY; PRT; 121 AA.
AC Q923F7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Baculoviral IAP repeat-containing 5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RX Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC004702; AA04702.1; -.
DR MGP; MGI:1203517; Birc5.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IMP.

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DR GO; GO:0006916; P:anti-apoptosis; IMP.
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 1.
DR SMART; SM00238; BIR; 1.
DR PROSITE; PS0143; BIR_REPEAT_2; 1.
SQ SEQUENCE 121 AA; 14154 MW; 1E0EC7E01BA65585 CRC64;

Query Match 71.5%; Score 556; DB 11; Length 121;
Best Local Similarity 81.7%; Pred. No. 3.1e-44;
Matches 98; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 1 MGAPLPPAWQPLKDHRISTFKNWPFLGCACTPERMAAGFHCPTNEPDLAQCFK 60
Db 1 MGAPLPPAWQPLKDHRISTFKNWPFLGCACTPERMAAGFHCPTNEPDLAQCFK 60

QY 61 FKELEGWEPDDPIEHHKHSGCCAFSLVKQFELTLGFLKLDREKAKNIKAKETNNK 120
Db 61 FKELEGWEPDDPIEHHKHSGCCAFSLVKQFELTLGFLKLDREKAKNIKAKETNNK 120

RESULT 4
Q9DDK0
ID Q9DDK0 PRELIMINARY; PRT; 142 AA.
AC Q9DDK0;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Survivin.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
SEQUENCE FROM N.A.
RX Langer J.S., Johnson A.L., Bridgham J.T.;
RT "Molecular cloning and characterization of chicken survivin.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF322051; AAG42494.1; -.
DR HSSP; O15392; IE31.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 1.
DR SMART; SM00238; BIR; 1.
DR PROSITE; PS0143; BIR_REPEAT_2; 1.
SQ SEQUENCE 142 AA; 15955 MW; 1323CCBD5EE2F551 CRC64;

Query Match 62.5%; Score 486; DB 13; Length 142;
Best Local Similarity 61.8%; Pred. No. 1.2e-37;
Matches 84; Conservative 19; Mismatches 33; Indels 0; Gaps 0;

QY 3 APTLPPAWQPLKDHRISTFKNWPFLGCACTPERMAAGFHCPTNEPDLAQCFK 62
Db 5 AEMLPKWLVLVSTRAATFRNWPFTGCACTPERMAAGFHCPTNEPDLAQCFK 64

QY 63 ELEGWEPDDPIEHHKHSGCCAFSLVKQFELTLGFLKLDREKAKNIKAKETNNK 122
Db 65 ELEGWEPDDPIEHHKHSGCCAFSLVKQFELTLGFLKLDREKAKNIKAKETNNK 124

QY 123 EFETAKVRRATEIQ 138
Db 125 DIEDVAKGVRAIENM 140

RESULT 5
Q804H7
ID Q804H7 PRELIMINARY; PRT; 157 AA.
AC Q804H7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

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[illegible]

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OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2037392; PubMed=10917738;
RA Inohara N., Nunez G.;
RT "Genes with homology to mammalian apoptosis regulators identified in
RL zebrafish."
RL Cell Death Differ. 7:509-510(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Inohara N., Nunez G.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY057058; AAL18251.1;
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; P:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR SMART; PF00653; BIR; 1.
DR PROSITE; PS00238; BIR; 1.
DR PROSITE; PS0143; BIR REPEAT 2; 1.
SQ SEQUENCE 138 AA; 15294 MW; A8496849082DDC66 CRC64;

Query Match 46.4%; Score 361; DB 13; Length 128;
Best Local Similarity 52.4%; Pred. No. 4.8e-25;
Matches 65; Conservative 19; Mismatches 36; Indels 4; Gaps 1;

QY 16 DHRISTFKNWPFLEGCACCTPERMAEAGFIHCPTEPNEDLAQCFFCFKELEGWEPDDDDPIE 75
DB 5 EKRLCTSEWFRDCCQCTPLMAKAGFVHCPSNEPDVACCFCLKELEGWEPDDNPS 64

QY 76 EHKHSSGCAFLSVKKQFEELTLGEFLKLDREKANKIAK-ETNNKKKEPFEETAKKVVRA 131
DB 65 EHKHSSGCAFLSVKKQFEELTLGEFLKLDREKANKIAK-ETNNKKKEPFEETAKKVVRA 131

QY 132 RRAI 135
DB 125 RALI 128

RESULT 9
Q8JG75 PRELIMINARY; PRT; 160 AA.
AC Q8JG75;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Survivin.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Bolton M.A., Lan W., Powers S.E., McClelland M.L., Kuang J.,
RA Stukenberg P.T.;
RT "Aurora B kinase exists in a complex with survivin and INCENP and its
RT kinase activity is stimulated by survivin binding and
RT phosphorylation."
RL Mol. Biol. Cell 0:0-0(2002).
DR EMBL; AY115553; AAM76714.1;
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; P:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR SMART; PF00653; BIR; 1.
DR PROSITE; PS00238; BIR; 1.
DR PROSITE; PS0143; BIR REPEAT 2; 1.
SQ SEQUENCE 160 AA; 18677 MW; B7C32E02119DC61B CRC64;

Query Match 45.8%; Score 356.5; DB 13; Length 160;
Best Local Similarity 54.1%; Pred. No. 1.6e-25;
Matches 66; Conservative 17; Mismatches 38; Indels 1; Gaps 1;

QY 16 DHRISTFKNWPFLEGCACCTPERMAEAGFIHCPTEPNEDLAQCFFCFKELEGWEPDDDDPIE 75
DB 25 DARLATFADWPFTECKCTPESMAKAGFVHCPTENEPDVACCFCLKELEGWEPDDDDPWT 84

QY 76 EHKHSSGCAFLSVKKQFEELTLGEFLKLDREKANKIAK-ETNNKKKEPFEETAKKVVRA 134
DB 85 EHKHSSGCAFLSVKKQFEELTLGEFLKLDREKANKIAK-ETNNKKKEPFEETAKKVVRA 134

QY 135 IE 136
DB 145 LE 146

RESULT 11
Q8AXI6 PRELIMINARY; PRT; 160 AA.
AC Q8AXI6;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Survivin.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.

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OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22341152; PubMed=12454937;
RA Murphy C.R., Sabell J.L., Sandler A.D., Dagle J.M.;
RT "Survivin mRNA is down-regulated during early Xenopus laevis
   embryogenesis.";
RL Dev. Dyn. 225:597-601(2002).
DR EMBL; AF442492; AAN76690.1; -.
DR GO; GO:0003622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0008916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 1.
DR SMART; SM00238; BIR; 1.
DR PROSITE; PS0143; BIR REPEAT 2; 1.
SQ SEQUENCE 160 AA; 18812 MW; 57538991C6190F4B CRC64;

Query Match 45.2%; Score 351.5; DB 13; Length 160;
Best Local Similarity 54.2%; Pred. No. 4.6e-25;
Matches 65; Conservative 16; Mismatches 38; Indels 1; Gaps 1;

QY 18 RISTFKNWPFLEGCACPTPMAEAGFIHCPTENEPDLAQCFCKELEGWEPDDPIBEH 77
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 27 RLATFADWFTENCXCTPENMAKAGVHCPTENEPDVACCFCKELEGWEPDDPWNH 86
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 78 KHSSGCALSVKQFEETLGFKLDRERAKNIAK-ETNKKKBPETAKKVRRAIE 136
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 87 SKRSVNCGLSLTKVNDLTMEGFLLEGDRISFYRKFTSTVQLQVEEMTAATKRLLE 146
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 12
Q9VEM2 PRELIMINARY; PRT; 153 AA.
AC Q9VEM2
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE CG12265 protein (B555472p).
GN CG12265.
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Randell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballou R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bereman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Borchan M.R., Bouck J., Brockstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Durkin B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck C.J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam J.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Matrei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

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RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleab J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Wang X.,
RA Svirskas R., Tector R., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RA Stapleton M., Brokstein P., Hong L., Acbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Lao G.,
RA Miranda A., Mungall C.J., Nunco J., Pacleab J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003716; AAP55399.1; -.
DR EMBL; AY071487; AAL49109.1; -.
DR HSPF; C15392; 1531.
DR Flybase; FBgn0038489; CG12265.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 1.
DR SMART; SM00238; BIR; 1.
DR PROSITE; PS0143; BIR REPEAT 2; 1.
SQ SEQUENCE 153 AA; 17455 MW; EE250E3B669EC359 CRC64;

Query Match 31.7%; Score 246.5; DB 5; Length 153;
Best Local Similarity 40.3%; Pred. No. 2.6e-15;
Matches 48; Conservative 20; Mismatches 50; Indels 1; Gaps 1;

QY 14 LKHRISTFRNWPFLGCACPTPMAEAGFIHCPTENEPDLAQCFCKELEGWEPDDP 73
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 27 LEQHRVSYKSWPPFPETASCSISKVABAGFYWTGKRENDTATCFVCGKTLDGWEPDDP 86
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 74 IEEHKCHSSGCALSVKQFEETLGFKLDRERAKNIAK-ETNKKKBP-ETAKKV 131
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 87 WKHRVHAPQCEFAKLSCPERNLTVSQFLGLGVVKGSIKTKAFKFSFVRENERKL 145
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 13
Q8BNX0 PRELIMINARY; PRT; 524 AA.
ID Q8BNX0
AC Q8BNX0
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Baculoviral IAP repeat-containing 6 (Fragment).
DE A430040A191K.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Aorta, and Vein;
RX MEDLINE=22354683; PubMed=12466851;
RA THE FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
   60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RL EMBL; AK079995; BAC37801.1; -.

```

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DR PIR; PT0546; PT0698.
DR PIR; PT0675; PT0675.
DR MGD; MGI:2444861; A430040A19R1k.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 1.
DR SMART; SM00238; BIR; 1.
DR PROSITE; PS50143; BIR_REPEAT_2; 1.
FT NON TER 524 524
SQ SEQUENCE 524 AA; 56194 MW; 6DA7DF987347D6FD CRC64;

Query Match 20.6%; Score 160; DB 11; Length 524;
Best Local Similarity 42.3%; Pred. No. 1.1e-06;
Matches 30; Conservative 10; Mismatches 31; Indels 0; Gaps 0;

QY 17 HRISTFKNWPFLGCACTPERMAEAGFIHCTENEPDLAQCFCKELEGWEPDDPIEE 76
Db 263 NRRTFTSWPHVGYRWAQPDMAQAGFYHQPASSGDDDRAMCFTCSVCLVCWEPTDEPWE 322
QY 77 HKHSSGCAFL 87
Db 323 HERHSPNCPFV 333

RESULT 14
Q8872 PRELIMINARY; PRT; 865 AA.
AC Q8872;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Baculoviral IAP repeat-containing 6 (Fragment).
GN A430040A19R1K.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22354683; PubMed=12466851;
RA Hausser H.P.; Bardroff M.; Pyrowolakis G.; Jentsch S.;
RT "A giant ubiquitin-conjugating enzyme related to IAP apoptosis
inhibitors."
RL J. Cell Biol. 141:1415-1422(1998).
CC -!- FUNCTION: CATALYZES THE COVALENT ATTACHMENT OF UBIQUITIN TO OTHER
PROTEINS (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: ATP + UBIQUITIN + PROTEIN LYSINE = AMP +
DIPHOSPHATE + PROTEIN N-UBIQUITYLLYSINE.
CC -!- PATHWAY: UBIQUITIN CONJUGATION; SECOND STEP.
CC -!- MISCELLANEOUS: A CYSTEINE RESIDUE IS REQUIRED FOR UBIQUITIN-
THIOLESTER FORMATION (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE UBIQUITIN-CONJUGATING ENZYME FAMILY.
EMBL; Y17267; CAA76720.1; -
DR PIR; T31067; T31067.
DR HSSP; Q13490; IQBH.
DR MGD; MGI:1276108; Birc6.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0004840; F:ubiquitin conjugating enzyme activity; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR GO; GO:0006512; P:ubiquitin cycle; IEA.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR000608; UBQ_conjugat.
DR Pfam; PF00653; BIR; 1.
DR Pfam; PF00179; UQ_con; 1.
DR ProDom; PD000461; UBQ_conjugat; 1.
DR SMART; SM00238; BIR; 1.
DR SMART; SM00212; UBCC; 1.
DR PROSITE; PS50143; BIR_REPEAT_2; 1.
DR PROSITE; PS50127; UBIQUITIN_CONJUGAT_2; 1.
DR Ligase; Ubl conjugation pathway.
SQ SEQUENCE 4845 AA; 528411 MW; 35C585F73B8CF84C CRC64;

Query Match 20.6%; Score 160; DB 11; Length 4845;
Best Local Similarity 42.3%; Pred. No. 1.2e-05;
Matches 30; Conservative 10; Mismatches 31; Indels 0; Gaps 0;

QY 17 HRISTFKNWPFLGCACTPERMAEAGFIHCTENEPDLAQCFCKELEGWEPDDPIEE 76
Db 263 NRRTFTSWPHVGYRWAQPDMAQAGFYHQPASSGDDDRAMCFTCSVCLVCWEPTDEPWE 322
QY 77 HKHSSGCAFL 87
Db 323 HERHSPNCPFV 333

Search completed: August 11, 2004, 14:17:08
Job time : 40 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 11, 2004, 14:10:05 ; Search time 53 Seconds
(without alignments)

757.014 Million cell updates/sec

Title: US-09-690-825-34

Perfect score: 778

Sequence: 1 MGAPLPPAWQPFLLKDHRS.....EFETAKVRRRAIEQLAAMD 142

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04:**

1: Geneseq1980s:**

2: Geneseq1990s:**

3: Geneseq2000s:**

4: Geneseq2001s:**

5: Geneseq2002s:**

6: Geneseq2003as:**

7: Geneseq2003bs:**

8: Geneseq2004s:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	778	100.0	142	2 AAW61359	Aw61359 Survivin
2	778	100.0	142	2 AAY49080	Aay49080 Human Sur
3	778	100.0	142	4 AAG53360	Ag53360 Human Her
4	778	100.0	142	5 AAU74571	Aau74571 Human sur
5	778	100.0	142	5 AAO14948	Aao14948 Survivin-
6	778	100.0	142	6 ABP72162	Abp72162 Human sur
7	778	100.0	142	7 ABR61582	Abr61582 Human sur
8	778	100.0	142	4 AAU29999	Aau29999 Novel hum
9	776	99.7	142	5 AAU74572	Aau74572 Human mut
10	772	99.2	142	5 AAU74574	Aau74574 Human mut
11	772	99.2	142	5 AAU74577	Aau74577 Human mut
12	768	98.7	142	5 AAU74575	Aau74575 Human mut
13	764	98.2	142	5 AAU74573	Aau74573 Human mut
14	762	98.0	141	6 ABU56477	Abu56477 Lung canc
15	762	97.9	142	5 AAU74576	Aau74576 Human mut
16	756.5	97.2	165	6 ADA09936	Ada09936 Human sur
17	750	96.4	142	5 AAU74580	Aau74580 Human mut
18	744	95.6	142	5 AAU74578	Aau74578 Human mut
19	742	95.4	142	5 AAU74581	Aau74581 Human mut
20	736	94.6	142	5 AAU74579	Aau74579 Human mut
21	699	89.8	125	5 AAU74582	Aau74582 Human del
22	660	84.8	140	2 AAW19749	Aaw19749 Mouse inh
23	660	84.8	140	5 AAU74583	Aau74583 Mouse sec
24	642	82.5	116	3 AAG02311	Ag02311 Human sec
25	436	56.0	75	7 ADB61824	Adb61824 Human inh

ALIGNMENTS

RESULT 1

AAW61359
ID AAW61359 standard; protein; 142 AA.

XX AAW61359;

DT 25-SEP-1998 (first entry)

DE Survivin protein.

KW survivin; apoptosis; cellular apoptosis; transplantation;

KW motor neuron degenerative disease; HIV infection; immunosuppression;

KW gastrointestinal perturbations; cardiovascular disorder.

XX OS Homo sapiens.

XX WO9822589-A2.

XX 28-MAY-1998.

XX 20-NOV-1997; 97WO-US021880.

XX 20-NOV-1996; 96US-0031435P.

XX 20-NOV-1997; 97US-00975080.

XX (UYVA) UNIV YALE.

XX Altieri DC;

XX WPI; 1998-312475/27.

XX N-PSDB; AAV27941.

XX Modulating apoptosis by controlling the survivin gene - useful for treating transplant rejection, degenerative disorders and tumours.

XX Disclosure; Fig 10; 108pp; English.

XX The survivin gene can be used to control apoptosis through modification of the gene. Survivin peptides can be used to inhibit cellular apoptosis, e.g. for enhancing the viability of organs and tissues prior to their transplantation, for preserving the growth of cells in culture or for treating conditions involving abnormal apoptosis, e.g. degenerative diseases such as motor neuron degenerative diseases, HIV infection, dermatological effects of ageing, disorders and diseases such as immunosuppression, gastrointestinal perturbations, cardiovascular disorders, apoptosis related to reperfusion damage, rejection of tissue transplantation and Alzheimer's disease. Agents which block Survivin activity can be used to treat e.g. tumours

Adb61823 Human inh
Abb61397 Drosophil
Adu06777 Fruit fly
Aau30231 Novel hum
Adb61822 Human inh
Abb97833 Human apo
Abb62249 Drosophil
Aaw19750 C. elegan
Aar98217 Neuronal
Aay09540 Human apo
Aay14080 Gonadotro
Aaw20033 Neuronal
Aaw20032 Neuronal
Aay09539 Human apo
Aay14079 Gonadotro
Aay88053 Human NAI
Adu07400 Protein d
Abp72166 Human inh
Aaw19751 C. elegan
Abb78046 Amino aci

XX SQ Sequence 142 AA; Best Local Similarity 100.0%; Score 778; DB 2; Length 142; Query Match 100.0%; Pred. No. 7.9e-78; Mismatches 0; Indels 0; Gaps 0; Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAPTLPPAWQPFKDHRISTFKNWPFLGGCACTPERMAEAGFIHCPTENEPDLAQCFPC 60
 DB 1 MGAPTLPPAWQPFKDHRISTFKNWPFLGGCACTPERMAEAGFIHCPTENEPDLAQCFPC 60

QY 61 FKELEGWEPDDPIEBHKHSSGCAFLSVKKQFEBTLGFEFLKDRERAKNKIAKETNNK 120
 DB 61 FKELEGWEPDDPIEBHKHSSGCAFLSVKKQFEBTLGFEFLKDRERAKNKIAKETNNK 120

QY 121 KKEFEETAKKVRRAIEQLAAMD 142
 DB 121 KKEFEETAKKVRRAIEQLAAMD 142

RESULT 2
 AAY49080
 ID AAY49080 standard; protein; 142 AA.
 XX
 AC AAY49080;
 XX
 DT 17-JAN-2000 (first entry)
 XX
 DE Human Survivin amino acid sequence.
 XX
 KW Survivin; IAP; apoptosis inhibitor; tumour cell; mitotic spindle;
 KW effector cell protease receptor-1; EPR-1; embryonic tissue; tubulin;
 KW abnormal cell growth; tumorigenesis.
 XX
 OS Homo sapiens.
 XX
 PN WO9950440-A2.
 XX
 PD 07-OCT-1999.
 XX
 PF 01-APR-1999; 93WO-US007205.
 XX
 PR 01-APR-1998; 98US-0080288P.
 XX
 PA (UYVA) UNIV YALE.
 XX
 PI Altieri DC;
 XX
 DR WPI; 1999-591329/50.
 DR N-PSDB; AAZ31037.
 XX
 PT Identifying agents that modulate Survivin interactions.
 XX
 PS Example; Fig 8A; 56pp; English.
 XX
 CC This is the amino acid sequence of the human survivin protein. Survivin
 CC is a 142 amino acid protein of approximately 16 kD. Survivin is a member
 CC of the IAP family of apoptosis inhibitors, and the gene is located on
 CC chromosome 17q25. The nucleic acid sequence of Survivin is related to the
 CC Effector Cell Protease Receptor-1 (EPR-1). Survivin is expressed in
 CC tumour cells and embryonic tissue. The sequence is used in the invention
 CC which involves identifying an agent that modulates interactions between
 CC Survivin and tubulin. Agents that modulate interaction between Survivin
 CC and tubulin or mitotic spindles may be administered to a mammal to
 CC modulate biological or pathological processes mediated by Survivin, for
 CC example, Survivin-mediated inhibition of cellular apoptosis. Thus an
 CC inhibiting agent may be used to block abnormal cell growth, for example
 CC during tumorigenesis. An agent that increases interaction may be used to
 CC extend cell growth in culture
 XX
 SQ Sequence 142 AA;

Query Match 100.0%; Score 778; DB 2; Length 142;
 Best Local Similarity 100.0%; Pred. No. 7.9e-78; Mismatches 0; Indels 0; Gaps 0; Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAPTLPPAWQPFKDHRISTFKNWPFLGGCACTPERMAEAGFIHCPTENEPDLAQCFPC 60
 DB 1 MGAPTLPPAWQPFKDHRISTFKNWPFLGGCACTPERMAEAGFIHCPTENEPDLAQCFPC 60

QY 61 FKELEGWEPDDPIEBHKHSSGCAFLSVKKQFEBTLGFEFLKDRERAKNKIAKETNNK 120
 DB 61 FKELEGWEPDDPIEBHKHSSGCAFLSVKKQFEBTLGFEFLKDRERAKNKIAKETNNK 120

QY 121 KKEFEETAKKVRRAIEQLAAMD 142
 DB 121 KKEFEETAKKVRRAIEQLAAMD 142

RESULT 3
 AAG65360
 ID AAG65360 standard; protein; 142 AA.
 XX
 AC AAG65360;
 XX
 DT 30-NOV-2001 (first entry)
 XX
 DE Human Her-3 polypeptide sequence.
 XX
 KW Her-3; epidermal growth factor; EGF; receptor/tyrosine kinase; human;
 KW antiinflammatory; cytostatic; antibacterial; antisense.
 XX
 OS Homo sapiens.
 XX
 PN US6277640-B1.
 XX
 PD 21-AUG-2001.
 XX
 PF 31-JUL-2000; 2000US-00630706.
 XX
 PR 31-JUL-2000; 2000US-00630706.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Bennett CP, Cowser LM;
 XX
 DR WPI; 2001-535134/59.
 DR N-PSDB; AAH47531.
 XX
 PT Antisense compounds capable of modulating expression of human Her-3,
 PT member of epidermal growth factor family of receptor/tyrosine kinases,
 PT useful for preventing or delaying infection, inflammation or tumor
 PT formation.
 XX
 PS Example 15; Col 57-70; 49pp; English.
 XX
 CC The invention provides antisense compounds capable of inhibiting the
 CC expression of human Her-3, a member of epidermal growth factor (EGF)
 CC family of receptor/tyrosine kinases. The antisense oligonucleotides are
 CC useful for inhibiting the expression of Her-3 in cells or tissues. They
 CC are commonly used as research reagents and in diagnostics for example, to
 CC elucidate the function of particular genes. The antisense compounds are
 CC also useful for distinguishing between functions of various members of a
 CC biological pathway and for research use. They are also utilized for
 CC diagnostics, therapeutics, prophylaxis and in kits. They are useful
 CC prophylactically, e.g. to prevent or delay infection, inflammation or
 CC tumor formation. The present sequence represents the human Her-3 sequence
 CC (GenBank Accession No. U75285)
 XX
 SQ Sequence 142 AA;

Query Match 100.0%; Score 778; DB 4; Length 142;
 Best Local Similarity 100.0%; Pred. No. 7.9e-78; Mismatches 0; Indels 0; Gaps 0; Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAPTLPPAWQPFKDHRISTFKNWPFLGGCACTPERMAEAGFIHCPTENEPDLAQCFPC 60

Db 1 MGAPLPPAWQPFLLKDHRISTFKNWPFLGGCACTPERMAEAGFIHCPTENEPDLAQCFPC 60
QY 61 FKELEGWEPDDPIIEHKKHSSGCAFLSVKKQFEEELTGEFLKLDREKAKKIAKETNNK 120
Db 61 FKELEGWEPDDPIIEHKKHSSGCAFLSVKKQFEEELTGEFLKLDREKAKKIAKETNNK 120
QY 121 KKEFEETAKKVRRAIEQLAAMD 142
Db 121 KKEFEETAKKVRRAIEQLAAMD 142
RESULT 4
AAU74571
ID AAU74571 standard; protein; 142 AA.
XX
AC AAU74571;
XX
DT 08-MAY-2002 (first entry)
XX
DE Human survivin polypeptide.
XX
KW Human; survivin; inhibitor of apoptosis protein; IAP; cytostatic; p21;
KW tubulin interaction; caspase-3; CDK4; zinc chelation activity; apoptosis;
KW dimerisation; ovary; breast; pancreas; central nervous system; blood;
KW lung; skin; lymph node; brain; kidney; liver; nasopharyngeal cavity;
KW thyroid; prostate; colon; rectum; cervix; endometrium; cancer; AIDS;
KW cell proliferative disorder; acquired immunodeficiency syndrome;
KW neurodegenerative disease; ischaemic injury; toxin-induced liver disease;
KW myelodysplastic syndrome; protein coordinate data.
XX
OS Homo sapiens.
XX
PN WC200202622-A2.
XX
PD 10-JAN-2002.
XX
PF 29-JUN-2001; 2001WO-05020872.
XX
PR 29-JUN-2000; 2000US-00608352.
XX
PA (SALK) SALK INST BIOLOGICAL STUDIES.
XX
PI Noel JP, Verdacia M, Hunter T, Huang H;
XX WPI; 2002-171638/22.
XX
DR Novel isolated crystalline survivin polypeptide, useful to screen and
PT design compounds that bind to or interact with inhibitor of apoptosis
PT protein and protein family members, and for design of novel therapeutics.
XX
PS Claim 42; Fig 2; 102pp; English.
XX
CC The invention relates to an isolated crystalline human survivin
CC polypeptide, an inhibitor or apoptosis protein (IAP). The polypeptide is
CC useful for determining the ability of a survivin binding agent to
CC modulate tubulin interaction, p21, caspase-3 and CDK4 requirement or zinc
CC chelation activity and for identifying an agent such as a peptide or
CC peptidomimetic which inhibits dimerisation of survivin. The ability of an
CC agent to modulate dimerisation can be determined through detection of a
CC change in apoptosis in a target cell expressing survivin. Binding agents
CC are useful for increasing apoptosis in a cell derived from a tissue
CC selected from ovary, breast, pancreas, lymph node, skin, blood, lung,
CC brain, kidney, liver, nasopharyngeal cavity, thyroid, central nervous
CC system, prostate, colon, rectum, cervix or endometrium, with a cell
CC proliferative disorder such as cancer. The molecules can also be used in
CC treatment or prevention of apoptosis which occurs as a part of AIDS,
CC neurodegenerative diseases, ischaemic injury, toxin-induced liver disease
CC and myelodysplastic syndromes. This sequence represents the human
XX survivin polypeptide
XX
SQ Sequence 142 AA;

Query Match 100.0%; Score 778; DB 5; Length 142;
Best Local Similarity 100.0%; Pred. No. 7.9e-78;
Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGAPLPPAWQPFLLKDHRISTFKNWPFLGGCACTPERMAEAGFIHCPTENEPDLAQCFPC 60
Db 1 MGAPLPPAWQPFLLKDHRISTFKNWPFLGGCACTPERMAEAGFIHCPTENEPDLAQCFPC 60
QY 61 FKELEGWEPDDPIIEHKKHSSGCAFLSVKKQFEEELTGEFLKLDREKAKKIAKETNNK 120
Db 61 FKELEGWEPDDPIIEHKKHSSGCAFLSVKKQFEEELTGEFLKLDREKAKKIAKETNNK 120
QY 121 KKEFEETAKKVRRAIEQLAAMD 142
Db 121 KKEFEETAKKVRRAIEQLAAMD 142
RESULT 5
AAO14948
ID AAO14948 standard; protein; 142 AA.
XX
AC AAO14948;
XX
DT 06-AUG-2002 (first entry)
XX
DE Survivin-like protein 6.
XX
KW Survivin-like protein; diagnosis; screening; cancer;
KW apoptosis abnormality; gene therapy.
XX
OS Unidentified.
XX
PN WO200233071-A1.
XX
PD 25-APR-2002.
XX
PF 16-OCT-2001; 2001WO-JP009071.
XX
PR 17-OCT-2000; 2000JP-00316721.
XX
PR 20-DEC-2000; 2000JP-00386809.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Tanaka H, Kaieda I;
XX WPI; 2002-435536/46.
XX
DR N-PSDB; AAL42859.
XX
PT Baculovirus IAP repeat domain or RING-finger domain-containing survivin-
PT like polypeptides and encoded DNAs, applicable in diagnosis and screening
PT compounds for treating various cancers and apoptosis abnormality.
XX
PS Disclosure; Page 122-123; 136pp; Japanese.
XX
CC The invention comprises the amino acid and coding sequences of survivin-
CC like proteins. The survivin-like DNA and protein sequences are useful in
CC diagnostics and screening compounds for treating various cancers and
CC apoptosis abnormality, including gene therapy. The present amino acid
CC sequence represents a survivin-like protein of the invention
XX
SQ Sequence 142 AA;
Query Match 100.0%; Score 778; DB 5; Length 142;
Best Local Similarity 100.0%; Pred. No. 7.9e-78;
Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGAPLPPAWQPFLLKDHRISTFKNWPFLGGCACTPERMAEAGFIHCPTENEPDLAQCFPC 60
Db 1 MGAPLPPAWQPFLLKDHRISTFKNWPFLGGCACTPERMAEAGFIHCPTENEPDLAQCFPC 60
QY 61 FKELEGWEPDDPIIEHKKHSSGCAFLSVKKQFEEELTGEFLKLDREKAKKIAKETNNK 120
Db 61 FKELEGWEPDDPIIEHKKHSSGCAFLSVKKQFEEELTGEFLKLDREKAKKIAKETNNK 120

QY 121 KKEFEETAKKVRRAIEQLAAMD 142
 DB 121 KKEFEETAKKVRRAIEQLAAMD 142

RESULT 6

ABP72162
 ID ABP72162 standard; protein; 142 AA.

AC ABP72162;

DT 22-APR-2003 (first entry)

XX Human Survivin.

XX Human; Survivin; inhibitor of apoptosis; cell death; apoptosis; cancer;
 KW cytostatic; cardiant; neuroprotective; gene therapy.

XX Homo sapiens.

PN WO2003004606-A2.

PD 16-JAN-2003.

XX 03-JUL-2002; 2002WO-US021002.

XX 03-JUL-2001; 2001US-00898158.

PA (UYCO) UNIV COLUMBIA NEW YORK.

XX Troy CM, Shelanski ML;

PI WPI; 2003-210351/20.

DR N-PSDB; ABZ58106.

XX New nucleic acid encoding an inhibitor-of-apoptosis protein, useful for
 PT treating cancer, neurodegenerative disorder or cardiomyopathy.

XX Disclosure; Fig 20A; 124pp; English.

XX The present sequence is the protein sequence of human Survivin protein.
 CC The invention provides a nucleic acid, such as an antisense
 CC oligonucleotide, which specifically hybridises to a nucleic acid encoding
 CC an inhibitor of apoptosis protein. Survivin is an example of an inhibitor
 CC of apoptosis or inducer of cell death protein of the invention. A claimed
 CC method for inducing a cell's death comprises contacting the cell with the
 CC nucleic acid under conditions permitting the nucleic acid to enter the
 CC cell, especially the use of a vector, liposome, or a mechanical or
 CC electrical means. The method is used to treat acute lymphocytic
 CC leukaemia, acute myelogenous leukaemia, lung cancer, breast cancer,
 CC ovarian cancer, prostate cancer, lymphoma, Hodgkin's disease, malignant
 CC melanoma, neuroblastoma, renal cell carcinoma and squamous cell carcinoma
 CC (all claimed). The invention also provides a second nucleic acid, which
 CC specifically hybridises to a nucleic acid encoding a protein, other than
 CC caspase-2, that induces cell death. A claimed method for inhibiting a
 CC cell's death comprises contacting the cell with the nucleic acid under
 CC conditions permitting the nucleic acid to enter the cell. The method is
 CC used to treat a neurodegenerative disorder (especially a brain disorder
 CC or central nervous system disorder), or a heart disorder (especially
 CC cardiomyopathy) in a human (all claimed)

XX Sequence 142 AA;

Query Match 100.0%; Score 778; DB 6; Length 142;
 Best Local Similarity 100.0%; Pred. No. 7.9e-78;
 Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAPTLPPAWQPFLLKDHRISTFKNWPFLGCACTPERMAEAGFHCPTENEPDLAQCFCC 60

DB 1 MGAPTLPPAWQPFLLKDHRISTFKNWPFLGCACTPERMAEAGFHCPTENEPDLAQCFCC 60

QY 61 FKELEGWEPDDPPIEHHKSHSSGCAFLSVKKQFELTLGFLKLDRAKNKIATETNNK 120

DB 61 FKELEGWEPDDPPIEHHKSHSSGCAFLSVKKQFELTLGFLKLDRAKNKIATETNNK 120

QY 121 KKEFEETAKKVRRAIEQLAAMD 142

DB 121 KKEFEETAKKVRRAIEQLAAMD 142

RESULT 7

ABR61582

ID ABR61582 standard; protein; 142 AA.

XX ABR61582;

XX 15-JAN-2004 (first entry)

XX Human survivin protein.

XX RasGAP; Aurora kinase; cytostatic; anti-tumoural; human; survivin.

XX Homo sapiens.

PN WO2003087395-A2.

PD 23-OCT-2003.

XX 15-APR-2003; 2003WO-IB002972.

XX 15-APR-2002; 2002US-0372483P.

PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

XX Garbay C, Gigoux V, Camonis J, L'hoste S, Samson J;

XX WPI; 2003-845340/78.

DR N-PSDB; ACF58071.

XX Identifying anti-tumoral compounds, comprises determining the capacity of
 PT a compound to inhibit interaction between RasGAP and Drosophila
 PT melanogaster (Dm) aurora kinase, or between RasGAP, Dm aurora kinase and
 PT aurora binding protein.

XX Disclosure; Page 67; Opp; English.

XX The invention relates to identifying a biologically active compound with
 CC anti-tumoural properties, where the compound is studied for its capacity
 CC to inhibit the interaction between: (a) RasGAP and the Drosophila
 CC melanogaster Aurora kinase or an orthologue of the kinase, or its
 CC fragment able to interact with RasGAP; or (b) RasGAP, an Aurora-binding
 CC protein and the D. melanogaster Aurora kinase or an orthologue of the
 CC kinase, or its fragment. The method is useful for identifying anti-
 CC tumoural agents. The present sequence represents a human survivin
 CC protein, an aurora-binding protein

XX Sequence 142 AA;

Query Match 100.0%; Score 778; DB 7; Length 142;
 Best Local Similarity 100.0%; Pred. No. 7.9e-78;
 Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAPTLPPAWQPFLLKDHRISTFKNWPFLGCACTPERMAEAGFHCPTENEPDLAQCFCC 60

DB 1 MGAPTLPPAWQPFLLKDHRISTFKNWPFLGCACTPERMAEAGFHCPTENEPDLAQCFCC 60

QY 61 FKELEGWEPDDPPIEHHKSHSSGCAFLSVKKQFELTLGFLKLDRAKNKIATETNNK 120

DB 61 FKELEGWEPDDPPIEHHKSHSSGCAFLSVKKQFELTLGFLKLDRAKNKIATETNNK 120

QY 121 KKEFEETAKKVRRAIEQLAAMD 142

DB 121 KKEFEETAKKVRRAIEQLAAMD 142

```
RESULT 8
AAU29999
ID AAU29999 standard; protein; 143 AA.
XX
AC AAU29999;
XX
DT 18-DEC-2001 (first entry)
XX
DE Novel human secreted protein #490.
XX
KW Human; vaccination; gene therapy; nutritional supplement;
KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200179449-A2.
XX
PD 25-OCT-2001.
XX
PF 16-APR-2001; 2001WO-US008656.
XX
PR 18-APR-2000; 2000US-00552929.
XX
PR 26-JAN-2001; 2001US-00770160.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
XX WPI; 2001-611725/70.
XX
XX Nucleic acids encoding a range of human polypeptides, useful in genetic
XX vaccination, testing and therapy.
XX
XX Claim 20; Page 219; 765pp; English.
XX
XX The invention relates to novel human secreted polypeptides. The
XX polypeptides and antibodies to the polypeptides are useful for
XX determining the presence of or predisposition to a disease associated
XX with altered levels of polypeptide. The polypeptides are also useful for
XX identifying agents (agonists and antagonists) that bind to them. Cells
XX expressing the proteins are useful for identifying a therapeutic agent
XX for use in treatment of a pathology related to aberrant expression or
XX physiological interactions of the polypeptide. Vectors comprising the
XX nucleic acids encoding the polypeptides and cells genetically engineered
XX to express them are also useful for producing the proteins. The proteins
XX are useful in genetic vaccination, testing and therapy, and can be used
XX as nutritional supplements. They may be used to increase stem cell
XX proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon
XX and/or nerve tissue growth or regeneration; immune suppression and/or
XX stimulation; as anti-inflammatory agents; and in treatment of leukaemias.
XX AAU29510-AAU33304 represent the amino acid sequences of novel human
XX secreted proteins of the invention
XX
XX Sequence 143 AA;
XX
XX Query Match 100.0%; Score 778; DB 4; Length 143;
XX Best Local Similarity 100.0%; Pred No. 7.9e-78;
XX Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGAPTLPPAQPFKDHRISTFKNWPFLGCACTPERMAEAGFIHCTPTNEPDLAQCFFC 60
DB 1 MGAPTLPPAQPFKDHRISTFKNWPFLGCACTPERMAEAGFIHCTPTNEPDLAQCFFC 60
QY 61 FKELEGWEPDDPIEEHHKSSGCAFLSVKKQFEELTLGFEFLKDRERAKNKIATETNNK 120
DB 61 FKELEGWEPDDPIEEHHKSSGCAFLSVKKQFEELTLGFEFLKDRERAKNKIATETNNK 120
QY 121 KGEFEETAKVRRRAIEQLAAMD 142
DB 121 KGEFEETAKVRRRAIEQLAAMD 142
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```
RESULT 9
AAU74572
ID AAU74572 standard; protein; 142 AA.
XX
AC AAU74572;
XX
DT 08-MAY-2002 (first entry)
XX
DE Human mutant L54M survivin polypeptide.
XX
KW Human; survivin; inhibitor of apoptosis protein; IAP; cytostatic; p21;
KW tubulin interaction; caspase-3; CDK4; zinc chelation activity; apoptosis;
KW dimerisation; ovary; breast; pancreas; central nervous system; blood;
KW lung; skin; lymph node; brain; kidney; liver; nasopharyngeal cavity;
KW thyroid; prostate; colon; rectum; cervix; endometrium; cancer; AIDS;
KW cell proliferative disorder; acquired immunodeficiency syndrome;
KW neurodegenerative disease; ischaemic injury; toxin-induced liver disease;
KW myelodysplastic syndrome; protein coordinate data; mutant; mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
XX FT Misc-difference 54
XX FT /note= "Wild-type Leu substituted by Met"
XX
XX WO200202622-A2.
XX
XX 10-JAN-2002.
XX
XX 29-JUN-2001; 2001WO-US020872.
XX
XX 29-JUN-2000; 2000US-00608352.
XX
XX (SALK ) SALK INST BIOLOGICAL STUDIES.
XX
XX Noel JP, Verdacia M, Hunter T, Huang H;
XX WPI; 2002-171638/22.
XX
XX Novel isolated crystalline survivin polypeptide, useful to screen and
XX design compounds that bind to or interact with inhibitor of apoptosis
XX protein and protein family members, and for design of novel therapeutics.
XX
XX Claim 7; Page; 102pp; English.
XX
XX The invention relates to an isolated crystalline human survivin
XX polypeptide, an inhibitor of apoptosis protein (IAP). The polypeptide is
XX useful for determining the ability of a survivin binding agent to
XX modulate tubulin interaction, p21, caspase-3 and CDK4 requirement or zinc
XX chelation activity and for identifying an agent such as a peptide or
XX peptidomimetic which inhibits dimerisation of survivin. The ability of an
XX agent to modulate dimerisation can be determined through detection of a
XX change in apoptosis in a target cell expressing survivin. Binding agents
XX are useful for increasing apoptosis in a cell derived from a tissue
XX selected from ovary, breast, pancreas, lymph node, skin, blood, lung,
XX brain, kidney, liver, nasopharyngeal cavity, thyroid, central nervous
XX system, prostate, colon, rectum, cervix or endometrium, with a cell
XX proliferative disorder such as cancer. The molecules can also be used in
XX treatment or prevention of apoptosis which occurs as a part of AIDS,
XX neurodegenerative diseases, ischaemic injury, toxin-induced liver disease
XX and myelodysplastic syndromes. This sequence represents a human mutant
XX survivin polypeptide. Note: This sequence is not featured in the printed
XX specification but was derived from the wild type protein shown in
XX AAU74571
XX
XX Sequence 142 AA;
```

```
Query Match 99.7%; Score 776; DB 5; Length 142;
Best Local Similarity 99.3%; Pred. No. 1.3e-77;
Matches 141; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGAPTLPPAQPFKDHRISTFKNWPFLGCACTPERMAEAGFIHCTPTNEPDLAQCFFC 60
```

Db 1 MGAPTLPPAWQFLKDHRISTFKWPFLEGGCACTPERMAEAGFIHCPTENPDMAQCFFC 60
 QY 61 FKELEGWEPDDPIEHHKHSGCCAFSLVKQFBEFLTGLGFLKDRERAKNKIAKETNNK 120
 Db 61 FKELEGWEPDDPIEHHKHSGCCAFSLVKQFBEFLTGLGFLKDRERAKNKIAKETNNK 120
 QY 121 KKEFEETAKKVRRAIEQLAAMD 142
 Db 121 KKEFEETAKKVRRAIEQLAAMD 142
 RESULT 10
 AAU74574
 ID AAU74574 standard; protein; 142 AA.
 AC AAU74574;
 XX
 DT 08-MAY-2002 (first entry)
 XX Human mutant T34E survivin polypeptide.
 DE
 KW Human; survivin; inhibitor of apoptosis protein; IAP; cytostatic; p21;
 KW tubulin interaction; caspase-3; CDK4; zinc chelation activity; apoptosis;
 KW dimerisation; ovary; breast; pancreas; central nervous system; blood;
 KW lung; skin; lymph node; brain; kidney; liver; nasopharyngeal cavity;
 KW thyroid; prostate; colon; rectum; cervix; endometrium; cancer; AIDS;
 KW cell proliferative disorder; acquired immunodeficiency syndrome;
 KW neurodegenerative disease; ischaemic injury; toxin-induced liver disease;
 KW myelodysplastic syndrome; protein coordinate data; mutant; mutein.
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 34 /note= "Wild-type Thr substituted by Glu"
 FT
 FN WO200202622-A2.
 PD 10-JAN-2002.
 XX
 PF 29-JUN-2001; 2001WO-US020872.
 XX
 PR 29-JUN-2000; 2000US-00608352.
 XX
 PA (SALK) SALK INST BIOLOGICAL STUDIES.
 XX
 PI Noel JP, Verdacia M, Hunter T, Huang H;
 XX
 DR WPI; 2002-171638/22.
 XX
 XX Novel isolated crystalline survivin polypeptide, useful to screen and
 PT design compounds that bind to or interact with inhibitor of apoptosis
 PT protein and protein family members, and for design of novel therapeutics.
 XX
 PS Claim 8; Page; 102pp; English.
 XX
 CC The invention relates to an isolated crystalline human survivin
 CC polypeptide, an inhibitor of apoptosis protein (IAP). The polypeptide is
 CC useful for determining the ability of a survivin binding agent to
 CC modulate tubulin interaction, p21, caspase-3 and CDK4 requirement or zinc
 CC chelation activity and for identifying an agent such as a peptide or
 CC peptidomimetic which inhibits dimerisation of survivin. The ability of an
 CC agent to modulate dimerisation can be determined through detection of a
 CC change in apoptosis in a target cell expressing survivin. Binding agents
 CC are useful for increasing apoptosis in a cell derived from a tissue
 CC selected from ovary, breast, pancreas, lymph node, skin, blood, lung,
 CC brain, kidney, liver, nasopharyngeal cavity, thyroid, central nervous
 CC system, prostate, colon, rectum, cervix or endometrium, with a cell
 CC proliferative disorder such as cancer. The molecules can also be used in
 CC treatment or prevention of apoptosis which occurs as a part of AIDS,
 CC neurodegenerative diseases, ischaemic injury, toxin-induced liver disease

CC and myelodysplastic syndromes. This sequence represents a human mutant
 CC survivin polypeptide. Note: This sequence is not featured in the printed
 CC specification but was derived from the wild type protein shown in
 CC AAU74571
 XX
 SQ Sequence 142 AA;
 Query Match 99.2%; Score 772; DB 5; Length 142;
 Best Local Similarity 99.3%; Pred. No. 3.6e-77;
 Matches 141; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MGAPTLPPAWQFLKDHRISTFKWPFLEGGCACTPERMAEAGFIHCPTENPDMAQCFFC 60
 Db 1 MGAPTLPPAWQFLKDHRISTFKWPFLEGGCACTPERMAEAGFIHCPTENPDMAQCFFC 60
 QY 61 FKELEGWEPDDPIEHHKHSGCCAFSLVKQFBEFLTGLGFLKDRERAKNKIAKETNNK 120
 Db 61 FKELEGWEPDDPIEHHKHSGCCAFSLVKQFBEFLTGLGFLKDRERAKNKIAKETNNK 120
 QY 121 KKEFEETAKKVRRAIEQLAAMD 142
 Db 121 KKEFEETAKKVRRAIEQLAAMD 142
 RESULT 11
 AAU74577
 ID AAU74577 standard; protein; 142 AA.
 XX
 AC AAU74577;
 XX
 DT 08-MAY-2002 (first entry)
 XX Human mutant T97E survivin polypeptide.
 DE
 KW Human; survivin; inhibitor of apoptosis protein; IAP; cytostatic; p21;
 KW tubulin interaction; caspase-3; CDK4; zinc chelation activity; apoptosis;
 KW dimerisation; ovary; breast; pancreas; central nervous system; blood;
 KW lung; skin; lymph node; brain; kidney; liver; nasopharyngeal cavity;
 KW thyroid; prostate; colon; rectum; cervix; endometrium; cancer; AIDS;
 KW cell proliferative disorder; acquired immunodeficiency syndrome;
 KW neurodegenerative disease; ischaemic injury; toxin-induced liver disease;
 KW myelodysplastic syndrome; protein coordinate data; mutant; mutein.
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 97 /note= "Wild-type Thr substituted by Glu"
 FT
 FN WO200202622-A2.
 PD 10-JAN-2002.
 XX
 PF 29-JUN-2001; 2001WO-US020872.
 XX
 PR 29-JUN-2000; 2000US-00608352.
 XX
 PA (SALK) SALK INST BIOLOGICAL STUDIES.
 XX
 PI Noel JP, Verdacia M, Hunter T, Huang H;
 XX
 DR WPI; 2002-171638/22.
 XX
 XX Novel isolated crystalline survivin polypeptide, useful to screen and
 PT design compounds that bind to or interact with inhibitor of apoptosis
 PT protein and protein family members, and for design of novel therapeutics.
 XX
 PS Claim 8; Page; 102pp; English.
 XX
 CC The invention relates to an isolated crystalline human survivin
 CC polypeptide, an inhibitor of apoptosis protein (IAP). The polypeptide is
 CC useful for determining the ability of a survivin binding agent to

CC modulate tubulin interaction, p21, caspase-3 and CDK4 requirement or zinc
 CC chelation activity and for identifying an agent such as a peptide or
 CC peptidomimetic which inhibits dimerisation of survivin. The ability of an
 CC agent to modulate dimerisation can be determined through detection of a
 CC change in apoptosis in a target cell expressing survivin. Binding agents
 CC are useful for increasing apoptosis in a cell derived from a tissue
 CC selected from ovary, breast, pancreas, lymph node, skin, blood, lung,
 CC brain, kidney, liver, nasopharyngeal cavity, thyroid, central nervous
 CC system, prostate, colon, rectum, cervix or endometrium, with a cell
 CC proliferative disorder such as cancer. The molecules can also be used in
 CC treatment or prevention of apoptosis which occurs as a part of AIDS,
 CC neurodegenerative diseases, ischaemic injury, toxin-induced liver disease
 CC and myelodysplastic syndromes. This sequence represents a human mutant
 CC survivin polypeptide. Note: This sequence is not featured in the printed
 CC specification but was derived from the wild type protein shown in
 CC AAU74571
 XX
 XX Sequence 142 AA;

Query Match 99.2%; Score 772; DB 5; Length 142;
 Best Local Similarity 99.3%; Pred. No. 3.6e-77;
 Matches 141; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MGAPTLPPAWQPFELKDHRISTFKNWPFLGCGACTPERMAEAGFIHCTPENEPLDAQCFPC 60
 Db 1 MGAPTLPPAWQPFELKDHRISTFKNWPFLGCGACTPERMAEAGFIHCTPENEPLDAQCFPC 60
 QY 61 FKELEGWEPDDDDPIEHHKHSKSCAFLSVKKQFELTLGFEFLKLDREAKNKIAKETNNK 120
 Db 61 FKELEGWEPDDDDPIEHHKHSKSCAFLSVKKQFELTLGFEFLKLDREAKNKIAKETNNK 120
 QY 121 KKEFEETAKKVRRAIEQLAAMD 142
 Db 121 KKEFEETAKKVRRAIEQLAAMD 142

RESULT 12
 AAU74575
 ID AAU74575 standard; protein; 142 AA.

AC AAU74575;
 XX
 DT 08-MAY-2002 (first entry)
 DE Human mutant H80A survivin polypeptide.
 DE
 KW Human; survivin; inhibitor of apoptosis protein; IAP; cytostatic; p21;
 KW tubulin interaction; caspase-3; CDK4; zinc chelation activity; apoptosis;
 KW dimerisation; ovary; breast; pancreas; central nervous system; blood;
 KW lung; skin; lymph node; brain; kidney; liver; nasopharyngeal cavity;
 KW thyroid; prostate; colon; rectum; cervix; endometrium; cancer; AIDS;
 KW cell proliferative disorder; acquired immunodeficiency syndrome;
 KW neurodegenerative disease; ischaemic injury; toxin-induced liver disease;
 KW myelodysplastic syndrome; protein coordinate data; mutant; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.

XX Key Location/Qualifiers
 XX Misc-difference 80
 FT /note= "Wild-type His substituted by Ala"

XX WO200202622-A2.

XX 10-JAN-2002.

XX 29-JUN-2001; 2001WO-US020872.

XX 29-JUN-2000; 2000US-00608352.

XX (SALK) SALK INST BIOLOGICAL STUDIES.

XX Noel JP, Verdacia M, Hunter T, Huang H;

XX WPI; 2002-171638/22.
 DR Novel isolated crystalline survivin polypeptide, useful to screen and
 PT design compounds that bind to or interact with inhibitor of apoptosis
 PT protein and protein family members, and for design of novel therapeutics.
 XX
 PS Claim 8; Page; 102pp; English.

XX The invention relates to an isolated crystalline human survivin
 CC polypeptide, an inhibitor of apoptosis protein (IAP). The polypeptide is
 CC useful for determining the ability of a survivin binding agent to
 CC modulate tubulin interaction, p21, caspase-3 and CDK4 requirement or zinc
 CC chelation activity and for identifying an agent such as a peptide or
 CC peptidomimetic which inhibits dimerisation of survivin. The ability of an
 CC agent to modulate dimerisation can be determined through detection of a
 CC change in apoptosis in a target cell expressing survivin. Binding agents
 CC are useful for increasing apoptosis in a cell derived from a tissue
 CC selected from ovary, breast, pancreas, lymph node, skin, blood, lung,
 CC brain, kidney, liver, nasopharyngeal cavity, thyroid, central nervous
 CC system, prostate, colon, rectum, cervix or endometrium, with a cell
 CC proliferative disorder such as cancer. The molecules can also be used in
 CC treatment or prevention of apoptosis which occurs as a part of AIDS,
 CC neurodegenerative diseases, ischaemic injury, toxin-induced liver disease
 CC and myelodysplastic syndromes. This sequence represents a human mutant
 CC survivin polypeptide. Note: This sequence is not featured in the printed
 CC specification but was derived from the wild type protein shown in
 CC AAU74571

XX Sequence 142 AA;

Query Match 98.7%; Score 768; DB 5; Length 142;
 Best Local Similarity 99.3%; Pred. No. 1e-76;
 Matches 141; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGAPTLPPAWQPFELKDHRISTFKNWPFLGCGACTPERMAEAGFIHCTPENEPLDAQCFPC 60
 Db 1 MGAPTLPPAWQPFELKDHRISTFKNWPFLGCGACTPERMAEAGFIHCTPENEPLDAQCFPC 60
 QY 61 FKELEGWEPDDDDPIEHHKHSKSCAFLSVKKQFELTLGFEFLKLDREAKNKIAKETNNK 120
 Db 61 FKELEGWEPDDDDPIEHHKHSKSCAFLSVKKQFELTLGFEFLKLDREAKNKIAKETNNK 120
 QY 121 KKEFEETAKKVRRAIEQLAAMD 142
 Db 121 KKEFEETAKKVRRAIEQLAAMD 142

RESULT 13
 AAU74573

ID AAU74573 standard; protein; 142 AA.

XX AAU74573;

XX 08-MAY-2002 (first entry)

XX Human mutant W10A survivin polypeptide.

XX Human; survivin; inhibitor of apoptosis protein; IAP; cytostatic; p21;
 KW tubulin interaction; caspase-3; CDK4; zinc chelation activity; apoptosis;
 KW dimerisation; ovary; breast; pancreas; central nervous system; blood;
 KW lung; skin; lymph node; brain; kidney; liver; nasopharyngeal cavity;
 KW thyroid; prostate; colon; rectum; cervix; endometrium; cancer; AIDS;
 KW cell proliferative disorder; acquired immunodeficiency syndrome;
 KW neurodegenerative disease; ischaemic injury; toxin-induced liver disease;
 KW myelodysplastic syndrome; protein coordinate data; mutant; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.

XX Key Location/Qualifiers

XX Misc-difference 10 /note= "Wild-type Trp substituted by Ala"

XX

XX WO200202622-A2.
 XX 10-JAN-2002.
 XX 29-JUN-2001; 2001WO-US020872.
 XX 29-JUN-2000; 2000US-00608352.
 XX (SALK) SALK INST BIOLOGICAL STUDIES.
 XX Noel JP, Verdacia M, Hunter T, Huang H;
 XX WPI; 2002-171638/22.
 XX Novel isolated crystalline survivin polypeptide, useful to screen and
 PT design compounds that bind to or interact with inhibitor of apoptosis
 PT protein and protein family members, and for design of novel therapeutics.
 XX
 XX Claim 8; Page; 102pp; English.
 XX The invention relates to an isolated crystalline human survivin
 CC polypeptide, an inhibitor or apoptosis protein (IAP). The polypeptide is
 CC useful for determining the ability of a survivin binding agent to
 CC modulate tubulin interaction, p21, caspase-3 and CDK4 requirement or zinc
 CC chelation activity and for identifying an agent such as a peptide or
 CC peptidomimetic which inhibits dimerization of survivin. The ability of an
 CC agent to modulate dimerization can be determined through detection of a
 CC change in apoptosis in a target cell expressing survivin. Binding agents
 CC are useful for increasing apoptosis in a cell derived from a tissue
 CC selected from ovary, breast, pancreas, lymph node, skin, blood, lung,
 CC brain, kidney, liver, nasopharyngeal cavity, thyroid, central nervous
 CC system, prostate, colon, rectum, cervix or endometrium, with a cell
 CC proliferative disorder such as cancer. The molecules can also be used in
 CC treatment or prevention of apoptosis which occurs as a part of AIDS,
 CC neurodegenerative diseases, ischaemic injury, toxin-induced liver disease
 CC and myelodysplastic syndromes. This sequence represents a human mutant
 CC survivin polypeptide. Note: This sequence is not featured in the printed
 CC specification but was derived from the wild type protein shown in
 CC AAU74571
 XX
 XX Sequence 142 AA;
 SQ
 Query Match 98.2%; Score 764; DB 5; Length 142;
 Best Local Similarity 99.3%; Pred. No. 2.8e-76;
 Matches 141; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MGAPTLPPAWQPFLLKDHRISTFKWPFLEGGCACTPERMAEAGFHCPTNEPDLAQCFCC 60
 DB 1 MGAPTLPPAAQPFLLKDHRISTFKWPFLEGGCACTPERMAEAGFHCPTNEPDLAQCFCC 60
 QY 61 FKELEGWEPDDDDPIEEHKHSGGCAFLSVKKQFELTLGFLKLDRAKNIKAKETNNK 120
 DB 61 FKELEGWEPDDDDPIEEHKHSGGCAFLSVKKQFELTLGFLKLDRAKNIKAKETNNK 120
 QY 121 KKEFEETAKVRRATEQLAAMD 142
 DB 121 KKEFEETAKVRRATEQLAAMD 142
 QY 121 KKEFEETAKVRRATEQLAAMD 142
 DB 121 KKEFEETAKVRRATEQLAAMD 142
 RESULT 14
 ABUS6477
 ID ABUS6477 standard; protein; 141 AA.
 XX
 XX AC ABUS6477;
 XX
 XX 02-APR-2003 (first entry)
 XX Lung cancer-associated polypeptide #70.
 DE Lung cancer-associated polypeptide; cytostatic; emphysema;
 XX anti-inflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
 KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
 KW

KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
 KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
 XX Unidentified.
 XX WO2002026443-A2.
 XX 31-OCT-2002.
 XX 18-APR-2002; 2002WO-US012476.
 XX 18-APR-2001; 2001US-0284770P.
 FR 10-MAY-2001; 2001US-0290492P.
 FR 09-NOV-2001; 2001US-0339245P.
 FR 13-NOV-2001; 2001US-0350666P.
 PR 29-NOV-2001; 2001US-0334370P.
 PR 12-APR-2002; 2002US-0372246P.
 XX (EOSB-) EOS BIOTECHNOLOGY INC.
 XX
 XX Aziz N, Murray R;
 XX WPI; 2003-093161/08.
 DR N-PSDB; ABX76199.
 XX
 XX Detecting a lung cancer-associated transcript in a cell from a patient
 PT for treating lung cancer, by contacting a biological sample from the
 PT patient with a polynucleotide that exhibits increased or decreased
 XX expression in lung cancer.
 PS Claim 27; Page 242; 453pp; English.
 XX The invention relates to a method for detecting a lung cancer-associated
 CC transcript in a cell from a patient, comprising contacting a biological
 CC sample from the patient with a polynucleotide that selectively hybridizes
 CC to a sequence that is at least 80 % identical to a gene that exhibits
 CC increased or decreased expression in lung cancer samples. Lung cancer-
 CC associated polynucleotides and polypeptides are used for identifying a
 CC compound that modulates a lung cancer-associated polypeptide, for
 CC inhibiting proliferation of a lung cancer-associated cell to treat lung
 CC cancer in a patient and for treating a mammal having lung cancer by
 CC administering a modulatory compound identified. The methods are useful
 CC for treating lung cancer, such as small cell lung cancer, non-small cell
 CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,
 CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
 CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
 CC bronchiectasis. The genes, polynucleotides and polypeptides are useful
 CC for diagnostic purposes and as targets for screening for therapeutic
 CC compounds that modulate lung cancer, such as antibodies. Sequences
 CC ABUS6408-ABUS6745 represent lung cancer-associated polypeptides of the
 CC invention
 XX
 XX Sequence 141 AA;
 SQ
 Query Match 98.0%; Score 762.5; DB 6; Length 141;
 Best Local Similarity 99.3%; Pred. No. 4e-76;
 Matches 141; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 1 MGAPTLPPAWQPFLLKDHRISTFKWPFLEGGCACTPERMAEAGFHCPTNEPDLAQCFCC 60
 DB 1 MGAPTLPPAWQPFLLKDHRISTFKWPFLEGGCACTPERMAEAGFHCPTNEPDLAQCFCC 60
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 DB 61 FKELEGWEPDDDDPIEEHKHSGGCAFLSVKKQFELTLGFLKLDRAKNIKAKETNNK 120
 QY 121 KKEFEETAKVRRATEQLAAMD 142
 DB 121 KKEFEETAKVRRATEQLAAMD 142
 RESULT 15
 AAU74576

ID AAU74576 standard; protein; 142 AA.
AC AAU74576;
XX
XX
XX 08-MAY-2002 (first entry)
XX
XX Human mutant H80A/E76A survivin polypeptide.
XX
XX Human; survivin; inhibitor of apoptosis protein; IAP; cytostatic; p21;
KW tubulin interaction; caspase-3; CDK4; zinc chelation activity; apoptosis;
KW dimerisation; ovary; breast; pancreas; central nervous system; blood;
KW lung; skin; lymph node; brain; kidney; liver; nasopharyngeal cavity;
KW thyroid; prostate; colon; rectum; cervix; endometrium; cancer; AIDS;
KW cell proliferative disorder; acquired immunodeficiency syndrome;
KW neurodegenerative disease; ischaemic injury; toxin-induced liver disease;
KW myelodysplastic syndrome; protein coordinate data; mutant; mutuin.
XX
XX Homo sapiens.
OS
OS Synthetic.
OS
XX
XX Key Location/Qualifiers
FH Misc-difference 76
FT FT /note= "Wild-type Glu substituted by Ala"
FT Misc-difference 80
FT FT /note= "Wild-type His substituted by Ala"
XX
XX WO200202622-A2.
XX
XX 10-JAN-2002.
XX
XX 29-JUN-2001; 2001WO-US020872.
XX
XX 29-JUN-2000; 2000US-00608352.
XX
XX (SALK) SALK INST BIOLOGICAL STUDIES.
XX
XX Noel JP, Verdacia M, Hunter T, Huang H;
PI WPI; 2002-171638/22.
XX
XX Novel isolated crystalline survivin polypeptide, useful to screen and
FT design compounds that bind to or interact with inhibitor of apoptosis
FT protein and protein family members, and for design of novel therapeutics.
XX
XX Claim 8; Page; 102pp; English.
XX
XX The invention relates to an isolated crystalline human survivin
CC polypeptide, an inhibitor or apoptosis protein (IAP). The polypeptide is
CC useful for determining the ability of a survivin binding agent to
CC modulate tubulin interaction, p21, caspase-3 and CDK4 requirement or zinc
CC chelation activity and for identifying an agent such as a peptide or
CC peptidomimetic which inhibits dimerisation of survivin. The ability of an
CC agent to modulate dimerisation can be determined through detection of a
CC change in apoptosis in a target cell expressing survivin. Binding agents
CC are useful for increasing apoptosis in a cell derived from a tissue
CC selected from ovary, breast, pancreas, lymph node, skin, blood, lung,
CC brain, kidney, liver, nasopharyngeal cavity, thyroid, central nervous
CC system, prostate, colon, rectum, cervix or endometrium, with a cell
CC proliferative disorder such as cancer. The molecules can also be used in
CC treatment or prevention of apoptosis which occurs as a part of AIDS,
CC neurodegenerative diseases, ischaemic injury, toxin-induced liver disease
CC and myelodysplastic syndromes. This sequence represents a human mutant
CC survivin polypeptide. Note: This sequence is not featured in the printed
CC specification but was derived from the wild type protein shown in
XX AAU74571
XX
XX Sequence 142 AA;
XX
XX Query Match 97.9%; Score 762; DB 5; Length 142;
XX Best Local Similarity 98.6%; Pred. No. 4.6e-76;
XX Matches 140; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1 MGAPILPPAWQPFLLKDHRISTFKWPFLEGGCACTPERMAEAGFIHCPTENEPDLAQCFPC 60

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GenCore version 5.1.6
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OM protein - protein search, using sw_model

Run on: August 11, 2004, 14:17:11 ; Search time 46 Seconds
(without alignments)
969.079 Million call updates/sec

Title: US-09-690-825-34
Perfect score: 778
Sequence: 1 MGAPLPPAWQPLKDHRS.....EFETAKKVRRAIEQLAAMD 142

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1292805 seqs, 313927144 residues

Total number of hits satisfying chosen parameters: 1292805

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
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11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
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14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	778	100.0	142	14	US-10-138-618-34
2	778	100.0	142	16	US-10-665-975-2
3	774	99.5	142	16	US-10-408-765A-2210
4	562	72.2	98	9	US-09-965-967-23
5	155	19.9	1403	8	US-08-913-322-22
6	155	19.9	1403	8	US-08-913-322-24
7	155	19.9	1403	14	US-10-285-408-1
8	151.5	19.5	172	14	US-10-041-859-8
9	148.5	19.1	172	14	US-10-041-859-10
10	148.5	18.7	172	14	US-10-041-859-11
11	144.5	18.6	172	14	US-10-041-859-12
12	143	18.4	346	14	US-10-041-859-2
13	139.5	17.9	127	12	US-10-424-539-246508
14	138.5	17.8	172	14	US-10-041-859-9
15	138	17.7	355	14	US-10-203-708-44

16	137	17.6	464	12	US-10-343-115-2	Sequence 2, Appl
17	136.5	17.5	68	14	US-10-041-859-14	Sequence 14, Appl
18	136.5	17.5	275	9	US-09-201-936-12	Sequence 12, Appl
19	136.5	17.5	275	14	US-10-323-643-9	Sequence 9, Appl
20	136.5	17.5	280	14	US-10-244-586-3	Sequence 3, Appl
21	136.5	17.5	298	14	US-10-235-026-2	Sequence 2, Appl
22	133.5	17.2	268	14	US-10-323-643-10	Sequence 10, Appl
23	132.5	17.0	68	9	US-09-201-936-29	Sequence 29, Appl
24	132.5	17.0	68	14	US-10-041-859-17	Sequence 17, Appl
25	131.5	16.9	68	9	US-09-201-936-28	Sequence 28, Appl
26	131.5	16.9	68	14	US-10-041-859-16	Sequence 16, Appl
27	131.5	16.9	68	14	US-10-041-859-18	Sequence 18, Appl
28	131	16.8	618	9	US-09-974-592-8	Sequence 8, Appl
29	131	16.8	618	9	US-09-201-936-8	Sequence 8, Appl
30	131	16.8	618	12	US-10-361-270-3	Sequence 3, Appl
31	131	16.8	618	12	US-10-260-708-63	Sequence 63, Appl
32	131	16.8	618	12	US-10-366-307-4	Sequence 4, Appl
33	131	16.8	618	14	US-10-153-668-338	Sequence 338, App
34	131	16.8	618	14	US-10-207-658-200	Sequence 200, App
35	131	16.8	618	14	US-10-232-286-2	Sequence 2, Appl
36	131	16.8	618	16	US-10-636-065-223	Sequence 223, App
37	130	16.7	236	12	US-10-024-433-2	Sequence 2, Appl
38	129.5	16.6	68	9	US-09-201-936-20	Sequence 20, Appl
39	129.5	16.6	496	9	US-09-974-592-10	Sequence 10, Appl
40	129.5	16.6	496	9	US-09-201-936-10	Sequence 10, Appl
41	129.5	16.6	496	16	US-10-636-085-225	Sequence 225, App
42	129.5	16.6	612	9	US-09-974-592-14	Sequence 14, Appl
43	129.5	16.6	612	14	US-10-232-286-14	Sequence 14, Appl
44	128	16.5	67	9	US-09-201-936-23	Sequence 23, Appl
45	128	16.5	148	10	US-09-764-861-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1
US-10-138-618-34
; Sequence 34, Application US/10138618
; Publication No. US20030100525A1
; GENERAL INFORMATION:
; APPLICANT: Altieri, Dario C.
; TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
; CELLULAR APOPTOSIS, AND ITS MODULATION
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
; STREET: 1800 M Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5869
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10138,618
; FILING DATE: 06-May-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/975,080
; FILING DATE: 20-NOV-1997
; APPLICATION NUMBER: US 60/031,435
; FILING DATE: 20-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler, Reid G.
; REGISTRATION NUMBER: 30,988
; REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-467-7000
; TELEFAX: 202-467-7176
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:

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;
; LENGTH: 142 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-10-138-618-34

Query Match          100.0%; Score 778; DB 14; Length 142;
Best Local Similarity 100.0%; Pred. No. 1.1e-72;
Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAPTLPPAWQPFLLKDHRISTFKNWPFLGCGACTPMAEAGFIHCPTENEPDLAQCFFC 60
DB 1 MGAPTLPPAWQPFLLKDHRISTFKNWPFLGCGACTPMAEAGFIHCPTENEPDLAQCFFC 60

QY 61 FKELEGWEPDDPIEEHKKHSSGCAFLSVKKQFEEITLGEFLKLDRAKKNIAKETNNK 120
DB 61 FKELEGWEPDDPIEEHKKHSSGCAFLSVKKQFEEITLGEFLKLDRAKKNIAKETNNK 120

QY 121 KKEFEETAKKVRRAIEQLAAMD 142
DB 121 KKEFEETAKKVRRAIEQLAAMD 142

RESULT 2
US-10-665-975-2
; Sequence 2, Application US/10665975
; Publication No. US20040138119A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Tamm, Ingo
; TITLE OF INVENTION: USE OF HEPATITIS VIRUS B X-INTERACTING
; TITLE OF INVENTION: PROTEIN (HBXIP) IN MODULATION OF APOPTOSIS
; FILE REFERENCE: BURNHAM.C05A
; CURRENT APPLICATION NUMBER: US/10/665,975
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: 60/412,109
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-665-975-2

Query Match          100.0%; Score 778; DB 16; Length 142;
Best Local Similarity 100.0%; Pred. No. 1.1e-72;
Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAPTLPPAWQPFLLKDHRISTFKNWPFLGCGACTPMAEAGFIHCPTENEPDLAQCFFC 60
DB 1 MGAPTLPPAWQPFLLKDHRISTFKNWPFLGCGACTPMAEAGFIHCPTENEPDLAQCFFC 60

QY 61 FKELEGWEPDDPIEEHKKHSSGCAFLSVKKQFEEITLGEFLKLDRAKKNIAKETNNK 120
DB 61 FKELEGWEPDDPIEEHKKHSSGCAFLSVKKQFEEITLGEFLKLDRAKKNIAKETNNK 120

QY 121 KKEFEETAKKVRRAIEQLAAMD 142
DB 121 KKEFEETAKKVRRAIEQLAAMD 142

RESULT 3
US-10-408-765A-2210
; Sequence 2210, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Rahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
```

```
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2210
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-2210

Query Match          99.5%; Score 774; DB 16; Length 142;
Best Local Similarity 99.3%; Pred. No. 2.8e-72;
Matches 141; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAPTLPPAWQPFLLKDHRISTFKNWPFLGCGACTPMAEAGFIHCPTENEPDLAQCFFC 60
DB 1 MGAPTLPPAWQPFLLKDHRISTFKNWPFLGCGACTPMAEAGFIHCPTENEPDLAQCFFC 60

QY 61 FKELEGWEPDDPIEEHKKHSSGCAFLSVKKQFEEITLGEFLKLDRAKKNIAKETNNK 120
DB 61 FKELEGWEPDDPIEEHKKHSSGCAFLSVKKQFEEITLGEFLKLDRAKKNIAKETNNK 120

QY 121 KKEFEETAKKVRRAIEQLAAMD 142
DB 121 KKEFEETAKKVRRAIEQLAAMD 142

RESULT 4
US-09-965-967-23
; Sequence 23, Application US/09965967
; Patent No. US20020177557A1
; GENERAL INFORMATION:
; APPLICANT: Shi, Yigong
; TITLE OF INVENTION: Compositions And Methods For Regulating Apoptosis
; FILE REFERENCE: PU-0031 (01-1739-1)
; CURRENT APPLICATION NUMBER: US/09/965,967
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: 60/236,574
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/256,830
; PRIOR FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-965-967-23

Query Match          72.2%; Score 562; DB 9; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.8e-50;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAPTLPPAWQPFLLKDHRISTFKNWPFLGCGACTPMAEAGFIHCPTENEPDLAQCFFC 60
DB 1 MGAPTLPPAWQPFLLKDHRISTFKNWPFLGCGACTPMAEAGFIHCPTENEPDLAQCFFC 60

QY 61 FKELEGWEPDDPIEEHKKHSSGCAFLSVKKQFEEITL 98
DB 61 FKELEGWEPDDPIEEHKKHSSGCAFLSVKKQFEEITL 98

RESULT 5
US-08-913-322-22
; Sequence 22, Application US/08913322
; Publication No. US20020137028A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Korneluk, Robert G.
; APPLICANT: MacKenzie, Alexander E.
; APPLICANT: Roy, Natalie
; APPLICANT: Robertson, George
; APPLICANT: Tamal, Katsu
; TITLE OF INVENTION: USER OF NEURONAL APOPTOSIS INHIBITOR
; FILE REFERENCE: 07891/013001
; CURRENT APPLICATION NUMBER: US/08/913,322
; CURRENT FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: PCT/IB97/00142
; EARLIER FILING DATE: 1997-01-17
; EARLIER APPLICATION NUMBER: GB 9601108.5
; EARLIER FILING DATE: 1996-01-19
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 1403
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-913-322-22

Query Match          19.9%; Score 155; DB 8; Length 1403;
Best Local Similarity 40.5%; Pred. No. 8,1e-07;
Matches 34; Conservative 15; Mismatches 29; Indels 6; Gaps 3;

QY      15 KDRHSIFKNWPF-LESCATCPREMAEAGFHCPTNEEDLAQCFCFKELEGNEPDDDP 73
Db      159 EARLARISNNFFVQG--ISPCVLSEAGFVF---TGKODTVQCFSCGGCLGNWEEGDDP 213
QY      74 IEEKXHSGCCAFLSVVKQFEELT 97
Db      214 WKERAKWPKCFERLSKKSSSEET 237

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RESULT 6
US-08-913-322-24
; Sequence 24, Application US/08913322
; Publication No. US20020137028A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Roy, Natalie
; APPLICANT: Robertson, George
; APPLICANT: Tamai, Katsu
; TITLE OF INVENTION: USER OF NEURONAL APOPTOSIS INHIBITOR
; TITLE OF INVENTION: (NAIP)
; FILE REFERENCE: 07891/013001
; CURRENT APPLICATION NUMBER: US/08/913,322
; CURRENT FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: PCT/IB97/00142
; EARLIER FILING DATE: 1997-01-17
; EARLIER APPLICATION NUMBER: GB 9601108.5
; EARLIER FILING DATE: 1996-01-19
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 1403
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-913-322-24

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Query Match      19.9%; Score 155; DB 8; Length 1403;
Best Local Similarity 40.5%; Pred. No. 8.le=07;
Matches 34; Conservative 15; Mismatches 29; Indels 6; Gaps 3;

QY 15 KDHRISTPKWPF-LEGCACTPERMAAGFIHCPTENEPDLAQCFCKLEGWEPDDP 73
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DB 159 EARLARLSRNPFYVQ--TSPCVLSEAGVF---TGKQDTVQCFCSCGCLGNWEGGDP 213
   ..:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 74 IEHKHSHSGCARLSVKVQPEELT 97
   ..:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Db 214 WKERAKWPKCEFLRSKKSSEIT 237
   ..:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

```

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RESULT 7
US-10-285-408-1
; sequence 1, Application US/10285408
; Publication No. US20030108967A1
; GENERAL INFORMATION:
; APPLICANT: IKEDA, Johe
; APPLICANT: SAKAI, Harumi
; TITLE OF INVENTION: Monoclonal Antibodies Against Human Apoptosis Inhibitory Protein 1
; TITLE OF INVENTION: and Method For Assaying the NAIP
; FILE REFERENCE: 2002-1440/MMC/00653
; CURRENT APPLICATION NUMBER: US/10/285,408
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: 09/830,338
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: PCT/JP99/05841
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 1403
; TYPE: PRN
; ORGANISM: Homo sapiens
US-10-285-408-1

Query Match          19.9%; Score 155; DB 14; Length 1403;
Best Local Similarity 40.5%; Pred. No. 8.1e-07;
Matches 34; Conservative 15; Mismatches 29; Indels 6; Gaps 3;

Oy      15 KDHISIFKNWPP-LESCACTPERMAGATHICPTENEPDLACQCFCKELEGWEPPDDP 73
       ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db       15G BEALKASRNWPFYVQG--ISPCLVLSEAGVF---TGKQDTVCQFCGGCLGNWEGDDP 213
       ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Oy      74 IEHHKHSSGCATLSVKKKOFEEIT 97
       :::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db     214 WKHAKWPCKCEFLRSKKSSEIIT 237
       :::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

```

```

RESULT 8
US-10-041-859-8
; Sequence 8, Application US/10041859
; Publication No. US20030049796A1
; GENERAL INFORMATION:
; APPLICANT: HUANG, QIHONG
; APPLICANT: REED, JOHN C.
; APPLICANT: DEVERAUX, QUINN L.
; APPLICANT: MAEDA, SUSUMU
; TITLE OF INVENTION: INHIBITOR OF APOPTOSIS PROTEINS AND NUCLEIC ACIDS AND
; TITLE OF INVENTION: METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 087102/027 2537
; CURRENT APPLICATION NUMBER: US/10/041.859
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,478
; PRIOR FILING DATE: 2001-01-08
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Bombyx mori
US-10-041-859-8

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Query Match	19.5%	Score 151.5	DB 14	Length 172
Best Local Similarity	36.9%	Pred. No. 1.4e-07		
Matches	31	Conservative 16	Mismatches 33	Indels 5 Gaps 2
QY	12	PFLKDRHISTKQWPTLEGACATPERMAAGPIHCTENEPDLAQCFPCFKEGWEPPD	71	
DB	65	PVEEARLATFKDWP--RRMRQKPELABAGFFY--TGQGDKTCFYCGGLKDWESDD	119	
QY	72	DPBEHKHSGGCAFLSVKKQFEE	95	
DB	120	VPVECHARNWEDRCAYVLCKICYSE	143	

RESULT 9

US-10-041-859-10

; Sequence 10, Application US/10041859

; Publication No. US20030049796A1

; GENERAL INFORMATION:

; APPLICANT: HUANG, QIHONG

; APPLICANT: REED, JOHN C.

; APPLICANT: DEVERAUX, QUINN L.

; APPLICANT: MAEDA, SUSUMU

; TITLE OF INVENTION: INHIBITOR OF APOPTOSIS PROTEINS AND NUCLEIC ACIDS AND

; FILE REFERENCE: 087102/027 2537

; CURRENT APPLICATION NUMBER: US/10/041,859

; PRIOR FILING DATE: 2002-01-07

; PRIOR APPLICATION NUMBER: 60/260,478

; PRIOR FILING DATE: 2001-01-08

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 10

; LENGTH: 172

; TYPE: PRT

; ORGANISM: Trichoplusia ni

US-10-041-859-10

Query Match

Best Local Similarity 19.1%; Score 148.5; DB 14; Length 172;

Matches 32; Conservative 15; Mismatches 29; Indels 11; Gaps 3;

QY 12 PFLKDHRISTFKNWFLEGGAC---TPERMAEAGFIHCPTENEPDLAQCFKKELEGWE 68

Db 65 PFVEAARLRSFNDP-----RCMRQKPEELAEAGFFY---TGQGDTKCFYCDGGLKDW 116

QY 69 PDDPIEHHKSHSGCAFLSVKQFEE 95

Db 117 NDDVPWEQHWDFRCAYVLCKICFAE 143

RESULT 10

US-10-041-859-11

; Sequence 11, Application US/10041859

; Publication No. US20030049796A1

; GENERAL INFORMATION:

; APPLICANT: HUANG, QIHONG

; APPLICANT: REED, JOHN C.

; APPLICANT: DEVERAUX, QUINN L.

; APPLICANT: MAEDA, SUSUMU

; TITLE OF INVENTION: INHIBITOR OF APOPTOSIS PROTEINS AND NUCLEIC ACIDS AND

; FILE REFERENCE: 087102/027 2537

; CURRENT APPLICATION NUMBER: US/10/041,859

; PRIOR FILING DATE: 2002-01-07

; PRIOR APPLICATION NUMBER: 60/260,478

; PRIOR FILING DATE: 2001-01-08

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 11

; LENGTH: 172

; TYPE: PRT

; ORGANISM: Cydia pomonella granulovirus

US-10-041-859-11

Query Match

Best Local Similarity 18.7%; Score 145.5; DB 14; Length 172;

Matches 30; Conservative 15; Mismatches 26; Indels 11; Gaps 3;

QY 12 PFLKDHRISTFKNWFLEGGAC---TPERMAEAGFIHCPTENEPDLAQCFKKELEGWE 68

Db 65 PFVEAARLRSFNDP-----RCMRQKPEELAEAGFFY---TGQGDTKCFYCDGGLKDW 116

QY 69 PDDPIEHHKSHSGCAFLSVKQFEE 90

Db 117 PEDVPWEQHWDFRCAYVLCK 138

RESULT 11

US-10-041-859-12

; Sequence 12, Application US/10041859

; Publication No. US20030049796A1

; GENERAL INFORMATION:

; APPLICANT: HUANG, QIHONG

; APPLICANT: REED, JOHN C.

; APPLICANT: DEVERAUX, QUINN L.

; APPLICANT: MAEDA, SUSUMU

; TITLE OF INVENTION: INHIBITOR OF APOPTOSIS PROTEINS AND NUCLEIC ACIDS AND

; FILE REFERENCE: 087102/027 2537

; CURRENT APPLICATION NUMBER: US/10/041,859

; PRIOR FILING DATE: 2002-01-07

; PRIOR APPLICATION NUMBER: 60/260,478

; PRIOR FILING DATE: 2001-01-08

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 12

; LENGTH: 172

; TYPE: PRT

; ORGANISM: Orgyia pseudotsugata

US-10-041-859-12

Query Match

Best Local Similarity 18.6%; Score 144.5; DB 14; Length 172;

Matches 29; Conservative 13; Mismatches 32; Indels 5; Gaps 2;

QY 12 PFLKDHRISTFKNWFLEGGACCTPERMAEAGFIHCPTENEPDLAQCFKKELEGWE 71

Db 65 PFVEAARLRSFNDP-----RCMRQKPEELAEAGFFY---TGQGDTKCFYCDGGLKDW 119

QY 72 DPIEHHKSHSGCAFLSVK 90

Db 120 APWQHARWYDRCEYVLCK 138

RESULT 12

US-10-041-859-2

; Sequence 2, Application US/10041859

; Publication No. US20030049796A1

; GENERAL INFORMATION:

; APPLICANT: HUANG, QIHONG

; APPLICANT: REED, JOHN C.

; APPLICANT: DEVERAUX, QUINN L.

; TITLE OF INVENTION: INHIBITOR OF APOPTOSIS PROTEINS AND NUCLEIC ACIDS AND

; FILE REFERENCE: 087102/027 2537

; CURRENT APPLICATION NUMBER: US/10/041,859

; PRIOR FILING DATE: 2002-01-07

; PRIOR APPLICATION NUMBER: 60/260,478

; PRIOR FILING DATE: 2001-01-08

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

; LENGTH: 346

; TYPE: PRT

; ORGANISM: Bombyx mori

US-10-041-859-2

Query Match

Best Local Similarity 18.4%; Score 143; DB 14; Length 346;

Matches 35; Conservative 22; Mismatches 46; Indels 14; Gaps 4;

QY 18 RISTFKNWFLEGGACCTPERMAEAGFIHCPTENEPDLAQCFKKELEGWE 77

Db 185 RLATFKDWP---RRMRQKPEELAEAGFFY---TGQGDTKCFYCDGGLKDW 239

QY 78 KKHSSGCAFLSVKQFEEFLKIDPERAKNTAKP---TNNKKKFFETAPK 120

Db 240 ARWDFRCAYVQVKGRIYQ-----KVKSEATAISASEEEQAATNDSTKRWAGEGK 291

RESULT 13

US-10-424-599-246508
; Sequence 246508, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalick David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; PRIOR APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 246508
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_64628C.1.pep
US-10-424-599-246508

Query Match 17.9%; Score 139.5; DB 12; Length 127;
Best Local Similarity 27.0%; Pred. No. 1.7e-06;
Matches 31; Conservative 21; Mismatches 46; Indels 17; Gaps 3;
Qy 18 RISTFX---NWPELEGCACTPERVABAGFIHCPTENEPDLAQCFCKELGWP-DDD 72
Db 10 RIKYKGRKNKWPYKRDTPVLDKLAAGFIHKPLSNHTDNVECFCLCETAVNGWDSHDND 69
Qy 73 PIEBKHSSCAFLSVKKOFELTLGFLKDRANKIAKTNKKKEPET 127
Db 70 PFRRHIOHAPACAWML-----ICVARGRPVSLDSSGVNQQNPDST 112

RESULT 14

US-10-041-859-9
; Sequence 9, Application US/10041859
; Publication No. US20030049796A1
; GENERAL INFORMATION:
; APPLICANT: HUANG, QIHONG
; APPLICANT: REED, JOHN C.
; APPLICANT: DEVERAUX, QUINN L.
; APPLICANT: MAEDA, SUSUMU
; TITLE OF INVENTION: INHIBITOR OF APOPTOSIS PROTEINS AND NUCLEIC ACIDS AND
; TITLE OF INVENTION: METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 087102/027 2537
; CURRENT APPLICATION NUMBER: US/10/041,859
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,478
; PRIOR FILING DATE: 2001-01-08
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 9
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Spodoptera frugiperda
US-10-041-859-9

Query Match 17.8%; Score 138.5; DB 14; Length 172;
Best Local Similarity 34.5%; Pred. No. 3.2e-06;
Matches 30; Conservative 16; Mismatches 30; Indels 11; Gaps 3;
Qy 12 PFLKDHRISTPKNWPFLGGAC---TPERABAGFIHCPTENEPDLAQCFCKELGWE 68
Db 65 PFVEAARLSPKDPF-----RCWPKPELAAGFFY---TGGDKTKGFCYDGLKWE 116
Qy 69 PDDDPBIEBKHSSGCAFLSVKKQFEE 95

Db 117 NHDVPWEQHARWDFRCAYVLCIKCYAE 143

RESULT 15

US-10-203-708-44
; Sequence 44, Application US/10203708
; Publication No. US20030149238A1
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; APPLICANT: SMITHKLINE BEECHAM P.L.C.
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50013
; CURRENT APPLICATION NUMBER: US/10/203,708
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/04703
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/182,172
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 60/186,084
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 44
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-203-708-44

Query Match 17.7%; Score 138; DB 14; Length 355;
Best Local Similarity 32.7%; Pred. No. 8.7e-06;
Matches 33; Conservative 14; Mismatches 38; Indels 16; Gaps 4;
Qy 18 RISTFKNWPFLGCACTPERVABAGFIHCPTENEPDLAQCFCKELGWPDDDDPIEEH 77
Db 90 RLASFVDWELT--AEVFPPELLAAAGFFH---TGHQDKVRCFCYGLQSWKRGDDPWTEH 144
Qy 78 KHSSSGCAFL-----SVKKOFELTLGFLKDRER 108
Db 145 AKWFPSCQFLRSKGRDFVHSVQETHSQL-LGSMYSATSPR 184

Search completed: August 11, 2004, 14:22:45
Job time : 47 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 11, 2004, 14:14:55 ; Search time 19 Seconds
(without alignments)
385.836 Million cell updates/sec

Title: US-09-690-825-34
Perfect score: 778
Sequence: 1 MGAPTLPPAWQPFKDHRISTFKNWPFLEGGCACTPERMAEAGFIHCPTNEPDLAQCFEC 142

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51525971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A COMB.pcp.*
2: /cgn2_6/ptodata/2/iaa/5B COMB.pcp.*
3: /cgn2_6/ptodata/2/iaa/6A COMB.pcp.*
4: /cgn2_6/ptodata/2/iaa/6B COMB.pcp.*
5: /cgn2_6/ptodata/2/iaa/PCRIUS COMB.pcp.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	778	100.0	142	3	US-08-975-080-34
2	778	100.0	142	4	US-09-283-144-3
3	246.5	31.7	153	4	US-09-738-946-4
4	219	28.1	137	4	US-09-283-144-15
5	155	19.9	1151	3	US-08-836-134-23
6	155	19.9	1151	4	US-09-493-784-23
7	155	19.9	1232	3	US-08-836-134-2
8	155	19.9	1232	4	US-09-493-784-2
9	155	19.9	1295	4	US-09-705-872-3
10	155	19.9	1403	4	US-09-705-872-1
11	140	18.0	75	4	US-08-557-759-22
12	136.5	17.5	275	2	US-08-511-485-12
13	136.5	17.5	275	3	US-08-836-134-21
14	136.5	17.5	275	4	US-09-493-784-21
15	136.5	17.5	275	4	US-09-201-936-12
16	136.5	17.5	275	4	US-09-011-356-12
17	136.5	17.5	298	4	US-09-127-928-2
18	136.5	17.5	377	4	US-09-502-528-3
19	133.5	17.2	268	3	US-08-836-134-22
20	133.5	17.2	268	4	US-09-493-784-22
21	132.5	17.0	68	2	US-08-511-485-29
22	132.5	17.0	68	4	US-09-201-936-29
23	132.5	17.0	68	4	US-09-011-356-29
24	131.5	16.9	68	2	US-08-511-485-28
25	131.5	16.9	68	4	US-09-201-936-28
26	131.5	16.9	68	4	US-09-011-356-28
27	131	16.8	618	2	US-08-511-485-8

28	131	16.8	618	3	US-09-212-971-8	Sequence 8, Appl
29	131	16.8	618	3	US-08-800-929A-8	Sequence 8, Appl
30	131	16.8	618	3	US-08-569-749-2	Sequence 2, Appl
31	131	16.8	618	4	US-09-617-053A-8	Sequence 8, Appl
32	131	16.8	618	4	US-09-069-023-29	Sequence 29, Appl
33	131	16.8	618	4	US-09-201-936-8	Sequence 8, Appl
34	131	16.8	618	4	US-09-011-356-8	Sequence 8, Appl
35	131	16.8	618	4	US-09-672-717-223	Sequence 223, App
36	131	16.8	618	5	PCT-US96-12860-2	Sequence 2, Appl
37	130	16.7	236	3	US-09-121-979-4	Sequence 4, Appl
38	130	16.7	236	3	US-09-332-319-4	Sequence 2, Appl
39	130	16.7	236	4	US-09-239-867-2	Sequence 2, Appl
40	129.5	16.6	68	2	US-08-511-485-20	Sequence 20, Appl
41	129.5	16.6	68	4	US-09-201-936-20	Sequence 20, Appl
42	129.5	16.6	68	4	US-09-011-356-20	Sequence 20, Appl
43	129.5	16.6	496	2	US-08-511-485-10	Sequence 10, Appl
44	129.5	16.6	496	3	US-09-212-971-10	Sequence 10, Appl
45	129.5	16.6	496	3	US-08-800-929A-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-08-975-080-34
; Sequence 34, Application US/08975080
; Patent No. 6245523
; GENERAL INFORMATION:
; APPLICANT: Altieri, Dario C.
; TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
; CELLULAR APOPTOSIS, AND ITS MODULATION
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
; STREET: 1800 M Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5869
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,080
; FILING DATE: 20-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/031,435
; FILING DATE: 20-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler, Reid G.
; REGISTRATION NUMBER: 30,988
; REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-467-7000
; TELEFAX: 202-467-7176
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 142 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-975-080-34

Query Match 100.0%; Score 778; DB 3; Length 142;
Best Local Similarity 100.0%; Pred. No. 1e-79;
Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGAPTLPPAWQPFKDHRISTFKNWPFLEGGCACTPERMAEAGFIHCPTNEPDLAQCFEC 60
DB 1 MGAPTLPPAWQPFKDHRISTFKNWPFLEGGCACTPERMAEAGFIHCPTNEPDLAQCFEC 60

Qy	61	FKELEGEWEPDDPIBEHKHSGGCAFJSVKQFELTIGFLKIDREAKNKIaketNNK	120
Db	61	FKELEGEWEPDDPIBEHKHSGGCAFJSVKQFELTIGFLKIDREAKNKIaketNNK	120
Qy	121	KKEFEETAKKVRAIEQLAAMD	142
Db	121	KKEFEETAKKVRAIEQLAAMD	142

```

RESULT 2
US-09-283-144-3
; Sequence 3, Application US/092831144
; Patent No. 6346389
; GENERAL INFORMATION:
; APPLICANT: Yale University
; TITLE OF INVENTION: Method for Selectively Modulating the Interactions
; TITLE OF INVENTION: between Survivin and Tubulin
; FILE REFERENCE: 44574-5033-US
; CURRENT APPLICATION NUMBER: US/09/283,144
; CURRENT FILING DATE: 1999-04-01
; EARLIER APPLICATION NUMBER: US 60/080,288
; EARLIER FILING DATE: 1998-04-01
; EARLIER APPLICATION NUMBER: US 08/975,080
; EARLIER FILING DATE: 1997-11-20
; EARLIER APPLICATION NUMBER: PCT/US97/21880
; EARLIER FILING DATE: 1997-11-20
; EARLIER APPLICATION NUMBER: US 60/031,435
; EARLIER FILING DATE: 1996-11-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of Survivin
; US-09-283-144-3

```

RESULT 3
 US-09-738-946-4
 ; Sequence 4, Application US/09738946
 ; Patent No. 6579701
 ; GENERAL INFORMATION:
 ; APPLICANT: EXELIXIS, INC.
 ; TITLE OF INVENTION: DROSOPHILA HOMOLOGUES OF GENES AND PROTEINS IMPLICATED IN CANCER
 ; TITLE OF INVENTION: METHODS OF USE
 ; FILE REFERENCE: EX00-043C
 ; CURRENT APPLICATION NUMBER: US/09/738,946
 ; CURRENT FILING DATE: 2000-12-14
 ; PRIOR APPLICATION NUMBER: 60/170,832
 ; PRIOR FILING DATE: 1999-12-14
 ; PRIOR APPLICATION NUMBER: 60/170,838
 ; PRIOR FILING DATE: 1999-12-14
 ; PRIOR APPLICATION NUMBER: 60/178,580
 ; PRIOR FILING DATE: 2000-01-28

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; PRIOR APPLICATION NUMBER: 60/185,879
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/185,880
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/186,150
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/189,701
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent version 3.0
; SEQ ID NO 4
; LENGTH: 153
; TYPE: PRF
; ORGANISM: Drosophila melanogaster
US-09-738-946-4

Query Match          31.7%;   Score 246.5;   DB 4;   Length 153;
Best Local Similarity 40.3%;   Pred.No. 5.4e-20;
Matches 48; Conservative 20; Mismatches 50; Indels 1; Gaps 1;

Qy 14 LKHRISTFKNWPFLGCACCTPERMAEAGIHCFCTENEPDLAQOFFCKBLEGWEPDDP 73
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 27 LEQHRVSVKSWPPETASCSISKMFAEGFWTGTKEENTATCFVCVKTLDGWEPDDP 86
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

Qy 74 IEEHKHSSCCALSVKKQKFEBLTLGBFLKLDRERAKNTAKETNNKKKPF-BETAKV 131
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 87 WKEHVHAPQCEFAKUSCPERNLTVSQFLBILGTVVKGSIEKTCKAFKFSFVRENEKRLL 145

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RESULT 4
US-09-283-144-15
; Sequence 15, Application US/09283144
; Patent No. 6346389
; GENERAL INFORMATION:
; APPLICANT: Yale University
; TITLE OF INVENTION: Method for Selectively Modulating the Interactions
; TITLE OF INVENTION: between Survivin and Tubulin
; FILE REFERENCE: 44574-5033-US
; CURRENT APPLICATION NUMBER: US/09/283,144
; CURRENT FILING DATE: 1999-04-01
; EARLIER APPLICATION NUMBER: US 60/080,288
; EARLIER FILING DATE: 1998-04-01
; EARLIER APPLICATION NUMBER: US 08/975,080
; EARLIER FILING DATE: 1997-11-20
; EARLIER APPLICATION NUMBER: PCT/US97/21880
; EARLIER FILING DATE: 1997-11-20
; EARLIER APPLICATION NUMBER: US 60/031,435
; EARLIER FILING DATE: 1996-11-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Amino acid sequence from beginning of coding region of
; OTHER INFORMATION: Survivin gene
US-09-283-144-15

```

RESULT 5
US-08-836-134-23
; Sequence 23, Application US/08836134A
; Patent No. 6020127
; GENERAL INFORMATION:

APPLICANT: Mackenzie, Alex E.
APPLICANT: Korneluk, Robert G.
APPLICANT: Mahadevan, Mani S.
APPLICANT: McLean, Michael
APPLICANT: Roy, Natalie
APPLICANT: Ikeda, John-e
TITLE OF INVENTION: Neuronal Apoptosis Inhibitor Protein, Gene Sequence and
Patent No. 6020127
TITLE OF INVENTION: Mutations Causative of Spinal Muscular Atrophy
FILE REFERENCE: 3477-112, 033477/139914
CURRENT APPLICATION NUMBER: US/08/836,134A
CURRENT FILING DATE: 1997-06-20
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 23
LENGTH: 1151
TYPE: PRT
ORGANISM: Homo sapiens
US-08-836-134-23

Query Match 19.9%; Score 155; DB 3; Length 1151;
Best Local Similarity 40.5%; Pred. No. 1.4e-08;
Matches 34; Conservative 15; Mismatches 29; Indels 6; Gaps 3;
QY 15 KDHRISTFKWPF-LEGCACTPERMAEAGFIHCPTENEPDLAQCFKCELEGEWEPDDDP 73
DB 168 EEARLASFRNWPFFVQ--ISPCVLSEAGFV---TGKQDTVQCFCGCGCLGNWEEGDDP 222
QY 74 IEHKKHSSGCALSVKQFEELT 97
DB 223 WKEHAKWFPKCEFLRSKKSSEIT 246

RESULT 6
US-09-493-784-23
Sequence 23, Application US/09493784
Patent No. 6429011
GENERAL INFORMATION:
APPLICANT: Mackenzie, Alex E.
APPLICANT: Korneluk, Robert G.
APPLICANT: Mahadevan, Mani S.
APPLICANT: McLean, Michael
APPLICANT: Roy, Natalie
APPLICANT: Ikeda, John-e
TITLE OF INVENTION: Neuronal Apoptosis Inhibitor Protein, Gene Sequence and
Patent No. 6429011
TITLE OF INVENTION: Mutations Causative of Spinal Muscular Atrophy
FILE REFERENCE: 3477-112, 033477/139914
CURRENT APPLICATION NUMBER: US/09/493,784
CURRENT FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 08/836,134
PRIOR FILING DATE: 1997-06-20
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 23
LENGTH: 1151
TYPE: PRT
ORGANISM: Homo sapiens
US-09-493-784-23

Query Match 19.9%; Score 155; DB 4; Length 1151;
Best Local Similarity 40.5%; Pred. No. 1.4e-08;
Matches 34; Conservative 15; Mismatches 29; Indels 6; Gaps 3;
QY 15 KDHRISTFKWPF-LEGCACTPERMAEAGFIHCPTENEPDLAQCFKCELEGEWEPDDDP 73
DB 168 EEARLASFRNWPFFVQ--ISPCVLSEAGFV---TGKQDTVQCFCGCGCLGNWEEGDDP 222
QY 74 IEHKKHSSGCALSVKQFEELT 97
DB 223 WKEHAKWFPKCEFLRSKKSSEIT 246

RESULT 7
US-08-836-134-2
Sequence 2, Application US/08836134A
Patent No. 6020127
GENERAL INFORMATION:
APPLICANT: Mackenzie, Alex E.
APPLICANT: Korneluk, Robert G.
APPLICANT: Mahadevan, Mani S.
APPLICANT: McLean, Michael
APPLICANT: Roy, Natalie
APPLICANT: Ikeda, John-e
TITLE OF INVENTION: Neuronal Apoptosis Inhibitor Protein, Gene Sequence and
Patent No. 6020127
TITLE OF INVENTION: Mutations Causative of Spinal Muscular Atrophy
FILE REFERENCE: 3477-112, 033477/139914
CURRENT APPLICATION NUMBER: US/08/836,134A
CURRENT FILING DATE: 1997-06-20
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 1232
TYPE: PRT
ORGANISM: Homo sapiens
US-08-836-134-2

Query Match 19.9%; Score 155; DB 3; Length 1232;
Best Local Similarity 40.5%; Pred. No. 1.5e-08;
Matches 34; Conservative 15; Mismatches 29; Indels 6; Gaps 3;
QY 15 KDHRISTFKWPF-LEGCACTPERMAEAGFIHCPTENEPDLAQCFKCELEGEWEPDDDP 73
DB 159 EEARLASFRNWPFFVQ--ISPCVLSEAGFV---TGKQDTVQCFCGCGCLGNWEEGDDP 213
QY 74 IEHKKHSSGCALSVKQFEELT 97
DB 214 WKEHAKWFPKCEFLRSKKSSEIT 237

RESULT 8
US-09-493-784-2
Sequence 2, Application US/09493784
Patent No. 6429011
GENERAL INFORMATION:
APPLICANT: Mackenzie, Alex E.
APPLICANT: Korneluk, Robert G.
APPLICANT: Mahadevan, Mani S.
APPLICANT: McLean, Michael
APPLICANT: Roy, Natalie
APPLICANT: Ikeda, John-e
TITLE OF INVENTION: Neuronal Apoptosis Inhibitor Protein, Gene Sequence and
Patent No. 6429011
TITLE OF INVENTION: Mutations Causative of Spinal Muscular Atrophy
FILE REFERENCE: 3477-112, 033477/139914
CURRENT APPLICATION NUMBER: US/09/493,784
CURRENT FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 08/836,134
PRIOR FILING DATE: 1997-06-20
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 1232
TYPE: PRT
ORGANISM: Homo sapiens
US-09-493-784-2

Query Match 19.9%; Score 155; DB 4; Length 1232;
Best Local Similarity 40.5%; Pred. No. 1.5e-08;
Matches 34; Conservative 15; Mismatches 29; Indels 6; Gaps 3;
QY 15 KDHRISTFKWPF-LEGCACTPERMAEAGFIHCPTENEPDLAQCFKCELEGEWEPDDDP 73
DB 159 EEARLASFRNWPFFVQ--ISPCVLSEAGFV---TGKQDTVQCFCGCGCLGNWEEGDDP 213

QY 74 IEHKKHSSGCAFLSVKQFELT 97
Db 214 WKEHAKWFPKCEFLRSKKSSEIT 237

RESULT 9
US-09-705-872-3
; Sequence 3, Application US/09705872
; Patent No. 6617429
; GENERAL INFORMATION:
; APPLICANT: Joh-E IKEDA
; TITLE OF INVENTION: APOPTOSIS INHIBITORY PROTEIN, GENE ENCODING THE PROTEIN
; FILE REFERENCE: 2000-1110/LC/00653
; CURRENT APPLICATION NUMBER: US/09/705,872
; CURRENT FILING DATE: 2000-11-06
; PRIOR APPLICATION NUMBER: 09/239,797
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1295
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-705-872-3

Query Match 19.9%; Score 155; DB 4; Length 1295;
Best Local Similarity 40.5%; Pred. No. 1.6e-08;
Matches 34; Conservative 15; Mismatches 29; Indels 6; Gaps 3;

QY 15 KDHRISTFKWPP-LEGCACTPERMAEAGFIHCTPTNEPDLAQCFPCFKEGWEPPDDP 73
Db 159 BEARLASFRNFFYVQG--ISPCVLSEAGFVF--TGKQDTVQCFSCGCLGNWEEDDP 213
QY 74 IEHKKHSSGCAFLSVKQFELT 97
Db 214 WKEHAKWFPKCEFLRSKKSSEIT 237

RESULT 10
US-09-705-872-1
; Sequence 1, Application US/09705872
; Patent No. 6617429
; GENERAL INFORMATION:
; APPLICANT: Joh-E IKEDA
; TITLE OF INVENTION: APOPTOSIS INHIBITORY PROTEIN, GENE ENCODING THE PROTEIN
; FILE REFERENCE: 2000-1110/LC/00653
; CURRENT APPLICATION NUMBER: US/09/705,872
; CURRENT FILING DATE: 2000-11-06
; PRIOR APPLICATION NUMBER: 09/239,797
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1403
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-705-872-1

Query Match 19.9%; Score 155; DB 4; Length 1403;
Best Local Similarity 40.5%; Pred. No. 1.8e-08;
Matches 34; Conservative 15; Mismatches 29; Indels 6; Gaps 3;

QY 15 KDHRISTFKWPP-LEGCACTPERMAEAGFIHCTPTNEPDLAQCFPCFKEGWEPPDDP 73
Db 159 BEARLASFRNFFYVQG--ISPCVLSEAGFVF--TGKQDTVQCFSCGCLGNWEEDDP 213
QY 74 IEHKKHSSGCAFLSVKQFELT 97
Db 214 WKEHAKWFPKCEFLRSKKSSEIT 237

RESULT 11
US-08-657-759-22
; Sequence 22, Application US/08657759
; Patent No. 6511828
; GENERAL INFORMATION:
; APPLICANT: Thompson, Craig B.
; TITLE OF INVENTION: HUMAN AND DROSOPHILA INHIBITORS
; TITLE OF INVENTION: OF APOPTOSIS PROTEINS (IAPs)
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/657,759
; APPLICATION NUMBER: US/08/657,759
; FILING DATE: 31-MAY-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: ARCD:220
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 75 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-657-759-22

Query Match 18.0%; Score 140; DB 4; Length 75;
Best Local Similarity 39.7%; Pred. No. 2e-08;
Matches 31; Conservative 14; Mismatches 27; Indels 6; Gaps 3;

QY 15 KDHRISTFKWPP-LEGCACTPERMAEAGFIHCTPTNEPDLAQCFPCFKEGWEPPDDP 73
Db 3 BEARLASFRNFFYVQG--ISPCVLSEAGFVF--TGKQDTVQCFSCGCLGNWEEDDP 57
QY 74 IEHKKHSSGCAFLSVK 91
Db 58 WKEHAKWFPKCEFLRSK 75

RESULT 12
US-08-511-485-12
; Sequence 12, Application US/08511485
; Patent No. 5919912
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA

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; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/511,485
; FILING DATE: 04-AUG-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 07540/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 275 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: both
; MOLECULE TYPE: protein
; US-08-511-485-12

Query Match 17.5%; Score 136.5; DB 2; Length 275;
Best Local Similarity 36.4%; Pred. No. 2.6e-07;
Matches 28; Conservative 14; Mismatches 24; Indels 11; Gaps 3;

QY 18 RISTKNWPLEGCAC---TPERMAEAGFIHCPTENSPDLAOCFCFKELSGWEPDDDDPI 74
Db 111 RVKSFHNP-----RCMKORPEQMADAGFFY---TGYGNTKCFYCDGGLKDWEPEDVPW 162
QY 75 EHKHSSGCAFLSVKX 91
Db 163 EQHVRWFDRCAVYQLVK 179

RESULT 13
US-08-836-134-21
; Sequence 21, Application US/08836134A
; Patent No. 6020127
; GENERAL INFORMATION:
; APPLICANT: Mackenzie, Alex E.
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mahadevan, Mani S.
; APPLICANT: McLean, Michael
; APPLICANT: Roy, Natalie
; APPLICANT: Ikeda, John-e
; TITLE OF INVENTION: Neuronal Apoptosis Inhibitor Protein, Gene Sequence and
; TITLE OF INVENTION: Mutations Causative of Spinal Muscular Atrophy
; FILE REFERENCE: 3477-112, 033477/139914
; CURRENT APPLICATION NUMBER: US/08/836,134A
; CURRENT FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Cydia pomonella
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR primer
US-08-836-134-21

Query Match 17.5%; Score 136.5; DB 4; Length 275;
Best Local Similarity 36.4%; Pred. No. 2.6e-07;
Matches 28; Conservative 14; Mismatches 24; Indels 11; Gaps 3;

QY 18 RISTKNWPLEGCAC---TPERMAEAGFIHCPTENSPDLAOCFCFKELSGWEPDDDDPI 74
Db 111 RVKSFHNP-----RCMKORPEQMADAGFFY---TGYGNTKCFYCDGGLKDWEPEDVPW 162
QY 75 EHKHSSGCAFLSVKX 91
Db 163 EQHVRWFDRCAVYQLVK 179

RESULT 14
US-09-493-784-21
; Sequence 21, Application US/09493784
; Patent No. 6429011
; GENERAL INFORMATION:
; APPLICANT: Mackenzie, Alex E.
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mahadevan, Mani S.
; APPLICANT: McLean, Michael
; APPLICANT: Roy, Natalie
; APPLICANT: Ikeda, John-e
; TITLE OF INVENTION: Neuronal Apoptosis Inhibitor Protein, Gene Sequence and
; TITLE OF INVENTION: Mutations Causative of Spinal Muscular Atrophy
; FILE REFERENCE: 3477-112, 033477/139914
; CURRENT APPLICATION NUMBER: US/09/493,784
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 08/836,134
; PRIOR FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Cydia pomonella
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR primer
US-09-493-784-21

Query Match 17.5%; Score 136.5; DB 4; Length 275;
Best Local Similarity 36.4%; Pred. No. 2.6e-07;
Matches 28; Conservative 14; Mismatches 24; Indels 11; Gaps 3;

QY 18 RISTKNWPLEGCAC---TPERMAEAGFIHCPTENSPDLAOCFCFKELSGWEPDDDDPI 74
Db 111 RVKSFHNP-----RCMKORPEQMADAGFFY---TGYGNTKCFYCDGGLKDWEPEDVPW 162
QY 75 EHKHSSGCAFLSVKX 91
Db 163 EQHVRWFDRCAVYQLVK 179

RESULT 15
US-09-201-936-12
; Sequence 12, Application US/09201936
; Patent No. 6541457
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSEQ for Windows Version 3.0
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; SEQ ID NO 12
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Cydia pomonella
US-09-201-936-12

Query Match      17.5%; Score 136.5; DB 4; Length 275;
Best Local Similarity 36.4%; Pred. No. 2.6e-07;
Matches 28; Conservative 14; Mismatches 24; Indels 11; Gaps 3;

QY  18 RISTFQWPFLEGCAC---TPERMAEAGFIHCPTENEPDLAQCFKFELEGWEPDDPI 74
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  111 RVKSFHNWP-----RCMKQPEQWADAGFFY--TGyDNTKGFYCDGGLKDWEPEdVPW 162
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  75 BEHKHSHSGCAFLSVKK 91
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  163 EOHVRFEDRCAYVOLVK 179
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Job time : 20 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August '15, 2004, 21:13:29 ; Search time 2786 Seconds
(without alignments)
1522.049 Million cell updates/sec

Title: US-09-690-825-34
Perfect score: 778
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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9: gb_esti.*
10: gb_est2.*
11: gb_htc.*
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13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
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18: em_gss_inv.*
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28: gb_gss1.*

29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	778	100.0	517	10	AW411195 fh10h09.x
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6	778	100.0	553	14	CB138359 K-EST0131
7	778	100.0	563	12	BM835829 K-EST0111
8	778	100.0	574	14	CB111125 K-EST0152
9	778	100.0	580	10	AW409701 fh01802.x
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12	778	100.0	602	9	AL603004 DRFP2686K
13	778	100.0	605	12	BM841904 K-EST0119
14	778	100.0	613	10	AW409816 fh02810.x
15	778	100.0	624	14	CB135918 K-EST0188
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18	778	100.0	646	12	B1252508 602952974
19	778	100.0	682	10	BE796084 601531091
20	778	100.0	698	10	BE796061 601531059
21	778	100.0	703	10	BF219993 601296980
22	778	100.0	707	12	BG115707 602317179
23	778	100.0	718	12	BM827836 K-EST0100
24	778	100.0	726	13	BX421971 BX421971
25	778	100.0	742	10	BE907403 601500136
26	778	100.0	760	12	BM206268 603643029
27	778	100.0	766	12	BG682887 602651082
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29	778	100.0	772	12	BG750227 602709025
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31	778	100.0	815	12	BG335442 602403907
32	778	100.0	815	12	BG744230 602723337
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35	778	100.0	826	13	BU171608 AGENCOURT
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39	778	100.0	868	13	BQ832604 AGENCOURT
40	778	100.0	874	10	BE883968 601505487
41	778	100.0	875	10	BE898710 601681673
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ALIGNMENTS

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LOCUS K-EST0032467 S11SNUI Homo sapiens cDNA clone S11SNUI-12-C02 5',
DEFINITION 472 bp mRNA linear EST 04-MAR-2002
ACCESSION BM754864
VERSION BM754864.1 GI:19084482
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 472)


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QY      81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGluGlu 100
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QY      101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysLysLysLysLysLysLysLys 120
Db      322 TTTTGAACCTGGACAGAGAGAGCCAGCAACAAATTCAGAGGAAACCAACAATAAG 381
QY      121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaLysLysLysLysLysLys 140
Db      382 AAGAAAGAAATTTAGGAAACTGCGAAGAAAGTGGCGCGTGCATCGAGCAGCTGGCTGCC 441
QY      141 MetAsp 142
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LOCUS   AW411195
DEFINITION   f10h09.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2964713 5',
ACCESSION   AW411195
VERSION      AW411195.1 GI:6936736
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 517)
            NIH-MGC http://mgc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgabbs@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC)
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www.bio.llnl.gov/bbrp/image/image.html
            Plate: L1CM64 row: C column: 18
            Seq primer: -21M13 forward primer (ABI).
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                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:2964713"
                /issue_type="thabdomyosarcoma"
                /lab_host="DH10B (phage-resistant)"
                /clone_lib="NIH MGC 17"
                /notes="Organ: muscle; Vector: pOTB7; Site 1: EcoRI;
                Site 2: XhoI; cDNA made by oligo-dT priming.
                Directionally cloned into EcoRI/XhoI sites using the
                following 5' adaptor: GGACGAG(G). Size-selected >500bp
                for average insert size 1.8kb. Library constructed by
                Ling Hong in the laboratory of Gerald M. Rubin (University
                of California, Berkeley) using ZAP-cDNA synthesis kit
                (Stratagene) and Superscript II RT (Life Technologies)."
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ORIGIN

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Alignment Scores:      2,91e-74      Length:      517
Pred. No.:             778.00      Matches:      142
Score:                 100.00%      Conservative: 0
Percent Similarity:
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Best Local Similarity: 100.00%      Mismatches: 0
Query Match:           100.00%      Indels: 0
DB:                    10          Gaps: 0
US-09-690-825-34 (1-142) x AW411195 (1-517)
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QY      1 MetGlyAlaProThrLeuProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
Db      44 ATGGTGTCCCGGACGTTGGCCCTGCTGGCAGCCCTTTTCAAGGACCACCGCATCTCT 103
QY      21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
Db      104 ACATTCAAGAACTGGCCCTTCTTGGAGGGCTGGCCCTGCACCCCGAGGGATGGCCGAG 163
QY      41 AlaGlyPheIleHisCysPProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
Db      164 GCTGGCTTTCATCCACTGCCCTGAGACGACGACGACTTGGCCCGAGTGTTCCTTCTGC 223
QY      61 PheLysGluLeuGluGlyTrpGluProAspAspProLleGluHisLysLysHis 80
Db      224 TTCAAGGAGCTGGAAGCTGGGAGCCAGATGACGACCCCATAGAGGAACATAAAAGCAT 283
QY      81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGluGlu 100
Db      284 TCGTCCGTTGGCTTCTCTCTGTCAGAGACAGTGTGAAGAAATTAACCTTGGTGAA 343
QY      101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysLysLysLysLysLysLysLys 120
Db      344 TTTTGAACCTGGACAGAGAGAGCAACAAATTCGAAAGGAAACCAACAATAAG 403
QY      121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaLysLysLysLysLysLys 140
Db      404 AAGAAAGAAATTTAGGAAACTGCGAAGAAAGTGGCGCGTGCATCGAGCAGCTGGCTGCC 463
QY      141 MetAsp 142
Db      464 ATGGAT 469
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RESULT 4

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LOCUS     BG258128
DEFINITION   602379226P1 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:4510014 5',
ACCESSION   BG258128
VERSION      BG258128.1 GI:12767944
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 552)
            NIH-MGC http://mgc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgabbs@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: L1CM0391 row: C column: 07
            High quality sequence stop: 552.
            Location/Qualifiers
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                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:4510014"
                /tissue_type="embryonal carcinoma, cell line"
                /lab_host="DH10B (phage-resistant)"
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FEATURES

source

/clone_lib="NIH_MGC_92"
 /note="Organ: testis; Vector: PCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
 Average insert size 2.5 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
 Pred. No.: 3,14e-74 Length: 552
 Score: 778.00 Matches: 142
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 12 Gaps: 0

US-09-690-825-34 (1-142) x BG258128 (1-552)

QY 1 MetGlyAlaProThrLeuProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
 DB 32 ATGGTGGCCCGAGCTTGCCCTTGGCTGGAGCCCTTCTCAAGGACCCACCATCTCT 91
 QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
 DB 92 ACATTCAAGAACTGGCCCTTCTGGAGGCTGGCTGCACCCCGAGCGATGGCCGAG 151
 QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPheCys 60
 DB 152 GCTGGCTTCATCCACTGCCCTCCCTGAGAACGAGCAGACTGGCCCGAGTGTCTCTGC 211
 QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHisLysLysHis 80
 DB 212 TTCAGAGAGCTGGAGGCTGGAGCCAGATGACGACCCCATAGAGGACATATAAGCAT 271
 QY 81 SerSerGlyCysAlaPheLeuSerValLysGlnPheGluGlnLeuThrLeuGlyGlu 100
 DB 272 TCGTCCGGTGGCGTTCCTTCTGTCAAGAGCAGTTTCAGAAATTAACCCCTGGTGAA 331
 QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120
 DB 332 TTTTGAACATGGACAGAAAGAGCCCAAGAAATTCAGAAAGGAAACCAACAATAAG 391
 QY 121 LysLysGluPheGluGluThrAlaLysLysValArgAlaIleGluGlnLeuAlaAla 140
 DB 392 AAGAAAGATTTGAGGAACTGGGAGAAAGTGGCGGTCCATCGAGCAGCTGGCTGCC 451
 QY 141 MetAsp 142
 DB 452 ATGGAT 457

RESULT 5

BM839824

LOCUS

DEFINITION

K-ESR0116794 S13KM55 Homo sapiens cDNA clone S13KM55-32-F06 5',

mRNA sequence.

BM839824

VERSION

BM839824.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 552)

Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,

Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and

Kim, Y.S.

21C Frontier Korean EST Project 2001

Unpublished (2002)

Contact: Kim YS

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 32 row: F column: 06

High quality sequence stop: 552.

location/Qualifiers

1. .552

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="S13KM55-32-F06"

/tissue_type="myeloma"

/cell_line="KMS-5"

/lab_host="Top10F"

/clone_lib="S13KM55"

/note="Vector: pCNS; Site 1: EcoRI; Site 2: NotI; The poly

(A) + RNA was dephosphorylated with bacterial alkaline

phosphatase (BAP) and then dephosphorylated with tobacco acid

pyrophosphatase (TAP). The dephosphorylated mRNA was

ligated with DNA-RNA linker including EcoRI I site by

treatment of T4 RNA ligase and the first strand cDNA was

synthesized from oligo dt-selected mRNA by priming with

dt-tailed vector. The dt-tailed vector was adjusted to

have about 60nt. The cDNA vector was circularized with E.

coli DNA ligase after digestion of EcoRI which site is

also included in vector. An RNA strand converted to a DNA

strand by Okayama-Berg method. The obtained cDNA vectors

were used for transformation of competent cells E. coli

Top10F by electroporation method. The cDNA libraries

constructed by this method are full-length enriched cDNA

library."

ORIGIN

Alignment Scores:

Pred. No.: 3,14e-74 Length: 552
 Score: 778.00 Matches: 142
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 12 Gaps: 0

US-09-690-825-34 (1-142) x BM839824 (1-552)

QY 1 MetGlyAlaProThrLeuProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
 DB 78 ATGGTGGCCCGAGCTTGCCCTTGGCTGGAGCCCTTCTCAAGGACCCACCATCTCT 137
 QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
 DB 138 ACATTCAAGAACTGGCCCTTCTGGAGGCTGGCTGCACCCCGAGCGATGGCCGAG 197
 QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPheCys 60
 DB 198 GCTGGCTTCATCCACTGCCCTCCCTGAGAACGAGCAGACTGGCCCGAGTGTCTCTGC 257
 QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHisLysLysHis 80
 DB 258 TTCAAGAGAGCTGGAAGCTGGAGCCAGATGACGACCCCATAGAGGAAACATAAAGCAT 317
 QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
 DB 318 TCGTCCGGTGGCGTTCCTTCTGTCAAGAGCAGTTTGAAGAATTAACCCCTGGTGAA 377
 QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120
 DB 378 TTTTGAACATGGACAGAAAGAGCCCAAGAAATTCAGAAAGGAAACCAACAATAAG 437
 QY 121 LysLysGluPheGluGluThrAlaLysLysValArgAlaIleGluGlnLeuAlaAla 140
 DB 438 AAGAAAGATTTGAGGAACTGGGAGAAAGTGGCGGTCCATCGAGCAGCTGGCTGCC 497
 QY 141 MetAsp 142
 DB 498 ATGGAT 503

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RESULT 6
CBI38359
LOCUS
DEFINITION K-EST0191218 L5HLK1 Homo sapiens cDNA clone L5HLK1-23-G07 5', mRNA
sequence.
ACCESSION CBI38359
VERSION CBI38359.1 GI:28109974
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 553)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 23 row: G column: 07
High quality sequence stop: 553.
FEATURES
Source
1..553
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="L5HLK1-23-G07"
/sex="M"
/cell_line="HLK-1"
/lab_host="Top10p"
/clone_lib="L5HLK1"
/notes="Organ: Liver; Vector: PCNS-D2; Site 1: EcoRI;
Site 2: NotI; The poly (A) + RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tobacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including
EcoRI site by treatment of T4 RNA ligase and the first
strand cDNA was synthesized from oligo dT-selected mRNA by
priming with dT-tailed vector. The dT-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transfection of
competent cells E. coli Top10p by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."
ORIGIN
Alignment Scores:
Pred. No.: 3.15e-74 Length: 553
Score: 778.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0
US-09-690-825-34 (1-142) x CBI38359 (1-553)
Qy 1 MetGlyAlaProThrLeuProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
Db 40 ATGGGTGCCCCGAGGTTCGCCCTGCTGGCAGCCCTTTCTCAGGACCCAGCCGATCTCT 99
Qy 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
Db 100 ACATTCAAGAACTGGCCCTTCTTGGAGGGGTGGCGCTGCACCCGCGGATGCGCCGAG 159

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Qy 41 AlaGlyPheIleHisCysProThrGluAenGluProAspLeuAlaGlnCysPheCys 60
Db 160 GCTGGGTTTCATCCACATGCCCACTGAGAACGAGCCAGACTTGCCCACTGTTTCTTCGC 219
Qy 61 PheIysGluLeuGluGlyTrpGluProAspAspAspProIleGluGluHisLysHis 80
Db 220 TTCAGGAGCTGGAGGCTGGGAGCGGATGAGCCCATAGAGGACATATAAAGCAT 279
Qy 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
Db 280 TCGTCCGGTTGCGCTTCTTCTGTCAAGAGCAGTTTGAAGAATTAAACCTTGGTGA 339
Qy 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120
Db 340 TTTTGAACCTGACAGAGAGGACCAACACAAATTCGAAAGAACCAACCAATAG 399
Qy 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAla 140
Db 400 AAGAAAGAAATTTGAGGAAACTGCAAGAAAGTGCCTGCGCATCGAGCAGCTGCC 459
Qy 141 MetAsp 142
Db 460 ATGGAT 465
RESULT 7
CBI38359
LOCUS
DEFINITION K-EST0111069 S11SNUI Homo sapiens cDNA clone S11SNUI-73-H09 5',
mRNA sequence.
ACCESSION CBI38359
VERSION CBI38359.1 GI:19192238
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 563)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Kim,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 73 row: H column: 09
High quality sequence stop: 563.
FEATURES
Source
1..563
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S11SNUI-73-H09"
/sex="M"
/tissue_type="Stomach"
/cell_type="Lymphoblast-like"
/cell_line="SNU-1"
/lab_host="Top10p"
/clone_lib="S11SNUI"
/notes="Organ: Stomach; Vector: pME18-FL3; Site 1: XhoI;
Site 2: XhoI; The poly (A) + RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tobacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including SfiI
site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized with Superscript II using SfiI
oligo-dT primer. After first strand synthesis, RNA was
degraded by NaOH treatment and cDNA was amplified by PCR

```

reaction. The PCR products were digested with SfiI and cloned into DraIII-digested pME18S-FL3 vector. The obtained cDNA vectors were used for transformation of competent cells *E. coli* Top10[®] by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Alignment Scores:
 Pred. No.: 3.22e-74 Length: 563
 Score: 778.00 Matches: 142
 Percent Similarity: 100.00% Conservativity: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 12 Gaps: 0

US-09-690-825-34 (1-142) x BW835829 (1-563)

QY 1 MetGlyAlaProThrLeuProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
 Db 45 ATGGGTGCGCGAGCTTGCCCTTCTGGAGGGCTGGCCCTTCTCAAGGACCAACCGCATCTCT 104
 QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
 Db 105 ACATTCAAGAACTGGCCCTTCTGGAGGGCTGGCCCTTCTCAAGGACCAACCGCGAG 164
 QY 41 AlaGlyPheLeuHisCysProThrGluAsnGluProAspLeuAlaGlnCysPheCys 60
 Db 165 GCTGGCTTCATCCACTGCCCACTGAGACGAGCCAGACTTGGCCCACTGTTCTTCTG 224
 QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluHisLysLysHis 80
 Db 225 TTCAGAGAGCTGGAGCTGGAGCCAGATGACGCCATAGAGGAACATAAAGCAT 284
 QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluLeuThrLeuGlyGlu 100
 Db 285 TCGTCCGTTGCGCTTCTCTTCTGTCAGAACAGCAGTTTGAAGAATTAACCTTGTGAA 344
 QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120
 Db 345 TTTTGAACCTGCACAGAGAGAGCCAGAACAAATTTGCAAGAGAAACCAACATAAG 404
 QY 121 LysLysGluPheGluGluThrAlaLysLysValArgAlaIleGluGlnLeuAla 140
 Db 405 AAGAAAGAAATTTGAGGAATCTGCGAAGAGTGGCCGTCATCGAGCAGCTGCGTGC 464
 QY 141 MetAsp 142
 Db 465 ATGGAT 470

RESULT 8

CB111125

LOCUS

DEFINITION K-EST012661 L5HLK1 Homo sapiens cDNA clone L5HLK1-8-G05 5', mRNA

ACCESSION

CB111125

VERSION

EST.

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 574)

AUTHORS

Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.

TITLE

21C Frontier Korean EST Project 2001

JOURNAL

Unpublished (2002)

COMMENT

Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470

Fax: +82-42-860-4409
 Email: yongsung@mail.krribb.re.kr
 Plate: 8 row; G column: 05
 High quality sequence stop: 574.
 Location/Qualifiers
 1..574

FEATURES

source

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="L5HLK1-8-G05"
 /sex="M"
 /cell_line="HLK-1"
 /lab_host="Top10P"
 /clone_lib="L5HLK1"

/note=Organ: Liver; Vector: pcNS-D2; Site 1: EcoRI;
 Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
 bacterial alkaline phosphatase (BAP) and then decapped
 with tobacco acid pyrophosphatase (TAP). The decapped
 intact mRNA was ligated with DNA-RNA linker including
 EcoRI site by treatment of T4 RNA ligase and the first
 strand cDNA was synthesized from oligo dT-selected mRNA by
 priming with dT-tailed vector. The dT-tailed vector was
 adjusted to have about 60nt. The cDNA vector was
 circularized with *E. coli* DNA ligase after digestion of
 EcoRI which site is also included in vector. An RNA strand
 converted to a DNA strand by Okayama-Berg method. The
 obtained cDNA vectors were used for transformation of
 competent cells *E. coli* Top10[®] by electroporation method.
 The cDNA libraries constructed by this method are
 full-length enriched cDNA library."

ORIGIN

Alignment Scores:
 Pred. No.: 3.29e-74 Length: 574
 Score: 778.00 Matches: 142
 Percent Similarity: 100.00% Conservativity: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 14 Gaps: 0

US-09-690-825-34 (1-142) x CB111125 (1-574)

QY 1 MetGlyAlaProThrLeuProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
 Db 55 ATGGGTGCGCGAGCTTGCCCTTCTGGAGGGCTGGCCCTTCTCAAGGACCAACCGCATCTCT 114
 QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
 Db 115 ACATTCAAGAACTGGCCCTTCTGGAGGGCTGGCCCTTCTCAAGGACCAACCGCGAG 174
 QY 41 AlaGlyPheLeuHisCysProThrGluAsnGluProAspLeuAlaGlnCysPheCys 60
 Db 175 GCTGGCTTCATCCACTGCCCACTGAGACGAGCCAGACTTGGCCCACTGTTCTTCTGC 234
 QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluHisLysLysHis 80
 Db 235 TTCAGAGAGCTGGAGGCTGGAGCCAGATGACGCCATAGAGAAACATAAAGCAT 294
 QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluLeuThrLeuGlyGlu 100
 Db 295 TCGTCCGTTGCGCTTCTCTTCTGTCAGAACAGCAGTTTGAAGAATTAACCTTGTGAA 354
 QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120
 Db 355 TTTTGAACCTGCACAGAGAGCCAGAACAAATTTGCAAGAGAAACCAACCAATAG 414
 QY 121 LysLysGluPheGluGluThrAlaLysLysValArgAlaIleGluGlnLeuAla 140
 Db 415 AAGAAAGAAATTTGAGGAAACTGCGAAGAAAGTGGCCGTCATCGAGCAGCTGCGTGC 474
 QY 141 MetAsp 142
 Db 475 ATGGAT 480

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RESULT 9
AW409701
LOCUS
DEFINITION
  fho1e02.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2961098 5',
  mRNA sequence.
ACCESSION
  AW409701
VERSION
  AW409701.1 GI:6935175
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 580)
  NIH-MGC http://mgc.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-r@mail.nih.gov
  Tissue Procurement: ATCC
  cDNA Library Preparation: Ling Hong/Rubin Laboratory
  cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
  DNA Sequencing by: National Institutes of Health Intramural
  Sequencing Center (NISC)
  Clone distribution: MGC clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  www-bio.lnl.gov/bbrp/image/image.html
  Plate: LLCW55 row: I column: 3
  Seq primer: -21M13 forward primer (ABI).
FEATURES
    source
    1..580
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="IMAGE:2961098"
        /tissue_type="rhodomyosarcoma"
        /lab_host="DH10B (phage-resistant)"
        /clone_lib="NIH MGC 17"
        /note="Organ: muscle; Vector: pOTB7; Site 1: EcoRI;
        Site 2: XhoI; cDNA made by oligo-dT priming.
        Directionally cloned into EcoRI/XhoI sites using the
        following 5' adaptor: GGACGAG(G). Size-selected >500bp
        for average insert size 1.8kb. Library constructed by
        Ling Hong in the laboratory of Gerald M. Rubin (University
        of California, Berkeley) using ZAP-cDNA synthesis kit
        (Stratagene) and Superscript II RT (Life Technologies)."
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ORIGIN

```

Alignment Scores:
Pred. No.:      3,336-74      Length:      580
Score:          778.00      Matches:    142
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:     100.00%      Indels:    0
DB:              10          Gaps:      0
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US-09-690-825-34 (1-142) x AW409701 (1-580)

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Qy      1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
Db      53 ATGGGTGCCCCGACGTGGCCCCCTGCTGCGAGCCCTTTCTCAGGACCCACCGCATCTCT 112
Qy      21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
Db      113 ACATTCAAGAACTGGCCCTTTCTTGAGGGCTGCGCCTGCACCCCGAGCGGATGCCGAG 172
Qy      41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPheCys 60
Db      173 GCTGGGTTTCATCCACGTGCCCACTGAGACGACGACCTTGCCCGAGTTCCTTCCTGCG 232
Qy      61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHisLysLysHis 80
Db      233 TTCAGGAGCTGGAAGGCTGGAGGCCAGATGACGACCCCATAGAGGAACATTAAGGAT 292
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Qy      81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
Db      293 TCGTCGGGTTGCGCTTCTCTTGTCAAGAGCAGTTTGAAGAATTAAACCCCTTGTGTGA 352
Qy      101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
Db      353 TTTTGAACCTGGACAGAGAAAGAGCAACAATAATTCGAAGAGGAACCAACAATAG 412
Qy      121 LysLysGluPheGluGluThrAlaLysLysValArgAlaIleGluGlnLeuAlaAla 140
Db      413 AAGAAAGATTTCAGGAAACTGCGAAGAAAGTGCGCCGTGCCATCGAGCAGCTGGTGCC 472
Qy      141 MetAsp 142
Db      473 ATGGAT 478
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LOCUS
DEFINITION
  K-EST0177364 C1SNUL7 Homo sapiens cDNA clone C1SNUL7-12-G02 5',
  mRNA sequence.
ACCESSION
  CB128010
VERSION
  CB128010.1 GI:28090807
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 584)
  Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
  Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
  Kim,Y.S.
  21C Frontier Korean EST Project 2001
  Unpublished (2002)
  Contact: Kim YS
  Genome Research Center
  Korea Research Institute of Bioscience & Biotechnology
  52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
  Tel: +82-42-860-4470
  Fax: +82-42-860-4409
  Email: yongsung@mail.kribb.re.kr
  Plate: 12 row: G column: 02
  High quality sequence stop: 584.
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        /clone="C1SNUL7-12-G02"
        /sex="F"
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        /cell_type="Epithelial"
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        /lab_host="Top10F"
        /clone_lib="C1SNUL7"
        /note="Organ: Cervix; Vector: pCNS-D2; Site 1: EcoRI;
        Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
        bacterial alkaline phosphatase (BAP) and then decapped
        with tabacco acid pyrophosphatase (TAP). The decapped
        intact mRNA was ligated with DNA-RNA linker including
        EcoRI site by treatment of T4 RNA ligase and the first
        strand cDNA was synthesized from oligo dt-selected mRNA by
        priming with dt-tailed vector. The dt-tailed vector was
        adjusted to have about 60nt. The cDNA vector was
        circularized with E. coli DNA ligase after digestion of
        EcoRI which site is also included in vector. An RNA strand
        converted to a DNA strand by Okayama-Berg method. The
        obtained cDNA vectors were used for transformation of
        competent cells E. coli Top10F by electroporation method.
        The cDNA libraries constructed by this method are
        full-length enriched cDNA library."
```

ORIGIN

```

Alignment Scores:      3.36e-74      Length:      584
Pred. NO.:            778.00      Matches:      142
Score:                100.00%      Conservative: 0
Percent Similarity:   100.00%      Mismatches: 0
Best Local Similarity: 100.00%      Indels:      0
Query Match:         100.00%      Gaps:        0
DB:                  14

US-09-690-825-34 (1-142) x CB128010 (1-584)

Qy 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
Db 55 ATGGGTGCCCCGAGTTGGCCCTTCTTGGAGGCTGGCCCTTCTTCAAGGACCCGATCTCT 114
Qy 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
Db 115 ACATTCAGAACTGGCCCTTCTTGGAGGCTGGCCCTTCTTCAAGGACCCGATGGCCGAG 174
Qy 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
Db 175 GCTGGCTTCATCCACTGCCCCCACTGAGAACGAGCCAGACTTGGCCCGAGTTTCTTCTGC 234
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Db 235 TTCAAGGAGCTGGAAGGCTGGAGCCAGATGACGACCCCACTAGAGGAACATAAAAGCAT 294
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Db 355 TTTTGAACCTGGACAGAGAAAGAGCCAGCAACAAAAATTGCAAGGAAACCAACATAAG 414
Qy 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAlaA 140
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Qy 141 MetAsp 142
Db 475 ATGGAT 480

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LOCUS 602663774F1 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4808802 5',
DEFINITION mRNA sequence.
ACCESSION BG776624
VERSION BG776624.1 GI:14046941
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 585)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-x@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
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FEATURES
source

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/db_xref="taxon:9606"
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/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_59"
/notes="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggcgctcgcc); Site_2: SfiI (ggcattatggc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CAGCCGCTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCCGCGGCGGACATG-dt(30)BN-3',
(where B = A, C, G or N = A, C, G, or T). Average
insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
Library."

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ORIGIN

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Alignment Scores:      3.37e-74      Length:      585
Pred. NO.:            778.00      Matches:      142
Score:                100.00%      Conservative: 0
Percent Similarity:   100.00%      Mismatches: 0
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Query Match:         100.00%      Gaps:        0
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US-09-690-825-34 (1-142) x BG776624 (1-585)

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Qy 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
Db 106 ACATTCAGAACTGGCCCTTCTTGGAGGCTGGCCCTTGGAGGCTGGCCCTTGGAGGCTGGCCGAG 165
Qy 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
Db 166 GCTGGCTTCATCCACTGCCCCCACTGAGAACGAGCCAGACTTGGCCCGAGTTTCTTCTGC 225
Qy 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHisLysLysHis 80
Db 226 TTCAAGGAGCTGGAAGGCTGGAGCCAGATGACGACCCCACTAGAGGAACATAAAAGCAT 285
Qy 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
Db 286 TCGTCCCGTTGCGCTTCTTCTTCTGCAAGAACAGTTTGAAGAATTACCTTGTGTAA 345
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Db 346 TTTTGAACCTGGACAGAGAAAGAGCCAGCAACAAAAATTGCAAGGAAACCAACATAAG 405
Qy 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAlaA 140
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Qy 141 MetAsp 142
Db 466 ATGGAT 471

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RESULT 12

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DEFINITION DKFZp686k1620_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
ACCESSION AL603004
VERSION AL603004.1 GI:15166510
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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BM841904
LOCUS
DEFINITION
K-EST0119223 S13KMS5 Homo sapiens cDNA clone S13KMS5-34-A12 5', mRNA linear EST 06-MAR-2002
605 bp
mRNA
EST 06-MAR-2002
S13KMS5-34-A12 5',
sequence.
BM841904
ACCESSION
BM841904
VERSION
BM841904.1
KEYWORDS
GI:19198313
SOURCE
EST.
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 602)
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
JOURNAL
COMMENT
Contact: Kim YS
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Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 34 row: A column: 12
High quality sequence stop: 605.
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/note="Vector: pCNS; Site 1: EcoRI; Site 2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

BM841904
LOCUS
DEFINITION
K-EST0119223 S13KMS5 Homo sapiens cDNA clone S13KMS5-34-A12 5', mRNA linear EST 06-MAR-2002
605 bp
mRNA
EST 06-MAR-2002
S13KMS5-34-A12 5',
sequence.
BM841904
ACCESSION
BM841904
VERSION
BM841904.1
KEYWORDS
GI:19198313
SOURCE
EST.
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 602)
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
JOURNAL
COMMENT
Contact: Kim YS
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Korea Research Institute of Bioscience & Biotechnology
52 Eosun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 34 row: A column: 12
High quality sequence stop: 605.
Location/Qualifiers
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/note="Vector: pCNS; Site 1: EcoRI; Site 2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

BM841904
LOCUS
DEFINITION
K-EST0119223 S13KMS5 Homo sapiens cDNA clone S13KMS5-34-A12 5', mRNA linear EST 06-MAR-2002
605 bp
mRNA
EST 06-MAR-2002
S13KMS5-34-A12 5',
sequence.
BM841904
ACCESSION
BM841904
VERSION
BM841904.1
KEYWORDS
GI:19198313
SOURCE
EST.
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 602)
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
JOURNAL
COMMENT
Contact: Kim YS
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Korea Research Institute of Bioscience & Biotechnology
52 Eosun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 34 row: A column: 12
High quality sequence stop: 605.
Location/Qualifiers
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/organism="Homo sapiens"
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/tissue_type="myeloma"
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/lab_host="Top10F"
/clone_lib="S13KMS5"
/note="Vector: pCNS; Site 1: EcoRI; Site 2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

RESULT 13


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/cell_line="HLK-1"
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/clone_lib="LSHLK1"
/note="Organ: Liver; Vector: pcNS-D2; Site 1: EcoRI;
Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tobacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including
EcoRI site by treatment of T4 RNA ligase and the first
strand cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Oxayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Topiof by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

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ORIGIN

Alignment Scores:

Pred. No.:	3,648-74	Length:	624
Score:	778.00	Matches:	142
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	14	Gaps:	0

US-09-690-825-34 (1-142) x CBI35918 (1-624)

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DB	25	ATGGGTGCCCCGACGTTGCCCTGCTGGCAGCCCTTCTCAGGACCCACCGCATCTCT	84
QY	21	ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu	40
DB	85	ACATTCAAGAACTGGCCCTTCTTGGAGGGCTGCGCTGCACCCCGGAGCGGATGCCCGAG	144
QY	41	AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPheCys	60
DB	145	GCTGGCTTCATCCACTGCCCTGCTGACGACGAGCCAGACTTGGCCCGAGTGTCTCTTCTGC	204
QY	61	PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHisLysLysHis	80
DB	205	TTCAGGAGCTGGAGGCTGGGAGCCAGATGACGACCCCATAGAGGAACATATAAAGCAT	264
QY	81	SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu	100
DB	265	TGTCGCGGTGCGCTTCTCTTCTGCAAGAGCAGTTTGAAGAAATTAACCTTGGTGAA	324
QY	101	PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys	120
DB	325	TITTTGAAACTGGACAGAGAAAGAGCCAAAGACAAATTTGCAAGGAAACCAACAATTAAG	384
QY	121	LysLysGluPheGluGluThrAlaLysLysValArgAlaIleGluGlnLeuAlaAla	140
DB	385	AAGAAAGAAATTTGAGGAAATCGGAGAAAGTGGCGCGTGCATCGAGCAGCTGGCTGCC	444
QY	141	MetAsp	142
DB	445	ATGGAT	450

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 15, 2004, 16:29:32 ; Search time 457 Seconds
(without alignments)
1320.009 Million cell updates/sec

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

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Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	778	100.0	426	6 AAL42859	Aal42859 Survivin
3	778	100.0	429	9 ACF58071	Acf58071 Human sur
4	778	100.0	1024	7 ABZ83360	Abz83360 Toxicolog
5	778	100.0	1619	3 AAA08903	Aaa08903 Human sur
6	778	100.0	1619	5 AAS21617	Aas21617 DNA encod
7	778	100.0	1619	7 ABX76199	Abx76199 Lung canc
8	778	100.0	1619	7 AAL53734	Aal53734 Survivin

9	778	100.0	1619	7	AA049666	Human sur
10	778	100.0	1619	9	AD585228	Farnesyl
11	778	100.0	1662	7	ABZ58106	Human Sur
12	778	100.0	2404	7	ACA03988	CDNA down
13	748	96.1	1165	2	AAQ93052	Human EPR
14	721	92.7	740	7	ACA56320	Human sig
15	660	84.8	500	2	AAT72714	Mouse inh
16	660	84.8	955	5	AAS21530	DNA encod
17	642	82.5	393	3	AAC02317	Human sec
18	465	59.6	300	9	ADD33414	Mouse mit
19	382	49.1	14796	2	AAV27941	Survivin
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22	382	49.1	14796	6	ABL68655	Kidney ca
23	382	49.1	14796	6	ABL66326	Lung canc
24	382	49.1	14796	6	ABL56663	Lung canc
25	382	49.1	14796	6	ABN96924	Gene #342
26	246.5	31.7	598	4	ABL09161	Drosophil
27	246.5	31.7	624	9	ADC06776	Fruit fly
28	233	29.9	121	7	ABZ68313	Nucleotid
29	219	28.1	403	2	AAZ31036	5' flanki
30	214	27.5	1100	4	AAF82458	Human sur
31	201.5	25.9	1050	9	ADB67958	Human lun
32	184.5	23.7	2736	4	ABL09180	Drosophil
33	184.5	23.7	2926	4	ABL09178	Drosophil
34	184.5	23.7	5749	4	ABL18270	Drosophil
35	160	20.6	14490	4	AAH20191	Human apo
36	158	20.3	14843	4	ABL10865	Drosophil
37	158	20.3	20672	4	ABL10864	Drosophil
38	157	20.2	1075	2	AAT72715	C. elegan
39	155	19.9	5366	2	AAZ56273	Human apo
40	155	19.9	5366	2	AAZ58001	Gonadotro
41	155	19.9	5502	2	AAT30092	Neuronal
42	155	19.9	5502	2	AAT71263	Neuronal
43	155	19.9	5984	2	AAZ56272	Human apo
44	155	19.9	5984	2	AAZ58000	Gonadotro
45	155	19.9	5984	3	AAA39808	Human NAI

ALIGNMENTS

RESULT 1
AAZ31037
ID AAZ31037 standard; DNA; 426 BP.
XX AC AAZ31037;
XX AC AAZ31037;
DT 17-JAN-2000 (first entry)
XX 17-JAN-2000 (first entry)
DE Open reading frame of human Survivin gene.

Survivin; open reading frame; IAP; apoptosis inhibitor; tumour cell;
effector cell protease receptor-1; EPR-1; embryonic tissue; tubulin;
mitotic spindle; abnormal cell growth; tumorigenesis; ss.

XX Homo sapiens.
XX Key Location/Qualifiers
FH CDS 1..426
FT /*tag= a
FT /product= "Survivin"

XX WO3950440-A2.

XX 07-OCT-1999.

XX 01-APR-1999; 99WO-US007205.

XX 01-APR-1998; 98US-0080288P.

XX (UYUA) UNIV YALE.

XX Altieri DC;

```

XX WPI; 1999-591329/50.
DR P-PSDB; AAY49080.
XX
XX Identifying agents that modulate Survivin interactions.
XX Example; Fig 8B; 56pp; English.
XX
XX This sequence is the open reading frame of the human survivin gene.
XX Survivin is a 142 amino acid protein of approximately 16.5kD. Survivin is
XX a member of the IAP family of apoptosis inhibitors, and the gene is
XX located on chromosome 17q25. The nucleic acid sequence of Survivin is
XX related to the Effector Cell Protease Receptor-1 (EPR-1). Survivin is
XX expressed in tumour cells and embryonic tissue. The sequence is used in
XX the invention which involves identifying an agent that modulates
XX interactions between Survivin and tubulin. Agents that modulate
XX interaction between Survivin and tubulin or mitotic spindles may be
XX administered to a mammal to modulate biological or pathological processes
XX mediated by Survivin, for example Survivin-mediated inhibition of
XX cellular apoptosis. Thus an inhibiting agent may be used to block
XX abnormal cell growth, for example during tumourigenesis. An agent that
XX increases interaction may be used to extend cell growth in culture
XX
XX Sequence 426 BP; 115 A; 112 C; 113 G; 86 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:          9.17e-82          Length:          426
Score:              778.00           Matches:         142
Percent Similarity: 100.00%           Conservative:    0
Best Local Similarity: 100.00%       Mismatches:     0
Query Match:        100.00%          Indels:         0
DB:                 2                 Gaps:          0

US-09-690-825-34 (1-142) x AAZ31037 (1-426)
Qy 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
Db 1 ATGGGTGCGCCGACGTTGGCCCTGCTGGCAGCCCTTCTCAAGGACCAACCCGATCTCT 60
Qy 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
Db 61 ACATTCAAGAACTGGCGCTTCTTGGAGGCTGGCCCTGCGACCCCGAGCGGATGGCGGAG 120
Qy 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
Db 121 GCTGGCTTCATCCACTGCCCTGCTGGCAGCCGACACTTGGCCCGAGTGTTCCTCTGC 180
Qy 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluHisLysLysHis 80
Db 181 TTCAAGAGCTGGAAGCTGGAGCCGACAGATGACGACCCCATAGAGGAACATAAAGCAT 240
Qy 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
Db 241 TCGTCCGGTGGCGTTTCCTTCTGTCAAGAACGAGTTTGAAGAATTAACTTGTGTGA 300
Qy 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120
Db 301 TTTTGAACCTGGACAGAGAAGAGCCAGAACAAATTCGAAAGGAAACCAACATAAG 360
Qy 121 LysLysGluPheGluGluThrAlaLysLysValArgAlaIleGluGlnLeuAla 140
Db 361 AAGAAAGATTGAGGAAATTCGGAAGAAAGTGGCGCGTGCCTATCGAGCAGCTGGCTGCC 420
Qy 141 MetAsp 142
Db 421 ATGGAT 426

RESULT 2
AAJ42859
ID AAL42859 standard; DNA; 426 BP.
XX
XX AC
XX AAL42859;
XX

```

```

DT 05-AUG-2002 (first entry)
XX
XX Survivin-like protein coding sequence 6.
XX
XX Survivin-like protein; diagnosis; screening; cancer; gene; ds;
XX apoptosis abnormality; gene therapy.
XX
XX Unidentified.
XX
XX Key Location/Qualifiers
XX CDS 1..426
XX /tag= a
XX /partial
XX /product= "survivin-like protein 6"
XX /note= "No stop codon is given"
XX
XX WO200233071-A1.
XX
XX 25-APR-2002.
XX
XX 16-OCT-2001; 2001WO-JP009071.
XX
XX 17-OCT-2000; 2000JP-00316721.
XX
XX 20-DEC-2000; 2000JP-00386809.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Tanaka H, Kaieda I;
XX WPI; 2002-435536/46.
XX P-PSDB; AAO14948.
XX
XX Baculovirus IAP repeat domain or RING-finger domain-containing survivin-
XX like polypeptides and encoded DNAs, applicable in diagnosis and screening
XX compounds for treating various cancers and apoptosis abnormality.
XX
XX Disclosure; Page 123-124; 136pp; Japanese.
XX
XX The invention comprises the amino acid and coding sequences of survivin-
XX like proteins. The survivin-like DNA and protein sequences are useful in
XX diagnostics and screening compounds for treating various cancers and
XX apoptosis abnormality, including gene therapy. The present DNA sequence
XX encodes a survivin-like protein of the invention
XX
XX Sequence 426 BP; 115 A; 112 C; 113 G; 86 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:          9.17e-82          Length:          426
Score:              778.00           Matches:         142
Percent Similarity: 100.00%           Conservative:    0
Best Local Similarity: 100.00%       Mismatches:     0
Query Match:        100.00%          Indels:         0
DB:                 6                 Gaps:          0

US-09-690-825-34 (1-142) x AAL42859 (1-426)
Qy 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
Db 1 ATGGGTGCGCCGACGTTGGCCCTGCTGGCAGCCCTTCTCAAGGACCAACCCGATCTCT 60
Qy 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
Db 61 ACATTCAAGAACTGGCGCTTCTTGGAGGCTGGCCCTGCGACCCCGAGCGGATGGCGGAG 120
Qy 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
Db 121 GCTGGCTTCATCCACTGCCCTGCTGGCAGCCGACACTTGGCCCGAGTGTTCCTCTGC 180
Qy 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluHisLysLysHis 80
Db 181 TTCAAGAGCTGGAAGCTGGAGCCGACAGATGACGACCCCATAGAGGAACATAAAGCAT 240
Qy 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
Db 241 TCGTCCGGTGGCGTTTCCTTCTGTCAAGAACGAGTTTGAAGAATTAACTTGTGTGA 300
Qy 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120
Db 301 TTTTGAACCTGGACAGAGAAGAGCCAGAACAAATTCGAAAGGAAACCAACATAAG 360
Qy 121 LysLysGluPheGluGluThrAlaLysLysValArgAlaIleGluGlnLeuAla 140
Db 361 AAGAAAGATTGAGGAAATTCGGAAGAAAGTGGCGCGTGCCTATCGAGCAGCTGGCTGCC 420
Qy 141 MetAsp 142
Db 421 ATGGAT 426

```

Db 241 TCGTCCGGTTGGCTTCTCTGTCAAGAGCAGTTTGAAGATTAAACCTTTGGTGAA 300
Qy 101 PheLeuLysLeuAspArgGluArgAlaLysAlaLysAlaLysGluThrAsnLys 120
Db 301 TTTTGAACCTGGACAGAGAGAGCCCAAGAACAAATTCGAAGAGGAAACCAACAATAAG 360
Qy 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaLysGluGluLeuAla 140
Db 361 AAGAAGAATTGTAGGAAACTGCGNAGAAAGTGGCCGTGCAATCGAGCAGCTGGCTGCC 420
Qy 141 MetAsp 142
Db 421 ATGGAT 426
RESULT 3
ID ACP58071 standard; DNA; 429 BP.
AC ACP58071;
XX
XX 15-JAN-2004 (first entry)
XX Human survivin protein encoding DNA.
DE RasGAP; Aurora kinase; cytostatic; anti-tumoural; human; survivin; gene;
KW ds.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT 1. .429
CDS /*tag= a
FT /product= "survivin"
XX
XX WO2003087395-A2.
XX
XX 23-OCT-2003.
XX 15-APR-2003; 2003WO-IB002972.
XX 15-APR-2002; 2002US-0372483P.
XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
XX Garbay C, Gigoux V, Canonis J, L'hoste S, Samson J;
XX WPI: 2003-845340/78.
XX P-PSDB; ABR61582.
XX Identifying anti-tumoral compounds, comprises determining the capacity of
PT a compound to inhibit interaction between RasGAP and Drosophila
PT melanogaster (Dm) aurora kinase, or between RasGAP, Dm aurora kinase and
PT aurora binding protein.
XX
XX Disclosure; Page 67; Opp; English.
XX The invention relates to identifying a biologically active compound with
CC anti-tumoral properties, where the compound is studied for its capacity
CC to inhibit the interaction between: (a) RasGAP and the Drosophila
CC melanogaster Aurora kinase or an orthologue of the kinase, or its
CC fragment able to interact with RasGAP; or (b) RasGAP, an Aurora-binding
CC protein and the D. melanogaster Aurora kinase or an orthologue of the
CC kinase, or its fragment. The method is useful for identifying anti-
CC tumoural agents. The present sequence represents a DNA encoding a human
CC survivin protein, an aurora-binding protein
XX
SQ Sequence 429 BP; 116 A; 112 C; 114 G; 87 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9.25e-82 Length: 429
Score: 778.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-09-690-825-34 (1-142) x ACP58071 (1-429)
Qy 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
Db 1 ATGGGTGCCCGCAGTGTGCCCTTCTGTGGAGGCTGGCTGCGCTGACCCCGGCGGATGGCCGAG 60
Qy 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
Db 61 ACATTCAAGAACTGGCCCTTCTTGGAGGCTGGCTGCGCTGACCCCGGCGGATGGCCGAG 120
Qy 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
Db 121 GCTGGCTTCATCCACTGCCCTTCTTCTGTCAAGAGCAGTGTGGCCAGTGTTCCTTCTGTC 180
Qy 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHisLysLysHis 80
Db 181 TTCAGAGAGCTGGAAGGCTGGAGCCAGATGACCCCATAGAGGAACATATAAAGCAT 240
Qy 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluLeuThrLeuGlyGlu 100
Db 241 TCGTCCGGTTGGCTTCTTCTGTCAAGAGCAGTTTGAAGATTAAACCTTTGGTGAA 300
Qy 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysAlaLysGluThrAsnAsnLys 120
Db 301 TTTTGAACCTGGACAGAGAGAGCCCAAGAACAAATTCGAAGAGGAAACCAACAATAAG 360
Qy 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaLysGluGluLeuAla 140
Db 361 AAGAAGAATTGTAGGAAACTGCGNAGAAAGTGGCCGTGCAATCGAGCAGTGTGGCTGCC 420
Qy 141 MetAsp 142
Db 421 ATGGAT 426
RESULT 4
ABZ83360
ID ABZ83360 standard; cDNA; 1024 BP.
XX
XX AC ABZ83360;
XX
XX 14-MAY-2003 (first entry)
XX Toxicologically relevant human nucleotide sequence #519.
XX Toxicologically relevant gene; toxicological response; gene; ss.
XX Homo sapiens.
XX WO2003016500-A2.
XX
XX 27-FEB-2003.
XX
XX 16-AUG-2002; 2002WO-US026514.
XX
XX 16-AUG-2001; 2001US-0313080P.
XX (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
XX Neft RE, Dunn RT, Adkins K, Pickett GG, Kier LD, Schweiser K;
PI Alen P;
XX
XX WPI: 2003-268322/26.
XX
XX Determining a toxicological response to an agent, useful for screening of
PT drugs, comprises comparing the expression profile of one or more human
PT toxic response genes to a reference gene expression profile indicative of
PT toxicity.
XX
XX Claim 1; Page 183; 455pp; English..
PS

XX The present invention describes a method (M1) for determining a
 CC toxicological response to an agent, which comprises comparing the
 CC expression profile of one or more human toxic response genes to a
 CC reference gene expression profile indicative of toxicity, and so
 CC determining the presence of a toxic response to the agent. Also
 CC described: (1) an array comprising one or more polynucleotides selected
 CC from the genes corresponding to the partial sequences given in AB282842
 CC to AB284764, or their fragments of at least 20 nucleotides, or homologues
 CC ; and (2) determining if a gene putatively identified to be a toxic
 CC response gene plays a role on toxic response pathways by determining the
 CC expression profile of the gene after exposure of cells or a human subject
 CC to a known toxic pharmaceutical or industrial agent, comprising: (a)
 CC exposing cells to an agent or isolating cells from a human subject who
 CC was exposed to an agent; (b) obtaining the test gene expression profile
 CC for a putatively identified toxic response gene after exposure to a known
 CC toxic pharmaceutical or industrial agent; and (c) comparing the test
 CC profile to the expression profile of a gene with a similar function or
 CC comparing the test profile to the expression profile of that gene after
 CC exposure to other known toxic compounds. The methods are useful for
 CC predicting and determining toxicological responses on a cellular, organ
 CC or system level. The arrays comprising the human genes are useful for
 CC toxicological screening of drugs, pharmaceutical compounds and chemicals
 XX

SQ Sequence 1024 BP; 209 A; 248 C; 288 G; 279 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 2,97e-81 Length: 1024
 Score: 778.00 Matches: 142
 Percent Similarity: 100.00% Conservativeness: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 7 Gaps: 0

US-09-690-825-34 (1-142) x AB283360 (1-1024)

Qy 1 MetGlyAlaProThrLeuProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
 Db 50 ATGGGTGCCCCGAGCGTTCGCCCTTGGAGGGCTGCGCTGACCCCGGAGCGATGGCGGAG 109
 Qy 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
 Db 110 ACATTCAGAACTGCGCTTCTTGGAGGGCTGCGCTGACCCCGGAGCGATGGCGGAG 169
 Qy 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPheCys 60
 Db 170 GCTGGCTTCATCCACTGCCCTCCCTGAGACGAGCAGACACTGGCCCGAGTGTCTTCTGC 229
 Qy 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluHisLysLysHis 80
 Db 230 TTCAGAGAGTGGAGCTGGAGCCGACATGACGACCCCTATAGGACATATAAAGCAT 289
 Qy 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
 Db 290 TCGTCGGTTCGGCTTCTTCTTGTCTGACAGAGCGAGTTGAGAAATTAACCTTGTGAA 349
 Qy 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120
 Db 350 TTTTGAATCTGGACAGAAAGAGCCCAAGAAATTTGCAAGGAAACCAACAATAG 409
 Qy 121 LysLysGluPheGluGluThrAlaLysLysValArgAlaIleGluGlnLeuAlaLa 140
 Db 410 AAGAAAGATTTGAGGAATTCGGAAGAAAGTGGCGGTGCGCATTCGAGCAGTGGCTGCC 469
 Qy 141 MetAsp 142
 Db 470 ATGGAT 475

RESULT 5
 ID AAA08903
 XX AAA08903 standard; DNA; 1619 BP.
 AC AAA08903;

XX 01-AUG-2000 (first entry)
 DT Human survivin DNA.
 XX
 DE Survivin; inhibitor of apoptosis; IAP; caspase inhibitor; caspase-3;
 KW cell cycle regulation; cancer; cytostatic; antisense oligonucleotide; ss.
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 DE CDS 50..478
 FT /*tag= a
 FT /product= "survivin"
 XX
 PN WO200019781-A1.
 XX
 PD 06-APR-2000.
 XX
 PF 23-SEP-1999; 99WO-US022076.
 XX
 PF 29-SEP-1998; 98US-00163162.
 XX
 PR 05-APR-1999; 99US-00286407.
 XX
 XX (ISIS-) ISIS PHARM INC.
 PA
 XX Bennett CF, Ackermann EJ, Swayze EE, Cowsert LM;
 XX WPI; 2000-293103/25.
 XX
 DR Antisense molecules targeted to Survivin, useful for inducing apoptosis
 XX in cancer cells.
 PT
 XX Example 13; Page 61-62; 73pp; English.
 PS
 XX This is the DNA sequence of human survivin (GenBank U75285), a member of
 CC the IAP (inhibitor of apoptosis) Caspase inhibitor family. Survivin has
 CC been found to be involved in cell cycle regulation and is expressed in
 CC the G2/M phase of the cell-cycle in a cell cycle regulated manner and
 CC associates with microtubules of the mitotic spindle. Disruption of this
 CC interaction results in loss of survivin's anti-apoptotic function and
 CC increased caspase-3 activity during mitosis. Caspase-3 is associated with
 CC apoptotic cell death. It is therefore believed that survivin may
 CC counteract a default induction of apoptosis in the G2/M phase. It is also
 CC believed that the over expression of survivin in cancer may overcome this
 CC apoptotic check point, allowing undesired survival and division of cancer
 CC cells. Antisense oligonucleotides (ASO's) may be used to down regulate
 CC endogenous survivin and to increase caspase-3-dependent apoptosis in
 CC cells in the G2/M phase. A08910-49 are ASO's that were analyzed for
 CC effect on survivin mRNA levels by quantitative real-time PCR. The data
 CC obtained were averages from three experiments. It was found that ISIS
 CC 23667 (A08925) provided 70% inhibition of Survivin and ISIS 23672
 CC (A08930) provided 64% inhibition. The ASO's may be used to inhibit the
 CC expression of human survivin genes for the treatment of diseases
 CC associated with overexpression of survivin. In particular, they may be
 CC used to induce apoptosis in tumor cells
 XX
 SQ Sequence 1619 BP; 349 A; 392 C; 449 G; 429 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 5,49e-81 Length: 1619
 Score: 778.00 Matches: 142
 Percent Similarity: 100.00% Conservativeness: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 3 Gaps: 0

US-09-690-825-34 (1-142) x AAA08903 (1-1619)

Qy 1 MetGlyAlaProThrLeuProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
 Db 50 ATGGGTGCCCCGAGCGTTCGCCCTTGGAGGGCTGCGCTGACCCCGGAGCGATGGCGGAG 109

Example 17; Page 56; 120pp; English.

US-09-690-825-34 (1-142) x AA521617 (1-1619)

QY	1	MetGlyValaProThrLeuProPheAlaTTrpGlnProPheLeuLysAspHisArgLysSer	20
DB	50	ATGGGTGCCCGACAGTGGCCCTGGCTGGCAGCCCTTCTCAAGACACACCCCATCTCT	109
QY	21	ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu	40
DB	110	ACATTCAAGAACTGGGCCCTTCTGGAGGGCTGGCTGCACCCCGAGCGGATGGCGCAG	169
QY	41	AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys	60
DB	170	GCTGGCTTTCATCCATGCCCCACTGAGACAGACCCAGACTTGGCCCCAGTGTTTCTCTGC	229
QY	61	PheLysGluLeuGluGlyTrpGluProAspAspAspProIleGluHisLysLysHis	80
DB	230	TTCAAGAGAGCTGGAAGCTGGGAGCCAGATGACGAGCCCATAGAGGAACATAAAAGCAT	289
QY	81	SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu	100
DB	290	TGCTCCGGTGGCTTCTCTCTGTCRAGAAGCAGTTTGAAAGAAATAACCCCTGGTGAA	349

Qy	101	PhsLeuLYsLeuAspArgGluArgAlaLYsAsnLYsIleAlaLYsGluThrAsnAsnLYs	120
Db	350	TTTTTGAAACTGGACAGAGAAAGAGCCAAGACAAAAATTGCAAAAGGAACCAACAATAAG	409
Qy	121	LYsLYsGluPheGluGluThrAlaLYsLYsValArgArgAlaIleGluGlnLeuAlaAa	140
Db	410	AGAAAGAAATTTAGGAAACTGCGAAGAAAGTCCGCGTGCCATCGAGCAGCTGGCTGCC	469
Qy	141	MetAsp 142	
Db	470	ATGGAT 475	
RESULT 7			
ABX76199			
ID	ABX76199 standard; DNA; 1619 BP.		
XX	ABX76199;		
XX	02-APR-2003 (first entry)		
XX	Lung cancer-associated polynucleotide #70.		
DE			
XX	Lung cancer-associated polynucleotide; gene; ds; cystostatic; emphysema;		
KW	antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;		
KW	small cell lung cancer; benign lesion; precancerous lesion; bronchitis;		
KW	chronic obstructive pulmonary disease; hypersensitivity pneumonitis;		
KW	interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.		
XX			
OS	Unidentified.		
XX			
PN	WO200286443-A2.		
XX			
PD	31-OCT-2002.		
XX			

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PF 18-APR-2002; 2002WO-US012476.
XX
PR 18-APR-2001; 2001US-0284770P.
PR 10-MAY-2001; 2001US-0290492P.
PR 09-NOV-2001; 2001US-0339245P.
PR 13-NOV-2001; 2001US-0350666P.
PR 29-NOV-2001; 2001US-0334370P.
XX 12-APR-2002; 2002US-0372246P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Aziz N, Murray R;
XX
DR WPI; 2003-093161/08.
DR P-PSDB; ABUS6477.
XX
XX Detecting a lung cancer-associated transcript in a cell from a patient
PT for treating lung cancer, by contacting a biological sample from the
PT patient with a polynucleotide that exhibits increased or decreased
PT expression in lung cancer.
XX
PS Claim 22; Page 242; 453pp; English.
XX
XX The invention relates to a method for detecting a lung cancer-associated
CC transcript in a cell from a patient, comprising contacting a biological
CC sample from the patient with a polynucleotide that selectively hybridizes
CC to a sequence that is at least 80 % identical to a gene that exhibits
CC increased or decreased expression in lung cancer samples. Lung cancer-
CC associated polynucleotides and polypeptides are used for identifying a
CC compound that modulates a lung cancer-associated polypeptide, for
CC inhibiting proliferation of a lung cancer-associated cell to treat lung
CC cancer in a patient and for treating a mammal having lung cancer by
CC administering a modulatory compound identified. The methods are useful
CC for treating lung cancer, such as small cell lung cancer, non-small cell
CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,
CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
CC bronchiectasis. The genes, polynucleotides and polypeptides are useful
CC for diagnostic purposes and as targets for screening for therapeutic
CC compounds that modulate lung cancer, such as antibodies. Sequences
CC ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the
CC invention
XX
SQ Sequence 1619 BP; 349 A; 392 C; 449 G; 429 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 5,49e-81 Length: 1619
Score: 778.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-09-690-825-34 (1-142) x ABX76199 (1-1619)

Qy 1 MetGlyAlaProThrLeuProProAlaTyrGlnProPheLeuLysAspHisArgIleSer 20
Db 50 ATGGGTGCCCGACGTTGGCCCTGCTGGCAGCCCTTTCTCAAGGACCACCGCATCTCT 109
Qy 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
Db 110 ACATTCAGAACTGGCCCTCTTGGAGGGCTGGCCCTGCACCCCGAGCGGATGGCCGAG 169
Qy 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
Db 170 GCTGGCTTCATCCACTGCCCACTGAGACGAGCCAGACTTGGCCCGAGTGTCTTCTCTCG 229
Qy 61 PheLysGluLeuGluGlyTyrGluProAspAspProIleGluHisLysLysHis 80
Db 230 TTCAAGGAGCTGGAAGCTGGAGCCGACATGACGACCCCATAGAGGAACATAAAAGCAT 289
Qy 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100

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Db 290 TCGTCGGTTCGGCTTCTTCTGTCAAGAGCAGTTTGAGGAATTAACCCCTGGTGAA 349
Qy 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAspAsnLys 120
Db 350 TTTTGAACCTGGACAGAGAAAGAGCCCAAGACAAATTCGAAAGGAAACCAACAATAG 409
Qy 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAla 140
Db 410 AAGAAAGAAATTTAGGAAACTGCGAAGAAAGTGGCGCGTCATCGAGCAGCTGGCTGCC 469
Qy 141 MetAsp 142
Db 470 ATGGAT 475

RESULT 8
AAL53734
ID AAL53734 standard; RNA; 1619 BP.
XX
AC AAL53734;
XX
DT 07-FEB-2003 (first entry)
XX
DE Survivin DNA sequence SEQ ID No 28.
XX
KW Target RNA; target RNA: support-attached test compound; flow cytometry;
KW mass spectrometry; high-throughput screening; ds.
XX
OS Homo sapiens.
XX
PN WO200283837-A1.
XX
PD 24-OCT-2002.
XX
PF 11-APR-2002; 2002WO-US011758.
PR 11-APR-2001; 2001US-0282966P.
XX
XX (PTCT-) PTC THERAPEUTICS INC.
XX
XX Almstead NG;
XX
XX WPI; 2003-075534/07.
XX
XX Identifying a test compound that binds to a target RNA molecule by
XX separating the detectably labeled target RNA: support-attached test
XX compound complex from uncomplexed target RNA molecules and test compounds
XX by flow cytometry.
XX
XX Example; Page 81; 131pp; English.
XX
XX The invention relates to a novel method for identifying a test compound
XX that binds to a target RNA molecule comprising separating the detectably
XX labeled target RNA: support-attached test compound complex from
XX uncomplexed target RNA molecules and test compounds. The separating
XX process is carried out by flow cytometry and determining a structure of
XX the type of test compound of the RNA: support-attached test compound
XX complex by mass spectrometry. The method is useful for high-throughput
XX screening of libraries of compounds to identify pharmaceutical leads.
XX This polynucleotide sequence represents a DNA sequence related to the
XX detecting method of the invention
XX
SQ Sequence 1619 BP; 349 A; 392 C; 449 G; 429 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 5,49e-81 Length: 1619
Score: 778.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-09-690-825-34 (1-142) x AAL53734 (1-1619)

```


QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
DB 50 ATGGGTGCCCCACGTTGCCCTCCCTGGCAGCCCTTCTCAAGGACCCACCGCATCTCT 109
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 110 ACATTCAAGAACTGGCCCTTCTTGAGGGCTGCGCTGCACCCGAGCGGATGCCGAG 169
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
DB 170 GTGGGCTTCATCCACTGCCCCACTGAGAACGAGCCAGACTTGGCCCACTGTTCTTCTG 229
QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHisLysLysHis 80
DB 230 TTCAGGAGCTGGAAGCTGGAGGCGAGTGCAGTGCAGCCCTAGAGAGACATATAAAGCAT 289
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
DB 290 TCGTCGGTGGCGCTTCTCTCTGCAAGAACTGCAAGAAAGTGCCTGCGCATCGAGCAGCTGCTGCC 349
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysLysLysLysLysLysLys 120
DB 350 TTTTGTAAACTGGACAGAGAAAGAGCCAAAGAAATTCGAAGGAAACCAACATTAAG 409
QY 121 LysLysGluPheGluGluThrAlaLysLysValArgAlaIleGluGluLeuAlaAla 140
DB 410 AAGAAAGAAATTTGAGGAACTGCAAGAAAGTGCCTGCGCATCGAGCAGCTGCTGCC 469
QY 141 MetAsp 142
DB 470 ATGGAT 475
RESULT 9
ID AAD49666 standard; DNA; 1619 BP.
AC AAD49666;
XX
XX
XX 24-MAR-2003 (first entry)
DE Human survivin DNA.
XX
XX Amyloidosis; haemophilia; Alzheimer's disease; atherosclerosis; cancer;
KW gigantism; dwarfism; hypothyroidism; hyperthyroidism; cystic fibrosis;
KW autoimmune disorder; aging; inflammation; diabetes; obesity; anorectic;
KW neurodegenerative disorder; Parkinson's disease; gene therapy; viricide;
KW haemostatic; antibacterial; neutropic; neuroprotective; cytostatic; XIAP;
KW fungicide; human; survivin; gene; ds.
OS Homo sapiens.
XX
XX WO200283953-A1.
PN
XX
XX 24-OCT-2002.
XX
XX 11-APR-2002; 2002WO-US011757.
XX
XX 11-APR-2001; 2001US-0282965P.
XX
XX (PTCT-) PTC THERAPEUTICS INC.
XX
XX Rando R, Welch E;
XX
XX WPI; 2003-075561/07.
XX
XX Identifying a test compound that binds to a target RNA molecule for
PT treating or preventing amyloidosis, hemophilia, cancer, gigantism,
PT diabetes, by contacting a detectably labeled target RNA molecule with a
PT library of test compounds.
XX
XX Example; Page 89-90; 152pp; English.
XX
XX The invention relates to a method for identifying a test compound that

CC binds to a target RNA molecule, which comprises contacting a detectably
CC labelled target RNA molecule with a library of test compounds under
CC conditions that permit direct binding of the labelled target RNA to a
CC member of the library of test compounds so that a detectably labeled
CC target RNA: test compound complex is formed. The method is useful for
CC screening libraries of compounds for those that are selectively bind to a
CC pre-selected target RNA. The compounds are useful for inhibiting the
CC formation of a specific bound RNA: host cell factor complexes in vivo.
CC They are also useful for treating or preventing diseases associated with
CC overproduction or decreased protein function, such as amyloidosis,
CC haemophilia, Alzheimer's disease, atherosclerosis, cancer, gigantism,
CC dwarfism, hypothyroidism, hyperthyroidism, autoimmune disorders, aging,
CC inflammation, cystic fibrosis, diabetes, obesity, neurodegenerative
CC disorders, Parkinson's disease or infections (bacterial, viral, fungal).
CC The invention is also used in gene therapy. The present sequence is human
CC survivin DNA. This sequence is used to illustrate the method of the
CC invention
XX
SQ Sequence 1619 BP; 349 A; 392 C; 449 G; 429 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 5,49e-81 Length: 1619
Score: 778.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
US-09-630-825-34 (1-142) x AAD49666 (1-1619)
QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
DB 50 ATGGGTGCCCCACGTTGCCCTCCCTGGCAGCCCTTCTCAAGGACCCACCGCATCTCT 109
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 110 ACATTCAAGAACTGGCCCTTCTTGAGGGCTGCGCTGCACCCGAGCGGATGCCGAG 169
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
DB 170 GTCGCTTCATCCACTGCCCCACTGAGAACGAGCCAGACTTGGCCCACTGTTCTTCTG 229
QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHisLysLysHis 80
DB 230 TTCAGGAGCTGGAAGCTGGAGGCGAGTGCAGTGCAGCCCTAGAGAGACATATAAAGCAT 289
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
DB 290 TCGTCGGTGGCGCTTCTCTCTGCAAGAACTGCAAGAAAGTTCGAAGAAATTAACCTTGGTGA 349
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysLysLysLysLysLysLys 120
DB 350 TTTTGTAAACTGGACAGAGAAAGAGCCAAAGAAATTCGAAGGAAACCAACATTAAG 409
QY 121 LysLysGluPheGluGluThrAlaLysLysValArgAlaIleGluGluLeuAlaAla 140
DB 410 AAGAAAGAAATTTGAGGAACTGCAAGAAAGTGCCTGCGCATCGAGCAGCTGCTGCC 469
QY 141 MetAsp 142
DB 470 ATGGAT 475
RESULT 10
ADE85228
ID ADE85228 standard; DNA; 1619 BP.
XX
XX ADE85228;
AC
XX
XX 29-JAN-2004 (first entry)
XX
XX Farnesyl transferase inhibitor modulated leukemia associated gene #447.
DE ss; cytostatic; farnesyl transferase inhibitor; gene expression;
XX
KW

KW quinolinone; leukemia; cancer.

XX Homo sapiens.

XX WO2003038129-A2.

XX 08-MAY-2003.

XX 30-OCT-2002; 2002WO-US034784.

XX 30-OCT-2001; 2001US-0338997P.

XX 30-OCT-2001; 2001US-0340081P.

XX 30-OCT-2001; 2001US-0340938P.

XX 30-OCT-2001; 2001US-0341012P.

XX (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.

XX Raponi M;

XX WPI; 2003-513497/48.

XX Determining whether a patient will respond to treatment with a farnesyl transferase inhibitor, by analyzing the expression of gene that is differentially modulated in the presence of the inhibitor.

XX Disclosure; SEQ ID NO 447; 346pp; English.

XX The invention relates to a method of determining whether a patient will respond to treatment with a farnesyl transferase inhibitor (FTI), by analyzing the expression of gene that is differentially modulated in the presence of an FTI. The method is useful for determining whether a patient will respond to treatment with a FTI such as (B)-6-[amino(4-chlorophenyl)(1-methyl-1H-imidazol-5-yl)methyl]-4-(3-chlorophenyl)-1-methyl-2-(1H)quinolinone, monitoring the therapy of a patient, treating a patient with leukemia with FTI if the analysis indicates that the patient will respond. This sequence corresponds to a gene whose expression may be modulated in the presence of FTI.

XX Sequence 1619 BP; 349 A; 392 C; 449 G; 429 T; 0 U; 0 Other;

XX Alignment Scores:

XX Pred. No.: 5,49e-81 Length: 1619

XX Score: 778.00 Matches: 142

XX Percent Similarity: 100.00% Conservativeness: 0

XX Best Local Similarity: 100.00% Mismatches: 0

XX Query Match: 100.00% Indels: 0

XX DB: 9 Gaps: 0

XX US-09-690-825-34 (1-142) x ADE85228 (1-1619)

XX QY 1 MetGlyAlaProThrLeuProAlaTrpGlnProPheLeuLysAspHisAlaGlySer 20

XX Db 50 ATGGTGCCCGACGAGTGGCCCTTCTGCGAGCCCTTCTCAAGGACCAACCCGATCTCT 109

XX QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40

XX Db 110 ACATTCAAGAACTGGCCCTTCTTGAGGGCTGGCCCTGCGCTGCACCCCGAGCGATGGCCGAG 169

XX QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60

XX Db 170 GCTGCTTCATCCACTGCCCTCCCTGAGACGAGCCAGCTGGCCGAGTCTTCTCTGTC 229

XX QY 61 PheLysGluLeuGluGlyTyrGluProAspAspProIleGluHisLysLysHis 80

XX Db 230 TTCAAGGAGCTGGAAGCTGGAGCCAGATGACGACCCCATAGAGGAACATAAAAGCAT 289

XX QY 81 SerSerGlyCysAlaPheLeuSerValLysGlnPheGluLeuThrLeuGlyGlu 100

XX Db 290 TCGTCCCGTTCGCTTCTTCTTCTGTCGAAGAGCAGTTTGAAGAATTAAACCTTGTGTAA 349

XX QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120

XX Db 350 TTTTGAACCTGGACAGAGAAGAGCCAGACAAATTCGAAGGAACCAACAATAG 409

QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAlaAla 140

Db 410 AAGAAGAAATTGAGAACTCGGAAGAAAGTGGCCGCTGCATCGACACATGGCTGCC 469

QY 141 MetAsp 142

Db 470 ATGGAT 475

RESULT 11

ABZ58106

ID ABZ58106 standard; cDNA; 1662 BP.

XX AC ABZ58106;

XX 22-APR-2003 (first entry)

XX Human Survivin cDNA.

XX Human; Survivin; inhibitor of apoptosis; cell death; apoptosis; cancer;

XX cytostatic; cardiant; neuroprotective; gene therapy; gene; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 43..471

XX FT /tag= a

XX FT /product= "Survivin"

XX WO2003004606-A2.

XX 16-JAN-2003.

XX 03-JUL-2002; 2002WO-US021002.

XX 03-JUL-2001; 2001US-00898158.

XX (UYCO) UNIV COLUMBIA NEW YORK.

XX Troy CM, Shelanski ML;

XX WPI; 2003-210351/20.

XX P-PSDB; ABP72162.

XX New nucleic acid encoding an inhibitor-of-apoptosis protein, useful for treating cancer, neurodegenerative disorder or cardiomyopathy.

XX Disclosure; Fig 20B; 124pp; English.

XX The present sequence is that of cDNA encoding human Survivin protein. The invention provides a nucleic acid, such as an antisense oligonucleotide, which specifically hybridizes to a nucleic acid encoding an inhibitor of apoptosis protein. Survivin is an example of an inhibitor of apoptosis or inducer of cell death protein of the invention. A claimed method for inducing a cell's death comprises contacting the cell with the nucleic acid under conditions permitting the nucleic acid to enter the cell, especially the use of a vector, liposome, or a mechanical or electrical means. The method is used to treat acute lymphocytic leukaemia, acute myelogenous leukaemia, lung cancer, breast cancer, ovarian cancer, prostate cancer, lymphoma, Hodgkin's disease, malignant melanoma, neuroblastoma, renal cell carcinoma and squamous cell carcinoma (all claimed). The invention also provides a second nucleic acid, which specifically hybridizes to a nucleic acid encoding a protein, other than caspase-2, that induces cell death. A claimed method for inhibiting a cell's death comprises contacting the cell with the nucleic acid under conditions permitting the nucleic acid to enter the cell. The method is used to treat a neurodegenerative disorder (especially a brain disorder or central nervous system disorder), or a heart disorder (especially cardiomyopathy) in a human (all claimed).

XX Sequence 1662 BP; 396 A; 389 C; 451 G; 426 T; 0 U; 0 Other;

XX Alignment Scores:

Pred. No.: 5,698-81 Length: 1662
 Score: 778.00 Matches: 142
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 7 Gaps: 0

US-09-690-825-34 (1-142) x ABZ59106 (1-1662)

QY 1 MetGlyAlaProThrLeuProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
 DB 43 ATGGGTGCGCGACGTTGCCCGCTGCTGGCAGCGCTTCTCAAGGACCCACCGCATCTCT 102
 QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
 DB 103 ACATTCAAGAACTGGCCCTTTCTGGAGGCTCGCGCTGCACCCCGGACCGATGGCGGAG 162
 QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
 DB 163 GCTGGCTTCATCCACTGCCCGCTGAGAACGAGCGAGACTTGGCCCGAGTGTCTTCTGTC 222
 QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProlleGluGluHisLysLysHis 80
 DB 223 TTCAAGGAGCTGGAAGGTGGAGCGCAGATGACGACCCCATAGAGGAACATAAAAGCAT 282
 QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
 DB 283 TGTCTCGGTGGCTTCTCTCTCAAGAGCAGTTTGAAGATTAAACCTTGGTGAA 342
 QY 101 PheLeuLysLeuAspArgGluArgAlaLysLysLysLysLysLysLysLysLysLys 120
 DB 343 TTTTGTAAACTGGACAGAGAAAGAGCCAAAGAACAAAATTGCAAGGAAACCAACAATAAG 402
 QY 121 LysLysGluPheGluGluThrAlaLysLysValArgAlaLysLysLysLysLysLys 140
 DB 403 AAGAAAGAAATTTGAGAAACTCCGAAGAAAGTGGCCCGTGCATCGACGACGCTGGCTGCC 462

QY 141 MetAsp 142

DB 463 ATGGAT 468

RESULT 12

ID ACRA03988 standard; cDNA; 2404 BP.

AC ACRA03988;

DT 27-MAY-2003 (first entry)

XX cDNA downregulated in senescent cells Incyte ID NO: 251651.4.

XX Human; senescence; s6; gene; cancer; proliferative disorder; leukaemia;
 KW adenocarcinoma; lymphoma; melanoma; myeloma; sarcoma; testatocarcinoma;
 KW adrenal gland cancer; bladder cancer; bone cancer; bone marrow cancer;
 KW brain cancer; breast cancer; cervical cancer; colon cancer; heart cancer;
 KW oesophageal cancer; gall bladder cancer; glioma; glioblastoma; kidney cancer;
 KW liver cancer; lung cancer; muscle cancer; ovarian cancer; penile cancer;
 KW pancreatic cancer; parathyroid gland cancer; prostate cancer;
 KW salivary gland cancer; skin cancer; small intestine cancer;
 KW spleen cancer; stomach cancer; testicular cancer; thymic cancer;
 KW thyroid cancer; uterine cancer.

XX Homo sapiens.

XX US2002192679-A1.

XX 19-DEC-2002.

XX 07-FEB-2002; 2002US-00071766.

XX 09-FEB-2001; 2001US-0268380P.

XX (CHEN/) CHEN H.

XX Chen H;

XX WPI: 2003-32858/31.

XX New combination comprising cDNAs or their complements, useful for
 PT detecting changes in expression of genes encoding proteins associated
 PT with senescence, and in diagnosing, staging or treating proliferative
 PT diseases, e.g. cancer.

XX Example 13; Page 135-136; 195pp; English.

XX The invention relates to a combination comprising a plurality of cDNAs,
 CC or their complements that are differentially expressed in cancer and
 CC other proliferative disorders. The combination is useful in detecting
 CC changes in expression of genes encoding proteins that are associated with
 CC senescence and in diagnosing, staging, treating, or monitoring the
 CC progression or treatment of subjects with proliferative diseases such as
 CC cancer e.g. adenocarcinoma, leukaemia, lymphoma, melanoma, myeloma,
 CC sarcoma, testatocarcinoma; cancer of the adrenal gland, bladder, bone,
 CC bone marrow, brain, breast, cervix, colon, oesophagus, gall bladder,
 CC ganglia, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid
 CC gland, penis, prostate, salivary glands, skin, small intestine, spleen,
 CC stomach, testis, thymus, thyroid and uterus. The present sequence
 CC represents cDNA of genes that are downregulated in senescent cells

XX SQ Sequence 2404 BP; 525 A; 588 C; 634 G; 628 T; 0 U; 29 Other;

Alignment Scores:

Pred. No.: 9,338-81 Length: 2404
 Score: 778.00 Matches: 142
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 7 Gaps: 0

US-09-690-825-34 (1-142) x ACRA03988 (1-2404)

QY 1 MetGlyAlaProThrLeuProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
 DB 56 ATGGGTGCGCGACGTTGCCCGCTGCTGGCAGCGCTTCTCAAGGACCCACCGCATCTCT 115

QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
 DB 116 ACATTCAAGAACTGGCCCTTTCTGGAGGCTCGCGCTGCACCCCGGACCGATGGCGGAG 175

QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
 DB 176 GCTGGCTTCATCCACTGCCCGCTGAGAACGAGCGAGACTTGGCCCGAGTGTCTTCTGTC 235

QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProlleGluGluHisLysLysHis 80
 DB 236 TTCAAGGAGCTGGAAGGCTGGGAGCGCAGATGACGACCCCATAGAGGAACATAAAAGCAT 295

QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
 DB 296 TGTCTCGGTGGCTTCTCTCTGTCAGAGCAGTGTGAAGATTAAACCTTGGTGAA 355

QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysLysLysLysLysLysLys 120
 DB 356 TTTTGTAAACTGGACAGAGAAAGCCAGAACAAAATTGCAAGGAAACCAACAATAAG 415

QY 121 LysLysGluPheGluGluThrAlaLysLysValArgAlaLysLysLysLysLysLys 140
 DB 416 AAGAAAGAAATTTGAGAAACTCGAGAAAGTGGCCCGTGCATCGACGACGCTGGCTGCC 475

QY 141 MetAsp 142

DB 476 ATGGAT 481

RESULT 13

AAQ93052/c

ID AAQ93052 standard; cDNA; 1165 BP.

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XX AAQ93052;
XX AC
XX DT 25-MAR-2003 (revised)
XX DT 07-DEC-1995 (first entry)
XX DE Human EPR-1 cDNA.
XX KW Effector cell protease receptor-1; EPR-1; lymphocyte;
XX KW lymphoproliferative disorder; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT CDS 37..1050
XX FT /*tag= a
XX FN WO9520655-A1.
XX PD 03-AUG-1995.
XX PF 18-JAN-1995; 95WO-US000666.
XX PR 28-JAN-1994; 94US-00189309.
XX PA (SCRI ) SCRIPPS RES INST.
XX PI Altieri DC;
XX DR WPI; 1995-275440/36.
XX DR P-PSDB; AAR76744.
XX PT New effector cell protease receptor-1 protein - used to develop prods.
XX PT for inducing lymphocyte proliferation or diagnosis and treatment of
XX PT lymphoproliferative disorders.
XX PS Claim 10; Page 154-155; 181pp; English.
XX CC Immunoscreening of a human lymphocyte expression library in lambda- gt11
XX CC using a MAB raised against human EPR-1 yielded clone lambda-104. This was
XX CC used as a probe in further screening of human cDNA libraries, and a
XX CC consensus EPR-1 cDNA sequence was deduced from 28 isolated clones. The
XX CC DNA can be used for prodn. of recombinant EPR-1. (Updated on 25-MAR-2003
XX CC to correct FN field.)
XX SQ Sequence 1165 BP; 293 A; 331 C; 300 G; 241 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.15e-77 Length: 1165
Score: 748.00 Matches: 1165
Percent Similarity: 99.30% Conservative: 1
Best Local Similarity: 98.59% Mismatches: 1
Query Match: 96.14% Indels: 1
DB: 2 Gaps: 0

US-09-690-825-34 (1-142) x AAQ93052 (1-1165)

QY 1 MetGlyAlaProThrLeuProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
DB 1114 ATGGGTGCCCGGACGTTGCCCTTCTGGCAGCCCTTTCTCAAGACACCGCATCTCT 1055
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 1054 ACATTCAAGAACTGGCCCTTTCTTGGAGGGCTGGCG-TGCACCCCGGAGCGGATGGCCGAG 996
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
DB 995 GCTGGCTTCATCCATGCCCATCTGAGACGACGACGACGATTTGGCCAGTGTCTTCTTGC 936
QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluHisLysHis 80
DB 935 TTCAAGGAGCTGAAGCTGGGAGCCAGATGACGACCCCATAGAGGACATATAAAGCAT 876

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81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
875 TCGTCCGGTTCGGCTTTCCTTCTGTCAAGAAGCAGTTTGAGAAATTAAACCTTGGTGA 816
101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
815 TTTTGAACCTGGACAGAGAAAGAGCCAAAGAAATTTGCAAGGAAACCAACATAAG 756
121 LysLysGluPheGluGluThrAlaLysLysValArgAlaIleGluGlnLeuAlaAla 140
755 AAGAAAGAAATTTGAGAAACTGCGAAGAAAGTGGCGTGCATCGAGCAGCTGCCTCG 696
141 MetAsp 142
695 ATGGAT 690

RESULT 14
ACAS6320
ID ACAS6320 standard; cDNA; 740 BP.
XX ACAS6320;
AC ACAS6320;
XX 06-JUN-2003 (first entry)
XX Human signalling pathway polynucleotide probe SEQ ID NO 918.
XX Human; probe; ss; array element; Parkinson's disease;
XX signalling pathway population; cancer; adenocarcinoma; leukaemia;
XX immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
XX Homo sapiens.
XX OS
XX US6500938-B1.
XX 31-DEC-2002.
XX 30-JAN-1998; 98US-00016434.
XX 30-JAN-1998; 98US-00016434.
XX (INCY-) INCYTE GENOMICS INC.
XX Au-Young J, Seilhamer JJ;
XX WPI; 2003-352189/33.
XX Combination of polynucleotide probes, useful as array elements in a
XX microarray for monitoring the expression of a number of target
XX polynucleotides.
XX Claim 1; SEQ ID NO 918; 65pp; English.
XX The invention relates to a combination which, comprises a number of
XX polynucleotide probes comprising a sequence selected from one of the 1490
XX sequences mentioned in the specification. The combination is useful as an
XX array element in a microarray for monitoring the expression of a number
XX of target polynucleotides. The microarray is particularly useful in the
XX diagnosis and treatment of cancer and immunopathology and neuropathology.
XX The microarray is useful in diagnostics and treatment regimens, drug
XX discovery and development, toxicological and carcinogenicity studies,
XX forensics and pharmacogenomics. The microarray is also useful for
XX monitoring progression of diseases and for developing sophisticated
XX profiles for the effects of currently available therapeutic drugs. The
XX combination is also useful for purifying a subpopulation of mRNAs, cDNAs
XX and genomic fragments and in research and diagnostic applications. The
XX array can detect changes in expression in a large number of genes coding
XX for different signaling pathway populations which can be used to diagnose
XX various diseases including cancer e.g. adenocarcinoma and leukaemia,
XX immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease
XX and Parkinson's disease. The present sequence represents a polynucleotide
XX probe of the invention. Note: The sequence data for this patent did not
XX form part of the printed specification but was obtained in electronic
XX format directly from USPTO at

```
CC seqdata.uspto.gov/sequence.html?DocID=06500938B1
XX SQ Sequence 740 BP; 170 A; 186 C; 189 G; 184 T; 0 U; 11 Other;

Alignment Scores:
Pred. No.: 9,096-75 Length: 740
Score: 721.00 Matches: 135
Percent Similarity: 95.74% Conservative: 6
Best Local Similarity: 95.74% Mismatches: 0
Query Match: 92.67% Indels: 1
DB: 7 Gaps: 0

US-09-690-825-34 (1-142) x ACA56320 (1-740)
QY 2 GlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSerThr 21
DB 22 GGGTGGCNCNCCTTGGCACT-SCCTGGCNCCTTCTCAAGGACCACCGCATCTCTACA 80
QY 22 PheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGluAla 41
DB 81 TTCAAGAACTGGCCCTTCTTGGAGGGCTGCGCTGCACCCCGAGCGATGCGGAGGCT 140
QY 42 GlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCysPhe 61
DB 141 GCTTCATCCATGCCCCACTGANAACGAGCGAGACTTGGCCAGTGTCTCTGCTTC 200
QY 62 LysGluLeuGluGlyTrpGluProAspAspProIleGluGluHisLysLysHisSer 81
DB 201 AAGGAGCTGGAAGGTGGGAGCGAGATGACGACCCCATAGAGGAACATAAAGCATTCG 260
QY 82 SerGlyCysAlaPheLeuSerValLysGlnPheGluGluLeuThrLeuGlyGluPhe 101
DB 261 TCCGGTGGCGCTTCTTCTGTCAAGAGCAGTTTGAAGAATTAAACCTTGGTGAATT 320
QY 102 LeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLysLys 121
DB 321 TTGAACTCGACAGAGAAAGAGCCAAAGAAATTTGCAAGGAAACCAACCAATAAGAG 380
QY 122 LysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAlaMet 141
DB 381 AAAGAATTTGAGGAACCTCGAAGAAAGTGCGCGCCGTCATCGAGCAGCTGCTGCCATG 440
QY 142 Asp 142
DB 441 GAT 443

RESULT 15
ID AAT72714
XX AAT72714 standard; DNA; 500 BP.
AC AAT72714;
XX AAT72714;
DT 16-SEP-1997 (first entry)
XX Mouse inhibitor of apoptosis protein homologue MIHD DNA.
DE Inhibitor of apoptosis protein; IAP; mammalian IAP homologue; MIHD;
XX degenerative disease; infectious disease; autoimmune disease; cancer;
KW gene therapy; diagnosis; ss.
XX Mus musculus.
XX Key Location/Qualifiers
XX CDS 48..470
XX /*tag= a
XX WO9723501-A1.
XX 03-JUL-1997.
XX 20-DEC-1996; 96WO-AU000827.
XX 22-DEC-1995; 95AU-00007275.
XX FR
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XX (AMRA-) AMRAD OPERATIONS PTY LTD.
XX PA Vaux DL;
XX PI
XX WPI; 1997-350966/32.
XX P-PSDB; AAM19749.
XX Isolated protein homologues of viral inhibitors of apoptosis - used to
XX modulate apoptosis for treatment of degenerative, infectious or
XX auto-immune diseases and cancer.
XX Claim 28; Page 71-72; 136pp; English.
XX An isolated nucleic acid molecule (AAT72714) codes for mammalian IAP
XX homologue D (MIHD) (AAM19749), a murine homologue of baculovirus
XX inhibitor of apoptosis protein (IAP). It was isolated following a
XX database search for sequences showing homology to a consensus sequence
XX (see also AAM19744) for IAP homologues. Animal IAP homologue nucleic
XX acids (see also AAT72710-13 and AAT72715-17) can be used to produce
XX polypeptides useful in methods for modulating apoptosis in animal cells,
XX specifically for treatment, by inhibition, of degenerative and infectious
XX disease or, by promotion, of cancer and autoimmune disease, and can be
XX used for gene therapy of these diseases
XX SQ Sequence 500 BP; 134 A; 131 C; 135 G; 100 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 7,486-68 Length: 500
Score: 660.00 Matches: 118
Percent Similarity: 92.86% Conservative: 12
Best Local Similarity: 84.29% Mismatches: 10
Query Match: 84.83% Indels: 0
DB: 2 Gaps: 0

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QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
DB 48 ATGGGAGCTCGGCGCTGCCCGATCTGGCAGCTGTACCTCAAGAACTACCAGCATGCC 107
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DB 108 ACCTTCAAGAACTGGCCCTTCTTGGAGGACTGGCGCTGCACCCCGAGCGAATGGCGGAG 167
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
DB 168 GCTGGCTTCATCACTGCCCTACCGAAGACGAGCTGATTTGGCCAGTGTCTTTTCTGC 227
QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHisLysLysHis 80
DB 228 TTTAAGGAATTGGAAGCTGGGAACCCGATGACAAACCCGATAGAGGAGCATAGAAGCAC 287
QY 81 SerSerGlyCysAlaPheLeuSerValLysGlnPheGluGluLeuThrLeuGlyGlu 100
DB 288 TCCCGCTGGCTGGCGCTTCTTCTCAAGAGAGCAGATGGAAGAACTAACCGTCAGTGAA 347
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
DB 348 TTTCTTGAACCTGGACACAGACAGAGAGCCAGACAAATTCGAAAGGAGAGACCAACAAG 407
QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAla 140
DB 408 CAAAAAGAGTTTGAAGAGACTGCAAGAGACTACCCGCTCAGTCAATTGAGCAGCTGGTGC 467

Search completed: August 15, 2004, 22:24:53
Job time : 463 secs
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DEFINITION Survivin-like polypeptide and its DNA.
ACCESSION BD185366
VERSION BD185366.1 GI:31877566
KEYWORDS JP 2002355062-A/6.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 426)
AUTHORS Tanaka, H. and Kaieda, I.
TITLE Survivin-like polypeptide and its DNA
JOURNAL Patent: JP 2002355062-A 6 10-DEC-2002;
TAKEDA CHEMICAL INDUSTRIES LTD
COMMENT OS Homo sapiens (human)
PN JP 2002355062-A/6
DD 10-DEC-2002
PF 16-OCT-2001 JP 2001318533
PI HIROSHI TANAKA, ISAO KAIEDA
PC C12N15/09, A61K31/7088, A61K38/55, A61K39/395, A61K48/00, A61P35/00,
PC A61P43/00, A61P43/00, C07K14/82, C07K16/32, C12N1/15, C12N1/19, PC
C12N1/21,
PC C12N5/10, C12P21/02, C12Q1/02, C12Q1/68, G01N33/15, G01N33/50, PC
G01N33/53,
PC G01N33/53, G01N33/566, G01N33/574, C12N15/00, C12N5/00, A61K37/64
CC Survivin-like polypeptide and its DNA
FH Key Location/Qualifiers
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FEATURES
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Pred. No.: 3,018-77 Length: 426
Score: 778.00 Matches: 142
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-690-825-34 (1-142) x BD185366 (1-426)

QY 1 MetGlyAlaProThrLeuProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
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QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
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QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPheCys 60
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QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluHisLysLysHis 80
DB 181 TTCAAGGAGCTGGAAGCTGGGAGCGAGATGACGCCCATAGAGGAACATATAAAGCAT 240
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DB 241 TCGTCCGGTTGCCCTTCTCTCTGTCAGAAAGCAGTTTGAAGAAATTAACCCCTTGGTGAA 300
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysLysLysLysLysLysLys 120
DB 301 TTTTGTAAACTGGACAGAGAAAGAGCCAGAACAAAAATTGCAAGGAAACCAACAATAAG 360
QY 121 LysLysGluPheGluGluThrAlaLysLysValArgAlaIleGluGlnLeuAla 140
DB 361 AAGAAAGAAATTTGAGGAACTGCGAAGAAAGTGGCCGCTGCCATCGAGCAGCTGGCTGCC 420

QY 141 MetAsp 142
DB 421 ATGGAT 426

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AR099347
LOCUS AR099347 1619 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 1 from patent US 6077709.
ACCESSION AR099347
VERSION AR099347.1 GI:12809113
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1619)
AUTHORS Bennett, C. Frank., Ackermann, E. J., Swayze, E. E. and Cowsett, L. M.
TITLE Antisense modulation of Survivin expression
JOURNAL Patent: US 6077709-A 1 20-JUN-2000;
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Score: 778.00 Matches: 142
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Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

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DB 170 GCTGGCTTCTACCTGCCCCCATGAGACGACGACAGCTTGGCCAGCTGTTCTTCGTC 229
QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluHisLysLysHis 80
DB 230 TTCAAGGAGCTGGAAGCTGGGAGCCAGATGACGCCCATAGAGGAACATATAAAGCAT 289
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
DB 290 TCGTCCGGTTGCCCTTCTCTCTGTCAGAAAGCAGTTTGAAGAAATTAACCCCTTGGTGAA 349
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysLysLysLysLysLysLys 120
DB 350 TTTTGTAAACTGGACAGAGAAAGAGCCAGAACAAAAATTGCAAGGAAACCAACAATAAG 409
QY 121 LysLysGluPheGluGluThrAlaLysLysValArgAlaIleGluGlnLeuAla 140
DB 410 AAGAAAGAAATTTGAGGAACTGCGAAGAAAGTGGCCGCTGCCATCGAGCAGCTGGCTGCC 469
QY 141 MetAsp 142
DB 470 ATGGAT 475

RESULT 5
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LOCUS BD273550 1619 bp DNA linear PAT 17-JUL-2003
DEFINITION Antisense modulation of survivin expression.
ACCESSION BD273550
VERSION BD273550.1 GI:33083318

KEYWORDS JP 2002539073-A/1.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1619)
 AUTHORS Bennett, F.C., Ackermann, E.J., Swayze, E.E. and Cowsett, L.M.
 TITLE Antisense modulation of survivin expression
 JOURNAL Patent: JP 2002539073-A 1 19-NOV-2002;
 ISIS PHARMACEUTICALS INC
 COMMENT OS Homo sapiens (human)
 PN JP 2002539073-A/1
 PD 19-NOV-2002
 PF 23-SEP-1999 JP 2000572239
 PR 29-SEP-1998 US 09/163162.05-APR-1999 US 09/286407 PI
 FRANK C BENNETT, ELIZABETH J ACKERMANN, ERIC E SWAYZE, LEX M PI
 COWSETT
 FC C07H21/04, A61K31/7088, A61K31/712, A61K48/00, A61P35/00 CC
 Antisense modulation of survivin expression
 FH Key Location/Qualifiers
 FT CDS (50)..(478).
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 /organism="Homo sapiens"
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 Pred. No.: 778.00 Matches: 142
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 Percent Similarity: 100.00% Conservative: 0
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 DB: 6 Gaps: 0
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 QY 21 ThrPheLysAsnTrpProPheLeuGluCysAlaCysThrProGluArgMetAlaGlu 40
 Db 110 ACATTCAAGAACTGGCCCTCTTGGAGGGCTGCGCTGCACCCCGAGCGATGGCCGAG 169
 QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPheCys 60
 Db 170 GCTGGCTTCATCCACTGCCCTGAGAACGAGCCAGACTTGGCCAGTGTCTTCTGTC 229
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 Db 230 TTCAAGGAGCTGGAGGCTGGAGCCAGATGACGCCATAGAGGAACATAAAGCAT 289
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 Db 290 TCGTCCGGTTCGCTTCTTCTGTCAGAGGAGCATTTGAAGATTAACCTTGGTGAA 349
 QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysLysLysLysGluThrAsnLys 120
 Db 350 TTTTGAACCTGGACAGAGAAAGAGCCAAAGAAATTTGCAAGGAACCAACAATAAG 409
 QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAla 140
 Db 410 AAGAAGAAATTTGAGAACTGCGAAGAAAGTGGCGGTGCGCATCGAGCAGCTGGCTGCC 469
 QY 141 MetAsp 142
 Db 470 ATGGAT 475
 RESULT 7
 AX775129 1619 bp DNA linear PAT 09-JUL-2003
 LOCUS Sequence 445 from Patent WO03038129.
 DEFINITION AX775129
 ACCESSION AX775129
 VERSION AX775129.1 GI:32486645
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1
 AUTHORS Raponi, M.
 TITLE Methods for assessing and treating leukemia

JOURNAL Patent: WO 03038129-A 445 08-MAY-2003;
Ortho-Clinical Diagnostics, Inc. (US)
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ORIGIN

Alignment Scores:
Pred. No.: 1 38e-76 Length: 1619
Score: 778.00 Matches: 142
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-690-825-34 (1-142) x AX775129 (1-1619)

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DB 50 ATGGGTGCCCCGACGTTGGCCCTGCTGGCAGCCCTTTCTCAAGGACCAACCGCATCTCT 109
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 110 ACATTCAAGAACTGGCCCTTTCTGGAGGCTGGCTGCACCCCGAGCGGATGCGCGAG 169
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPheCys 60
DB 170 GCTGGCTTCATCCACTGCCCTGAGAACGAGCAGACTTGGCCGAGTGTTCCTCTGC 229
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DB 230 TTCAGGAGCTGGAGGCTGGAGCGAGATGACGCCCATAGAGAAACATAAAAGCAT 289
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DB 290 TCGTCCGGTTGGCTTTCCTTCTGTCAGAGAGCAGTTTGAAGATTAAACCTTGGTGA 349
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DB 350 TTTTGAAGAACTGGACAGAGAAAGAGCAAGAAACAAAATTGCAAGGAAACCAACAAATAG 409
QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAlaAla 140
DB 410 AGAAGAAGATTGAGGAAACTGCGAAGAAAGTGGCCGCTGCCATCGAGCAGCTGCTGCC 469
QY 141 MetAsp 142
DB 470 ATGGAT 475

RESULT 8

AX779941
LOCUS AX779941 1619 bp DNA linear PAT 14-JUL-2003
DEFINITION Sequence 2098 from Patent WO03039443.
ACCESSION AX779941
VERSION AX779941.1 GI:32696935

KEYWORDS Homo sapiens (human)

SOURCE

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1
AUTHORS Haferlach, T., Schoch, C., Kern, W., Kohlmann, A., Schnittger, S.,
Dugas, M., Sills, R., Brors, B. and Mergenthaler, S.
TITLE Novel genetic markers for leukemias
JOURNAL Patent: WO 03039443-A 2098 15-MAY-2003;
Ludwig-Maximilians-Universitaet Muenchen (DE) ;
PD Dr. Dr. (DE) ; Schoch, Claudia (DE) ; Kern, Wolfgang (DE)

FEATURES

source
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ORIGIN

Alignment Scores:
Pred. No.: 1 38e-76 Length: 1619
Score: 778.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-690-825-34 (1-142) x AX779941 (1-1619)

QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
DB 50 ATGGGTGCCCCGACGTTGGCCCTGCTGGCAGCCCTTTCTCAAGGACCAACCGCATCTCT 109
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DB 110 ACATTCAAGAACTGGCCCTTTCTGGAGGCTGGCTGCACCCCGAGCGGATGCGCGAG 169
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DB 170 GCTGGCTTCATCCACTGCCCTGAGAACGAGCAGACTTGGCCGAGTGTTCCTCTGC 229
QY 61 PheLysGluLeuGluGlyTrpGluProAspAspAspProIleGluHisLysLysHis 80
DB 230 TTCAGGAGCTGGAGGCTGGAGCGAGATGACGCCCATAGAGAAACATAAAAGCAT 289
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluLeuThrLeuGlyGlu 100
DB 290 TCGTCCGGTTGGCTTTCCTTCTGTCAGAGAGCAGTTTGAAGATTAAACCTTGGTGA 349
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120
DB 350 TTTTGAAGAACTGGACAGAGAAAGAGCAAGAAACAAAATTGCAAGGAAACCAACAAATAG 409
QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAlaAla 140
DB 410 AGAAGAAGATTGAGGAAACTGCGAAGAAAGTGGCCGCTGCCATCGAGCAGCTGCTGCC 469
QY 141 MetAsp 142
DB 470 ATGGAT 475

RESULT 9

AF077350
LOCUS AF077350 1629 bp mRNA linear PRI 14-DEC-2000
DEFINITION Homo sapiens inhibitor of apoptosis homolog mRNA, complete cds.
ACCESSION AF077350
VERSION AF077350.1 GI:4959078

KEYWORDS Homo sapiens (human)

SOURCE

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1
AUTHORS Uren, A.G., Wong, L., Pakusch, M., Fowler, K.J., Burrows, F.J.,
Vaux, D.L. and Choo, K.H.
TITLE Survivin and the inner centromere protein INCENP show similar
cell-cycle localization and gene knockout phenotype
JOURNAL Curr. Biol. 10 (21), 1319-1328 (2000)

MEDLINE

PUBMED 11084331

REFERENCE

2 (bases 1 to 1629)

Uren, A.G. and Vaux, D.L.

AUTHORS

Direct Submission
Submitted (02-OCT-1997) Molecular Cancer Division, The Walter and
Eliza Hall Institute, Royal Parade, Parkville, Vic 3052, Australia

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ORIGIN
Alignment Scores:
Pred. No.: 1.39e-76 Length: 1629
Score: 778.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 85 ACATTCAGAACTGGCCCTCTTGGAGGGCTGGCCCTGCACCCCGGAGCGGATGGCGGAG 144
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPheCys 60
DB 145 GCTGGCTTCATCCACTGCCCCACCTGAGAACGAGCCAGACCTTGCCCGAGTGTTCCTGTCG 204
QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluHisLysLysHis 80
DB 205 TTCAAGGAGCTGGAAGCTGGAGCCAGATGACGACCCCATAGAGGAACATAAAGCAT 264
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
DB 265 TCGTCCGGTTCGGCTTTCCTTCCTGTCGCAAGAGCAGTTTGAAGAAATTAACCTTGTTGAA 324
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
DB 325 TTTTGAACCTGGACAGAAAGAGGCAAGACAAATTCGAAAGGAACCAACAATAAG 384
QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAlaIle 140
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QY 141 MetAsp 142
DB 445 ATGGAT 450

RESULT 10
BC034148 1643 bp mRNA linear PRI 12-NOV-2003
LOCUS Homo sapiens baculoviral IAP repeat-containing 5 (survivin), mRNA
DEFINITION (CDNA clone MGC:32768 IMAGE:4656567), complete cds.
ACCESSION BC034148
VERSION BC034148.1 GI:21707886
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1643)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Haieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.D.,
Scheetz,T.E., Brownstein,M.J., Ustin,T.B., Toshiyuki,S.,
Carrinici,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Faney,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whitting,M., Madan,A., Young,A.C., Shavchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,B.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Kzywinski,M.I., Skalska,U., Smalilus,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
12477932
2 (bases 1 to 1643)
Strausberg,R.
Direct Submission
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
JOURNAL
TITLE
REMARK
COMMENT
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www.shgc.stanford.edu
Contact: (Dickson, Mark) mcdpaxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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/notes="synonyms: API4, SURVIVIN, EPR-1"
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/db_xref="GI:21707887"
/db_xref="LocusID:332"
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/notes="BIR; Region: Baculoviral inhibition of apoptosis
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/db_xref="CDD:smart00238"

FEATURES
source
gene
CDS
misc_feature
ORIGIN

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Alignment Scores:

Pred. No.: 1,4e-76 Length: 1643
 Score: 778.00 Matches: 142
 Percent Similarity: 100.00% Conservativity: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-690-825-34 (1-142) x BC034148 (1-1643)

QY 1 MetGlyAlaProThrLeuProProlaTrpGlnProPheLeuLeuAspHisArgIleSer 20
 Db 45 ATGGGTGCCCCGACGTTGCCCTGCTGGCAGCCCTTCTCAAGGACCCACCGCATCTCT 104
 QY 21 ThrPheLysAsnTrpPropheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
 Db 105 ACATTCAAGAACTGGCCCTTCTTGAGGGCTCGGCTGCACCCGGGCGGATGCCCGAG 164
 QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
 Db 165 GCTGGCTTCATCCACTGCCCTGAGAACGAGCAGACTTGGCCAGTGTTCTCTTCG 224
 QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHisLysHis 80
 Db 225 TTCAAGGAGCTGGAAGGCTGGGAGCGCAGATGACGCCCATAGAGGAAACATAAAGCAT 284
 QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
 Db 285 TGTCCGTTGGCTTCTCTTCTGTCAGAGAGCAGTTGAGANTTAACCTTGCTGTA 344
 QY 101 PheLeuLysLeuAspArgGluAlaGlnAlaLysAsnLysIleAlaLysGluThrAsnLys 120
 Db 345 TTTTGAAGCTGGACAGAGAAAGAGCCAAAGAAACAAATTCGAAGGAAACCAACATAAG 404
 QY 121 LysLysGluPheGluThrAlaLysLysValArgArgAlaIleGluGluLeuAlaLa 140
 Db 405 AGAAGAAGATTGAGGAAACTGGAGAAAGTGGCCGTTGCCATCGAGCGTGGCTGCC 464
 QY 141 MetAsp 142
 Db 465 ATGGAT 470

RESULT 11

BC008718
 LOCUS
 DEFINITION Homo sapiens baculoviral IAP repeat-containing 5 (survivin), mRNA
 (cdna clone MGC:8592 IMAGE:2961114), complete cds.

ACCESSION BC008718

VERSION BC008718.2 GI:38196997

KEYWORDS

SOURCE MGC.

ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1653)

Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,

Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,

Altshul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,

Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,

Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,

Stapleton,M., Soares,M.B., Bonaldo,M.P., Casavant,T.L.,

Schetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,

Carninci,P., Frange,C., Roha,S., Loquellano,N.A., Peters,G.J.,

Abramson,R.D., Mullaly,S.J., Bosak,S.A., McEwan,P.J.,

McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,

Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Rulyk,S.W.,

Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,

Fahay,J., Helton,E., Kettner,M., Madan,A., Rodriguez,S.,

Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,

Bouffard,G.G., Blakesley,R.W., Touchman,O.W., Green,E.D.,

Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,

Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalilus,D.E.,

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

REMARK

COMMENT

Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 22389257
 2 (bases 1 to 1653)
 Strausberg,R.
 Direct Submission
 Submitted (25-MAY-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA

NTH-MGC Project URL: <http://mgc.nci.nih.gov>

On Nov 6, 2003 this sequence version replaced gi:14250533.

Contact: MGC help desk

Email: cgaps-k@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory

DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC),

Gaithersburg, Maryland

Web site: <http://www.nisc.nih.gov/>

Contact: nisc_mgc@nhri.nih.gov

Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,

Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,

Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,

Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,

McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,

Turgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,

Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAL Plate: 1 Row: 1 Column: 7

This clone was selected for full length sequencing because it

passed the following selection criteria: matched mRNA gi: 5453604.

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/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="MGC:8592 IMAGE:2961114"

/tissue_type="Muscle, rhabdomyosarcoma"

/clone_lib="NIH MGC 17"

/lab_host="DH10B-R"

/note="Vector: pOTB7"

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/notes="synonyms: API4, SURVIVIN, EPR-1"

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34..462

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HCTENEPDLAQCFCCFKELEGWPDPPDPIEEHKHSSGCCAFLSVKKQPELTIGEPL

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73..294

/notes="BIR, Region: Baculoviral inhibition of apoptosis

/protein_repeat"

/db_xref="CDD:smart00238"

ORIGIN

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Pred. No.: 1,41e-76 Length: 1653

Score: 778.00 Matches: 142

Percent Similarity: 100.00% Conservativity: 0

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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-690-825-34 (1-142) x BC008718 (1-1653)

Qy 1 MetGlyAlaProThrLeuProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
Db 34 ATGGTGTCCCGGAGCTTGCCCTGCTGGCAGCCCTTCTCAAGGACCAACCGCATCTCT 93
Qy 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
Db 94 ACATTCAAGAACTGGCCCTTCTTGAGGGCTGGCCCTGCACCCCGGAGCGATGGCCGAG 153
Qy 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
Db 154 GCTGCTTCATCCACTGCCCTGCTGAGAACGAGCCAGACTTGGCCCGAGTGTTCCTCTGC 213
Qy 61 PheLysGluLeuGluGlyTTPGluProAspAspProIleGluGluHisLysLysHis 80
Db 214 TTCAAGGAGCTGGAGGCTGGAGCCAGATGACGACCCCATAGAGGAACATAAAAAAGCAT 273
Qy 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
Db 274 TCGTCCGTTGCCGTTTCCCTTCTGTCAGAGAGCAGTTTGAAGAAATTAACCTTGGTGA 333
Qy 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
Db 334 TTTTGAACCTGGACAGAAAGAGCCCAAGACAAATTCGAAAGGAAACCAACAATAAG 393
Qy 121 LysLysGluPheGluGluThrAlaLysValArgArgAlaIleGluGlnLeuAlaA 140
Db 394 AAGAAAGAAATTTGAGAAACTGCGAAGAAAGTGGCCGTCCTCGAGCAGCTGGCTGCC 453
Qy 141 MetAsp 142
Db 454 ATGGAT 459

RESULT 12
AB095108 1630 bp mRNA linear MAM 27-NOV-2002
LOCUS Canis familiaris mRNA for survivin, complete cds.
DEFINITION AB095108
ACCESSION AB095108
VERSION AB095108.1 GI:24636590
KEYWORDS
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1
Inoue, C., Yamazaki, J., Kano, R. and Hasegawa, A.
Canis familiaris mRNA for survivin-protein, complete cds
Published Only in database (2002)
2 (bases 1 to 1630)
Inoue, C., Yamazaki, J., Kano, R. and Hasegawa, A.
Direct Submission
Submitted (01-NOV-2002) Rui Kano, Nihon University School of
Veterinary Medicine, Department of Pathobiology, Kameino1866,
Fujisawa, Kanagawa 252-8610, Japan (E-mail:Kano@vms.nihon-u.ac.jp,
Tel:81-466-84-3649, Fax:81-466-84-3649)
Location/Qualifiers
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55. 483
/product="survivin"
/protein_id="BAC22748.2"
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FEATURES
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1. 1630
/organism="Canis familiaris"
/mol_type="mRNA"
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5'UTR
CDS

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484. 1630

3'UTR
ORIGIN
Alignment Scores:
Pred. No.: 2,99e-76 Length: 1630
Score: 775.00 Matches: 141
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.30% Mismatches: 0
Query Match: 99.61% Indels: 0
DB: 4 Gaps: 0

US-09-690-825-34 (1-142) x AB095108 (1-1630)
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Qy 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
Db 115 ACATTCAAGAACTGGCCCTTCTTGAGGGCTGGCCCTGCACCCCGGAGCGATGGCAGAG 174
Qy 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
Db 175 GCGGCTTCATCCACTGCCCTGCTGAGAACGAGCCAGCTTGGCCCGAGTGTTCCTCTGC 234
Qy 61 PheLysGluLeuGluGlyTTPGluProAspAspProIleGluGluHisLysLysHis 80
Db 235 TTCAAGGAGCTGGAGGCTGGAGCCAGATGATGACCTATAGAGGAGCATAAAAACAT 294
Qy 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
Db 295 TCATCTGTTGCTGTTTCCCTTCTGTCAGAGAGCAGTTTGAAGAAATTAACCTTGGTGA 354
Qy 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
Db 355 TTTTGAACCTGGACAGAAAGAGCCCAAGACAAATTCGAAAGGAAACCAACAATAAG 414
Qy 121 LysLysGluPheGluGluThrAlaLysValArgArgAlaIleGluGlnLeuAlaA 140
Db 415 AAGAAAGAAATTTGAGAAACTGCGAAGAAAGTGGCCGTCCTCGAGCAGCTGGCTGCC 474
Qy 141 MetAsp 142
Db 475 ATGGAT 480

RESULT 13
AB028869 600 bp mRNA linear PRI 04-APR-2000
LOCUS Homo sapiens mRNA for survivin-beta, complete cds.
DEFINITION AB028869
ACCESSION AB028869
VERSION AB028869.1 GI:7416052
KEYWORDS survivin-beta.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (sites)
Kageyama, H., Islam, A., Takayasu, H. and Nakagawara, A.
An isoform of Survivin (Survivin-beta) Which Has 23 Amino Acids
Insertion into the BIR Domain
Unpublished
2 (bases 1 to 600)
Kageyama, H., Islam, A. and Nakagawara, A.
Direct Submission
Submitted (11-JUN-1999) Akira Nakagawara, Chiba Cancer Center
Research Institute, Division of Biochemistry; 666-2 Nitona,
Chuch-ku, Chiba, Chiba 260-8717, Japan
(E-mail:akiranak@chiba-cc.pref.chiba.jp,
Tel:81-43-264-5431(ex.5201), Fax:81-43-265-4459)
Location/Qualifiers
FEATURES

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/organism="Homo sapiens"
/mol_type="mRNA"
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27. 524
/codon_start=1
/product="survivin-beta"
/protein_id="BAA93676.1"
/db_xref="GI:7416053"
/translation="MGAPTLPPAWQPFLLKDHRISTFKNWPFLGCACTPRMABAGFI
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LAAMD"

ORIGIN
Alignment Scores:
Pred. No.:      1.08e-74      Length:      600
Score:          756.50      Matches:    142
Percent Similarity: 86.06%      Conservative: 0
Best Local Similarity: 86.06%      Mismatches: 0
Query Match:    97.24%      Indels:    23
DB:              9          Gaps:      1

US-09-690-825-34 (1-142) x AB028869 (1-600)
Qy      1 MetGlyAlaProThrLeuProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
Db      27 ATGGGTGCCCCACGTTGCCCTCGCTGGAGCGCCCTTCTCAAGGACCCCGCATCTCT 86
Qy      21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
Db      87 ACATTCAAGAACTGCGCTTCTTGGAGGCTGCGCTGCACCCCGGAGCGGATGCGCGAG 146
Qy      41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
Db      147 GCTGCTCTTCATCCACTGCCCTGAGAACCGAGCGAGACTTGGCCCACTGTTCTTCTGCG 206
Qy      61 PheLysGluLeuGluGlyTrpGluProAspAspProIle-----GluGluHis 77
Db      207 TTCAGGAGCTGGAAGGCTGGAGCCAGATGACGACCCCATTTGGCCCGGCGACGCTGCT 266
Qy      75 -----GluGluHis 77
Db      267 TACGCTCTGTATACCAGCACCTTTGGAGCGCCGAGCGCGCGATCACGAGAGAGGAACAT 326
Qy      78 LysLysHisSerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThr 97
Db      327 AAAAAAGCATTCGTCGGTTGCGCTTCTCTTCTGTCAGAGAGCAGTTTGAAGAAATTAAAC 386
Qy      98 LeuGlyGluPheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThr 117
Db      387 CTGTGTGAATTTTGAAACTGGACAGAGAAAGAGCAAAATTTGCAAGAGAAACC 446
Qy      118 AsnAsnLysLysLysGluPheGluThrAlaLysLysValArgArgAlaIleGluGln 137
Db      447 AACAAATAAGAAAGAAATTTGAGGAAACTGCGAAGAAAGTGGCGCGTCCATCGAGCAG 506
Qy      138 LeuAlaAlaMetAsp 142
Db      507 CTGGCTGCCATGGAT 521

RESULT 14
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LOCUS      AR097642      1165 bp      DNA      linear      PAT 14-FEB-2001
DEFINITION      Sequence 1 from patent US 6072028.
ACCESSION      AR097642
VERSION      AR097642.1      GI:12806372
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
Unclassified.
REFERENCE      1
AUTHORS      Altieri,D.C.
TITLE      Diagnostic methods useful in the characterization of
lymphoproliferative disease characterized by increased EPR-1
JOURNAL
FEATURES
source      1. .1165
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/mol_type="unassigned DNA"
ORIGIN
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REFERENCE      1 (bases 1 to 1165)
AUTHORS      Altieri,D.C.
TITLE      EPR-1 proteins, polypeptides, and nucleic acid molecules encoding
same
JOURNAL      Patent: US 6072028-A 1 06-JUN-2000;
FEATURES
source      1. .1165
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.:      2.03e-73      Length:      1165
Score:          748.00      Matches:    140
Percent Similarity: 99.30%      Conservative: 1
Best Local Similarity: 98.59%      Mismatches: 1
Query Match:    96.14%      Indels:    1
DB:              6          Gaps:      0

US-09-690-825-34 (1-142) x AR097642 (1-1165)
Qy      1 MetGlyAlaProThrLeuProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
Db      1114 ATGGGTGCCCCGACGTTGCCCTCGCTGGAGCGCCCTTCTCAAGGACCCCGCATCTCT 1055
Qy      21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
Db      1054 ACATTCAAGAACTGCGCTTCTTGGAGGCTGGCG-TGCACCCCGGAGCGGATGCGCGAG 996
Qy      41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
Db      995 GCTGGCTTTCATCCACTGCCCTGAGAACGAGCCAGACTTGGCCCGAGTGTTCCTTCTGCG 936
Qy      61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHisLysLysHis 80
Db      935 TTCAGGAGCTGGAAGGCTGGAGCGCCAGATGACGACCCCATAGAGGAACATAAAAGCAT 876
Qy      81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
Db      875 TCGTCCGGTTGCGCTTCTCTTCTGTCAGAGAGCAGTTTGAAGAAATTAAACCTTGGTGAA 816
Qy      101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
Db      815 TTTTGAACCTGGACAGAGAAAGAGCCAGCAAAATTTGCAAGAGGAACCAACAATAAG 756
Qy      121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAlaAla 140
Db      755 AAGAAAGAAATTTGAGGAAACTGCGAAGAAAGTGGCGCGTGCATCGAGCAGCTGGCGCTCG 696
Qy      141 MetAsp 142
Db      695 ATGGAT 690

RESULT 15
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LOCUS      AR154245      1165 bp      DNA      linear      PAT 08-AUG-2001
DEFINITION      Sequence 1 from patent US 6238875.
ACCESSION      AR154245
VERSION      AR154245.1      GI:15122298
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
Unclassified.
REFERENCE      1 (bases 1 to 1165)
AUTHORS      Altieri,D.C.
TITLE      Diagnostic methods useful in the characterization of
lymphoproliferative disease characterized by increased EPR-1
JOURNAL      Patent: US 6238875-A 1 29-MAY-2001;
FEATURES
source      1. .1165
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ORIGIN
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Alignment Scores: Pred. No.: 2.03e-73 Length: 1165
Score: 748.00 Matches: 140
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Best Local Similarity: 98.59% Mismatches: 1
Query Match: 96.14% Indels: 1
DB: 6 Gaps: 0

US-09-690-825-34 (1-142) x AR154245 (1-1165)

Qy	1	MetGlyAlaProThrLeuProProAlaTrrPrlProPheLeuLysAspHisArgIleSer	20
Db	1114	ATGGGTGCCCGGACGTTGGCCCTTGCTGGCAGCCCTTTCTCAAGGACCACCGCATCTCT	1055
Qy	21	ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu	40
Db	1054	ACATTCAAGAACTGGCCCTTCTTGGAGGGCTGCSC-TGCACCCCGGCGGATGGCCGAG	996
Qy	41	AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPheCys	60
Db	995	GCTGGCTTCATCCACTGCCCTCCCTGAGAACGAGCCAGACTTGGCCCACTGTTCTCTGC	936
Qy	61	PheLysGluLeuGluGlyTrrPrlProAspAspProIleGluHisLysLysHis	80
Db	935	TTCAAGAGCTGGAGGCTGGAGCCAGATGACGACCCCATAGAGGACATATAAAGCAT	876
Qy	81	SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluLeuThrLeuGlyGlu	100
Db	875	TCGTCGGTTGGCTTTCTCTTCTGTACAGAGCAGTTTGAAGAATTAACCCCTTGGTGAA	816
Qy	101	PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLeuLys	120
Db	815	TTTTTGAACCTGGACAGAGAGAGCCCAAGACAAATTCGAAAGGAAACCAACAATAAG	756
Qy	121	LysLysGluPheGluGluThrAlaLysLysValArgAlaIleGluGlnLeuAlaAla	140
Db	755	AAGAAGCAATTTGAGGAACCTGCGAAGAAAGTGGCCGTGCCATCGAGCAGCTGGCCTCG	696
Qy	141	MetAsp	142
Db	695	ATGGAT	690

Search completed: August 15, 2004, 23:26:24
Job time : 3690 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 15, 2004, 21:39:58 ; Search time 95 Seconds
(without alignments)

829.506 Million cell updates/sec

Title: US-09-690-825-34

Perfect score: 778

Sequence: 1 MGAPLPPMOPFLKDRHS.....EFEETAKKVRRAIQLAAMD 142

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=issued_patents NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOFC=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09690825 @CGN 1.1.69 @runat_11082004_140952_13557 -NCPU=6 -ICPU=3
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:*

1: /cgn2_6/ptodata/2/ina/5A.COMB.seq:*

2: /cgn2_6/ptodata/2/ina/5B.COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A.COMB.seq:*

4: /cgn2_6/ptodata/2/ina/6B.COMB.seq:*

5: /cgn2_6/ptodata/2/ina/PTJUS.COMB.seq:*

6: /cgn2_6/ptodata/2/ina/backfiles.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	778	100.0	426	4	US-09-283-144-2
2	778	100.0	1619	3	US-09-163-162-1
3	778	100.0	1619	3	US-09-286-407-1
4	778	100.0	1619	4	US-09-496-694B-97
c 5	748	96.1	1165	3	US-08-448-722A-1
c 6	748	96.1	1165	3	US-08-189-309B-1
7	721	92.7	740	4	US-09-016-434-918
8	660	84.8	955	4	US-09-496-694B-10
9	382	49.1	14796	3	US-08-975-080-35
10	382	49.1	14796	3	US-09-630-706-10
11	382	49.1	14796	4	US-09-496-694B-3
12	347	44.6	332	4	US-09-833-381-1331

13	246.5	31.7	624	4	US-09-738-946-3	Sequence 3, Appli
14	221	28.4	417	4	US-09-283-144-1	Sequence 1, Appli
15	155	19.9	5366	4	US-09-705-872-4	Sequence 4, Appli
16	155	19.9	5502	3	US-08-836-134-1	Sequence 1, Appli
17	155	19.9	5502	4	US-09-493-784-1	Sequence 1, Appli
18	155	19.9	5502	4	US-09-023-655-1459	Sequence 1459, Ap
19	155	19.9	5984	4	US-09-705-872-2	Sequence 2, Appli
20	136.5	17.5	1134	4	US-09-502-528-2	Sequence 1, Appli
21	136.5	17.5	1337	4	US-08-127-928-1	Sequence 1, Appli
22	136.5	17.5	1739	4	US-09-502-528-1	Sequence 1, Appli
23	131	16.8	1559	4	US-09-239-867-1	Sequence 1, Appli
24	131	16.8	2580	2	US-08-511-485-7	Sequence 7, Appli
25	131	16.8	2580	4	US-09-201-936-7	Sequence 7, Appli
26	131	16.8	2580	4	US-09-011-356-7	Sequence 7, Appli
27	131	16.8	2580	4	US-09-672-717-222	Sequence 222, App
28	131	16.8	2589	3	US-08-569-749-1	Sequence 1, Appli
29	131	16.8	2589	5	PCT-US96-12860-1	Sequence 1, Appli
30	131	16.8	3532	2	US-09-205-204-1	Sequence 1, Appli
31	131	16.8	3732	3	US-09-212-971-7	Sequence 7, Appli
32	131	16.8	3732	3	US-08-800-929A-7	Sequence 7, Appli
33	131	16.8	3732	4	US-09-617-053A-7	Sequence 3, Appli
34	130	16.7	711	3	US-09-121-979-3	Sequence 3, Appli
35	130	16.7	711	3	US-08-332-319-3	Sequence 3, Appli
36	129.5	16.6	2100	2	US-08-511-485-9	Sequence 9, Appli
37	129.5	16.6	2100	4	US-09-201-936-9	Sequence 9, Appli
38	129.5	16.6	2100	4	US-09-011-356-9	Sequence 9, Appli
39	129.5	16.6	2100	4	US-09-672-717-224	Sequence 224, App
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41	129.5	16.6	2691	3	US-08-800-929A-9	Sequence 9, Appli
42	129.5	16.6	2691	4	US-09-617-053A-9	Sequence 9, Appli
43	129.5	16.6	2862	3	US-08-569-749-13	Sequence 13, Appli
44	129.5	16.6	2862	5	PCT-US96-12860-13	Sequence 13, Appli
45	129.5	16.6	3151	3	US-09-212-971-13	Sequence 13, Appli

ALIGNMENTS

RESULT 1
US-09-283-144-2
; Sequence 2, Application US/09283144
; Patent No. 6346389
; GENERAL INFORMATION:
; APPLICANT: Yale University
; TITLE OF INVENTION: Method for Selectively Modulating the Interactions
; FILE REFERENCE: 44574-5033-US
; CURRENT APPLICATION NUMBER: US/09/283,144
; CURRENT FILING DATE: 1999-04-01
; EARLIER APPLICATION NUMBER: US 60/080,288
; EARLIER FILING DATE: 1998-04-01
; EARLIER APPLICATION NUMBER: US 08/975,080
; EARLIER FILING DATE: 1997-11-20
; EARLIER APPLICATION NUMBER: PCT/US97/21880
; EARLIER FILING DATE: 1997-11-20
; EARLIER APPLICATION NUMBER: US 60/031,435
; EARLIER FILING DATE: 1996-11-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 426
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence of open reading frame encoding
; OTHER INFORMATION: Survivin
US-09-283-144-2

Alignment Scores:
Pred. No.: 3 63e-93
Score: 778.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Length: 426
Matches: 142
Conservative: 0
Mismatch: 0
Indels: 0

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DB: 4 Gaps: 0
US-09-690-825-34 (1-142) x US-09-283-144-2 (1-426)

Qy 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
Db 1 ATGGGTGCCCGAGTTGGCCCTTCTGAGGGCTGGCCCTTCTCAAGGACCAACCGCATCTCT 60
Qy 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
Db 61 ACATTCAGAACTGGCCCTTCTTGGAGGCTGGCCCTGACCCCGAGCGGATGGCCGAG 120
Qy 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPheCys 60
Db 121 GCTGGCTTCATCCACTGCCCTTCTTGGAGGCTGGCCCTGACCCCGAGCGGATGGCCGAG 180
Qy 61 PhelysGluLeuGluGlyTTPGluProAspAspProIleGluHisLysLysHis 80
Db 181 TTCAAGGAGCTGGAGGCTGGAGCCAGATGACGCCCATAGAGGAACATAAAGCAT 240
Qy 81 SerSerGlyCysAlaPheLeuSerValLysGlnPheGluLeuThrLeuGlyGlu 100
Db 241 TCGTCCGTTGGCTTCTTCTGTCAGAGAGCAGTTTGAAGAAATAACCTTGGTGAA 300
Qy 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
Db 301 TTTTGGAACTGGACAGAGAGGCGCAAGACAAATTCGAAAGGAAACCAACAATAAG 360
Qy 121 LysLysGluPheGluGluThrAlaLysLysValArgAlaIleGluGlnLeuAlaAla 140
Db 361 AAGAAAGAAATTTGAGGAACTGCGAGAAAGTGGCGGTGCCATCGAGCAGCTGGCTGCC 420
Qy 141 MetAsp 142
Db 421 ATGGAT 426

RESULT 2
US-09-163-162-1
; Sequence 1, Application US/09163162
; Patent No. 6077709
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Ackermann, Elizabeth J.
; APPLICANT: Swayze, Eric E.
; APPLICANT: Cowsett, Lex M.
; TITLE OF INVENTION: ANTISENSE MODULATION OF Survivin EXPRESSION
; FILE REFERENCE: RTS-0008
; CURRENT APPLICATION NUMBER: US/09/163,162
; CURRENT FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 1
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (50)..(478)
US-09-163-162-1

Alignment Scores:
Pred. No.: 2,7e-92 Length: 1619
Score: 778.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-690-825-34 (1-142) x US-09-163-162-1 (1-1619)

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Db 50 ATGGGTGCCCGAGTTGGCCCTTCTGAGGGCTGGCCCTTCTCAAGGACCAACCGCATCTCT 109
Qy 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
Db 110 ACATTCAGAACTGGCCCTTCTTGGAGGCTGGCCCTGACCCCGAGCGGATGGCCGAG 169
Qy 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPheCys 60
Db 170 GCTGGCTTCATCCACTGCCCTTCTTGGAGGCTGGCCCTGACCCCGAGCGGATGGCCGAG 229

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Qy 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
Db 110 ACATTCAGAACTGGCCCTTCTTGGAGGCTGGCCCTGACCCCGAGCGGATGGCCGAG 169
Qy 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPheCys 60
Db 170 GCTGGCTTCATCCACTGCCCTTCTTGGAGGCTGGCCCTGACCCCGAGCGGATGGCCGAG 229
Qy 61 PhelysGluLeuGluGlyTTPGluProAspAspProIleGluHisLysLysHis 80
Db 230 TTCAAGGAGCTGGAGGCTGGAGCCAGATGACGCCCATAGAGGAACATAAAGCAT 289
Qy 81 SerSerGlyCysAlaPheLeuSerValLysGlnPheGluGluLeuThrLeuGlyGlu 100
Db 290 TCGTCCGTTGGCTTCTTCTGTCAGAGAGCAGTTTGAAGAAATAACCTTGGTGAA 349
Qy 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
Db 350 TTTTGGAACTGGACAGAGAGGCGCAAGACAAATTCGAAAGGAAACCAACAATAAG 409
Qy 121 LysLysGluPheGluGluThrAlaLysLysValArgAlaIleGluGlnLeuAlaAla 140
Db 410 AAGAAAGAAATTTGAGGAACTGCGAGAAAGTGGCGGTGCCATCGAGCAGCTGGCTGCC 469
Qy 141 MetAsp 142
Db 470 ATGGAT 475

RESULT 3
US-09-286-407-1
; Sequence 1, Application US/09286407A
; Patent No. 6165788
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Ackermann, Elizabeth J.
; APPLICANT: Swayze, Eric E.
; APPLICANT: Cowsett, Lex M.
; TITLE OF INVENTION: ANTISENSE MODULATION OF Survivin EXPRESSION
; FILE REFERENCE: ISPH-0349
; CURRENT APPLICATION NUMBER: US/09/286,407A
; CURRENT FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 48
; SEQ ID NO 1
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (50)..(478)
US-09-286-407-1

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Pred. No.: 2,7e-92 Length: 1619
Score: 778.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-690-825-34 (1-142) x US-09-286-407-1 (1-1619)

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Qy 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
Db 110 ACATTCAGAACTGGCCCTTCTTGGAGGCTGGCCCTGACCCCGAGCGGATGGCCGAG 169
Qy 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPheCys 60
Db 170 GCTGGCTTCATCCACTGCCCTTCTTGGAGGCTGGCCCTGACCCCGAGCGGATGGCCGAG 229

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Qy	61	PheLysGluLeuGluGlyTrrGluProAspAspAsprrleGluGluHisLysLysHis	80
Db	230	TTCAAGAGCTCGAAGGCTGGAGCCAGATGACACCCCATGAGAGAAACATATAAAGCAT	289
Qy	81	SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu	100
Db	290	TGTCGGGTGGCTTTCCTTCTGTCTAGAGAGAGATTGAGAAATTACCCCTGGTGAA	349
Qy	101	PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys	120
Db	350	TTTTTTAAACTGGACAGAGAGGCCAAGAACAAAAATTGCAAGAGAAACCCACCAATAG	409
Qy	121	LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAlaLa	140
Db	410	AGAAAGAAATTTGAGAAACTGCGAGAAAGTGTCGCCCTGCCATCGAGCAGCTGGCTGCC	469
Qy	141	MetAsp	142
Db	470	ATGGAT	475

Qy	101	PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys	120
Qy	102	LeuLysLeuLysLeuLysLeuLysLeuLysLeuLysLeuLysLeuLysLeuLysLeuLys	121
Db	350	TTTTTGAACCTGGACGAGAAGAGCCAGAACAAAAATTGCAAGGAAACCAACATTAAG	409
Qy	121	LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAlaAla	140
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Qy	141	MetAsp	142
Db	470	ATGGAT	475

QY 1 MetGlyAlaProThrLeuProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
 DB 1114 ATGGGTGCCCGACGTTGCCCTGCTGCTGAGCCCTTTCTCAAGGACCAACCGCATCTCT 1055
 QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
 DB 1054 ACATTCAAGAACTGGCCCTTTCTGGAGGCTGGCG-TGCACCCCGAGCGGATGGCCGAG 996
 QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPheCys 60
 DB 995 GCTGGCTTCATCCACTGCCCTGAGAACGACGACCTTGCCCGAGTTTCTTCTCTGC 936
 QY 61 PheLysGluLeuGluGlyTrpGluProAspAspAspProIleGluHisLysLysHis 80
 DB 935 TTCAAGGAGCTGGAGGCTGGAGCCAGATGACCAACCCCATAGAGAACTATAAAAGCAT 876
 QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
 DB 875 TCGTCCGGTGGCGCTTTCTCTGTCAAGAGCAGTTTGAAGAATTAAACCTTGGTGAA 816
 QY 101 PheLeuLysLeuAspArgGluA-GAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
 DB 815 TTTTGAAGAACTGGAGAACTGCGAAAGAGTGGCGCGTCCATCGAGCAGCTGGCGCTCG 696
 QY 141 MetAsp 142
 DB 695 ATGGAT 690

RESULT 6

US-08-189-309B-1/c
 ; Sequence 1, Application US/08189309B
 ; Patent No. 6238875
 ; GENERAL INFORMATION:
 ; APPLICANT: Altieri, Dario C.
 ; TITLE OF INVENTION: Diagnostic Methods Useful in the Characterization of
 ; TITLE OF INVENTION: Lymphoproliferative Disease Characterized by Increased EPR-1
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Office of Patent Counsel, The Scripps
 ; ADDRESSEE: Research Institute
 ; STREET: 10550 No. 6238875th Torrey Pines Road, TPC-8
 ; CITY: La Jolla
 ; STATE: CA
 ; COUNTRY: US
 ; ZIP: 92037
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/189,309B
 ; FILING DATE: 28-JAN-1994
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/988,897
 ; FILING DATE: 10-DEC-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/667,957
 ; FILING DATE: 12-MAR-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fitting, Thomas
 ; REGISTRATION NUMBER: 34,163
 ; REFERENCE/DOCKET NUMBER: 233.1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 784-2937
 ; TELEFAX: (619) 784-9399
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:

LENGTH: 1165 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 37..1047
 US-08-189-309B-1

Alignment Scores:
 Pred. No.: 1,44e-88 Length: 1165
 Score: 748.00 Matches: 140
 Percent Similarity: 99.30% Conservative: 1
 Best Local Similarity: 98.59% Mismatches: 1
 Query Match: 96.14% Indels: 1
 DB: 3 Gaps: 0

US-09-690-825-34 (1-142) x US-08-189-309B-1 (1-1165)

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 DB 1114 ATGGGTGCCCGACGTTGCCCTGCTGCTGAGCCCTTTCTCAAGGACCAACCGCATCTCT 1055
 QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
 DB 1054 ACATTCAAGAACTGGCCCTTTCTGGAGGCTGGCG-TGCACCCCGAGCGGATGGCCGAG 996
 QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPheCys 60
 DB 995 GCTGGCTTCATCCACTGCCCTGAGAACGACGACCTTGCCCGAGTTTCTTCTCTGC 936
 QY 61 PheLysGluLeuGluGlyTrpGluProAspAspAspProIleGluHisLysLysHis 80
 DB 935 TTCAAGGAGCTGGAGGCTGGAGCCAGATGACACCCCATAGAGAACTATAAAAGCAT 876
 QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
 DB 875 TCGTCCGGTGGCGCTTTCTCTGTCAAGAGCAGTTTGAAGAATTAAACCTTGGTGAA 816
 QY 101 PheLeuLysLeuAspArgGluA-GAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
 DB 815 TTTTGAAGAACTGGAGAAAGAGCCAAAGAACAAAAATTGCAAGGAAACCAACCAATAAG 756
 QY 121 LysLysGluPheGluGluThrAlaLysLysValArgAlaIleGluGlnLeuAlaAala 140
 DB 755 AAGAAAGAAATTGAGAAACTGCGAAGAAAGTGGCGCGTCCATCGAGCAGCTGGCGCTCG 696
 QY 141 MetAsp 142
 DB 695 ATGGAT 690

RESULT 7

US-09-016-434-918
 ; Sequence 918, Application US/09016434
 ; Patent No. 6500938
 ; GENERAL INFORMATION:
 ; APPLICANT: Janice Au-Young
 ; APPLICANT: Jeffrey J. Seilhamer
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
 ; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
 ; NUMBER OF SEQUENCES: 1490
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 ; STREET: 3174 PORTER DRIVE
 ; CITY: PALO ALTO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 918:
SEQUENCE CHARACTERISTICS:
LENGTH: 740 base pairs
TYPE: nucleic acid
STRADEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BRAITUT01
CLONE: 752848
US-09-016-434-918

Alignment Scores:
Pred. No.: 2,57e-85 Length: 740
Score: 721.00 Matches: 135
Percent Similarity: 95.74% Conservative: 0
Best Local Similarity: 95.74% Mismatches: 6
Query Match: 92.67% Indels: 1
DB: 4 Gaps: 0

US-09-690-825-34 (1-142) x US-09-016-434-918 (1-740)

QY 2 GlyAlaProThriLeuProAlaTrpGlnProPheLeuLysAspHisArgIleSerThr 21
DB 22 GGGTGGCNCNGTGGCACT-GCCTGGCNCCTTCTCAAGGACACCGCATCTCTACA 80
QY 22 PheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGluAla 41
DB 81 TTCAGAACTGGCCCTTCTTGGAGGCTGGCCTGCACCCCGAGCGGATGCCAGGCT 140
QY 42 GlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPheCysPhe 61
DB 141 GGCCTTCATCCACTGCCCACTGANAACAGAGCCAGACTTGGCCCACTGTTCTCTGCTTC 200
QY 62 LysGluLeuGluGlyTrpGluProAspAspProIleGluHisLysLysHisSer 81
DB 201 AAGGAGCTGGAAGGCTGGGAGCCAGATGACGCCCATGAGAACATTAAGAAGCATTCG 260
QY 82 SerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGluPhe 101
DB 261 TCGGTTGGCTTCTTCTCTGTCAGAAAGCAGTTTGAAGAATTAACCTTGGTGAATTT 320
QY 102 LeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLysLys 121
DB 321 TTGAATCTGACAGAAAGAGCCAGAACAAATTTGCAAGAAACCAACCAATTAAGAG 380
QY 122 LysGluPheGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAlaMet 141
DB 381 AAGAATTTGAGGAARACTGGAAGAAAGTGGCCGTCATCGAGCAGCTGGCTGCCATG 440
QY 142 Asp 142
DB 441 GAT 443

RESULT 8

US-09-496-694B-10

; Sequence 10, Application US/09496694B
; Patent No. 6335194
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Eric B. Swayze
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: ISPH-0439
; CURRENT APPLICATION NUMBER: US/09/496,694B
; CURRENT FILING DATE: 2000-02-02
; PRIOR APPLICATION NUMBER: 09/286,407
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 09/163,162
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 249
; SEQ ID NO 10
; LENGTH: 955
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURES:
; NAME/KEY: CDS
; LOCATION: (109)...(531)
US-09-496-694B-10

Alignment Scores:
Pred. No.: 3,9e-77 Length: 955
Score: 660.00 Matches: 118
Percent Similarity: 92.86% Conservative: 12
Best Local Similarity: 84.29% Mismatches: 10
Query Match: 84.83% Indels: 0
DB: 4 Gaps: 0

US-09-690-825-34 (1-142) x US-09-496-694B-10 (1-955)

QY 1 MetGlyAlaProThrLeuProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
DB 109 ATGGAGCTCCGGCGCTGCCCACTGTGGCAGCTGTACCTCAAGAACTACCCGATCGCC 168
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 169 ACCTTCAAGAACTGGCCCTTCTTGGAGGACTGGCCTGCCCCAGAGCGAATGGCGGAG 228
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPheCys 60
DB 229 GCTGGCTTCATCCACTGCCCTACCGAGACGAGCCTGATTGGCCCACTGTTTCTGTC 288
QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluHisLysLysHis 80
DB 289 TTTAAGAAATGGAGGCTGGGAACCCGATGACAAACCCGATAGAGGAGCATAGAAAGCAC 348
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
DB 349 TCCCTCGCTGGCTTCTTCTCACGTGTCAGAGAGCAGATGGAAGAACTAACCGTCAGTGA 408
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120
DB 409 TTTTGAATCTGGACAGACAGAGCCAGAACAAATTTGCAAGAGGAGACCAACAAAG 468
QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAlaAla 140
DB 469 CAAAAGAGTTTGAAGAGACTGCAAGAACTACCCGTCAGTCAATTGAGCAGCTGGCTGCC 528

RESULT 9

US-08-975-080-35

; Sequence 35, Application US/08975080

; Patent No. 6245523

; GENERAL INFORMATION:

; APPLICANT: Altieri, Dario C.

; TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS

; TITLE OF INVENTION: CELLULAR APOPTOSIS, AND ITS MODULATION

; NUMBER OF SEQUENCES: 35

; CORRESPONDENCE ADDRESS:

```

; ADDRESS: MORGAN, LEWIS & BOCKIUS LLP
; STREET: 1800 M Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5869
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,080
; FILING DATE: 20-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/031,435
; FILING DATE: 20-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler, Reid G.
; REGISTRATION NUMBER: 30,988
; REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-467-7000
; TELEFAX: 202-467-7176
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14796 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-975-080-35

Alignment Scores:
Pred. No.: 8.1e-39 Length: 14796
Score: 382.00 Matches: 73
Percent Similarity: 46.84% Conservative: 1
Best Local Similarity: 46.20% Mismatches: 0
Query Match: 49.10% Indels: 84
DB: 3 Gaps: 1

US-09-690-825-34 (1-142) x US-08-975-080-35 (1-14796)
Qy 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
Db 2811 ATGGGTGCGCGACGTTGCCCTTCTTGGAGGGCTGCCTGCACCCCGAGCGGGTGAGACTG 2870
Qy 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArg----- 37
Db 2871 ACATTCAAGAACTGGCCCTTCTTGGAGGGCTGCCTGCACCCCGAGCGGGTGAGACTG 2930
Qy 37 ----- 37
Db 2931 CCGGGCTCCTGGGGTCCCGCCCGCGCTTGCCTGTCCCTAGCGAGGCCACTGTGAC 2990
Qy 37 ----- 37
Db 2991 TGGGCTCGGGGTACAAAGCGCGCTCCCTCCCTGCTGTCCTCCCGAGCGGCCACTGT 3050
Qy 37 ----- 37
Db 3051 GGCTGGGCGCTTGGGTCCAGCGCGGCTCCCTCCCTGCTGTCCTCCCGAGCGGCCACTGT 3110
Qy 37 ----- 37
Db 3111 TGTGGCTGGGCTCGGGGTTCGGGGTCCCGGCTGCCACGTCCACTCAGAGCTGTGCTGCCCTTG 3170
Qy 38 ---MetAlaGluAlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGln 56
Db 3171 CAGATGGCCGAGGCTGGCTTCATCCACTGCCCTGCACCGAGCGGCCAGACTTGGGCCAG 3230
Qy 57 CysPhePheCysPheLysGluLeuGluGlyTrpGluProAspAspProfile 74
Db 3231 TGTTCCTGCTTCAAGGAGCTGGAGGGCTGGAGCCAGATGACGACCCCATG 3284

; ADDRESS: MORGAN, LEWIS & BOCKIUS LLP
; STREET: 1800 M Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5869
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/630,706
; FILING DATE: 2000-08-01
; NUMBER OF SEQ ID NOS: 94
; SEQ ID NO 10
; LENGTH: 14796
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2811)...(2921)
; NAME/KEY: CDS
; LOCATION: (3174)...(3283)
; NAME/KEY: CDS
; LOCATION: (5158)...(5275)
; NAME/KEY: CDS
; LOCATION: (11955)...(12044)
US-09-630-706-10

Alignment Scores:
Pred. No.: 8.1e-39 Length: 14796
Score: 382.00 Matches: 73
Percent Similarity: 46.84% Conservative: 1
Best Local Similarity: 46.20% Mismatches: 0
Query Match: 49.10% Indels: 84
DB: 3 Gaps: 1

US-09-690-825-34 (1-142) x US-09-630-706-10 (1-14796)
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Db 2811 ATGGGTGCGCGACGTTGCCCTTCTTGGAGGGCTGCCTGCACCCCGAGCGGGTGAGACTG 2870
Qy 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArg----- 37
Db 2871 ACATTCAAGAACTGGCCCTTCTTGGAGGGCTGCCTGCACCCCGAGCGGGTGAGACTG 2930
Qy 37 ----- 37
Db 2931 CCGGGCTCCTGGGGTCCCGCCCGCGCTTGCCTGTCCCTAGCGAGGCCACTGTGAC 2990
Qy 37 ----- 37
Db 2991 TGGGCTCGGGGTACAAAGCGCGCTCCCTCCCTGCTGTCCTCCCGAGCGGCCACTGT 3050
Qy 37 ----- 37
Db 3051 GGCTGGGCGCTTGGGTTCAGCGCGGCTCCCTCCCTGCTGTCCTCCCGAGCGGCCCTT 3110
Qy 37 ----- 37
Db 3111 TGTGGCTGGGCTCGGGGTTCGGGGTCCCGGCTGCCACGTCCACTCAGAGCTGTGCTGCCCTTG 3170
Qy 38 ---MetAlaGluAlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGln 56
Db 3171 CAGATGGCCGAGGCTGGCTTCATCCACTGCCCTGCACCGAGCGGCCAGACTTGGGCCAG 3230
Qy 57 CysPhePheCysPheLysGluLeuGluGlyTrpGluProAspAspProfile 74
Db 3231 TGTTCCTGCTTCAAGGAGCTGGAGGGCTGGAGCCAGATGACGACCCCATG 3284

RESULT 10
US-09-630-706-10
; Sequence 10, Application US/09630706
; Patent No. 6277640
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF HER-3 EXPRESSION
; FILE REFERENCE: RTS-0053
; CURRENT APPLICATION NUMBER: US/09/630,706
; CURRENT FILING DATE: 2000-08-01
; NUMBER OF SEQ ID NOS: 94
; SEQ ID NO 10
; LENGTH: 14796
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2811)...(2921)
; NAME/KEY: CDS
; LOCATION: (3174)...(3283)
; NAME/KEY: CDS
; LOCATION: (5158)...(5275)
; NAME/KEY: CDS
; LOCATION: (11955)...(12044)
US-09-630-706-10

RESULT 11
US-09-496-694B-3
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; Sequence 3, Application US/09496694B
; Patent No. 6335194
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Eric E. Swayze
; APPLICANT: Lex M. Cowart
; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: ISPH-0439
; CURRENT APPLICATION NUMBER: US/09/456,694B
; CURRENT FILING DATE: 2000-02-02
; PRIOR APPLICATION NUMBER: 09/286,407
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 09/163,162
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 249
; SEQ ID NO 3
; LENGTH: 14796
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2811)...(3283)
; NAME/KEY: CDS
; LOCATION: (3174)...(3283)
; NAME/KEY: CDS
; LOCATION: (5158)...(5275)
; NAME/KEY: CDS
; LOCATION: (11955)...(12044)
US-09-496-694B-3

Alignment Scores:
Pred. No.: 8,1e-39 Length: 14796
Score: 382.00 Matches: 73
Percent Similarity: 46.84% Conservative: 1
Best Local Similarity: 46.20% Mismatches: 0
Query Match: 49.10% Indels: 84
DB: 4 Gaps: 1

US-09-690-825-34 (1-142) x US-09-496-694B-3 (1-14796)

Qy 1 MetGlyAlaProThrLeuProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
Db 2811 ATGGGTGCCCCGACGTGCCCCCTGCTGGCAGCCCTTCTCAAGGACACCGCATCTCT 2870
Qy 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArg----- 37
Db 2871 ACATTCAAGAACTGGCCCTTCTTGGAGGCTCGCCCTGCACCCCGAGCGGGTGAGACTG 2930
Qy 37 ----- 37
Db 2931 CCGGGCTCTGGGTCCCCCGCCGCGCTTGCCTGTCCCTAGCGAGGCCACTGTGAC 2990
Qy 37 ----- 37
Db 2991 TGGGCTCGGGGTACAGCGCGCTTCCCTCCCGCTGCTGCCCGAGCGGCCACTGT 3050
Qy 37 ----- 37
Db 3051 GGCTGGGCCCCCTTGGGTCCAGCGCGGCTTCCCTCCCTGCTTGTCCCATCGAGGCCTT 3110
Qy 37 ----- 37
Db 3111 TGTGGCTGGGCTCGGGGTCCGGGTGCCACGTCCACTCAGAGTGTGTCCCTTG 3170
Qy 38 ---MetAlaGluAlaGlyPheLeHisCysProThrGluAsnGluProAspLeuAlaGln 56
Db 3171 CAGATGCGCGAGGCTGGCTTCATCCACTGCCCTCCCTCAGAGCGAGCGACTTGGCCGAG 3230
Qy 57 CysPhePheCysPheLysGluLeuGluGlyTrpGluProAspAspProIle 74
Db 3231 TGTTTCTTCTGCTTCAAGAGCTGGAGGCTGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 3284

RESULT 12
US-09-833-381-1331
; Sequence 1331, Application US/09833381
; Patent No. 6672186
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1331
; LENGTH: 332
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(332)
; OTHER INFORMATION: n = A,T,C or G
US-09-833-381-1331

Alignment Scores:
Pred. No.: 1,06e-36 Length: 332
Score: 347.00 Matches: 69
Percent Similarity: 72.45% Conservative: 2
Best Local Similarity: 70.41% Mismatches: 25
Query Match: 44.60% Indels: 2
DB: 4 Gaps: 0

US-09-690-825-34 (1-142) x US-09-833-381-1331 (1-332)

Qy 2 GlyAlaProThrLeuProAlaTrpGlnProPheLeuLysAspHisArgIleSerThr 21
Db 41 GGTGNCNGACNTTGNCCCTTGTGAGGCTCGCTCCACCCGNGGCGATGCGGCGG 100
Qy 22 PheLys-AsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGluAl 41
Db 101 TTCAGGAAGTGAACCTTGTGAGGCTCGCTCCACCCGNGGCGATGCGGCGG 160
Qy 41 aGlyPheLeHisCysProThrGluAsnGluProAspLeuAlaGlnCysPheCysPh 61
Db 161 TGGNTTCATCCANTGNCCTGNNACGAGCCANACTTGGTCCANTGTTNTTNTGCTA 220
Qy 61 eLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHisLysLysHis 81
Db 221 TAAGGACTGTAAAGCTGNGAGCCAGATGACGCCCNATAGAGGAACATATAAGCAATTC 280
Qy 81 r-SerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThr 97
Db 281 GTTACGGTTGGCTNNNNNTTCTGTCAAGAAACAGITTTGAAGATTAAACC 330

RESULT 13

US-09-738-946-3
; Sequence 3, Application US/09738946
; Patent No. 6597901

; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: DROSOPHILA HOMOLOGUES OF GENES AND PROTEINS IMPLICATED IN CANCER
; FILE REFERENCE: EX00-043C
; CURRENT APPLICATION NUMBER: US/09/738,946
; CURRENT FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: 60/170,832
; PRIOR FILING DATE: 1999-12-14
; PRIOR APPLICATION NUMBER: 60/170,838
; PRIOR FILING DATE: 1999-12-14
; PRIOR APPLICATION NUMBER: 60/178,580
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/185,879
; PRIOR FILING DATE: 2000-02-29

; PRIOR APPLICATION NUMBER: 60/185,880
 ; PRIOR FILING DATE: 2000-02-29
 ; PRIOR APPLICATION NUMBER: 60/186,150
 ; PRIOR FILING DATE: 2000-03-01
 ; PRIOR APPLICATION NUMBER: 60/189,701
 ; PRIOR FILING DATE: 2000-03-15
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 3
 ; LENGTH: 624
 ; TYPE: DNA
 ; ORGANISM: Drosophila melanogaster
 US-09-738-946-3

Alignment Scores:
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 Score: 246.50 Matches: 48
 Percent Similarity: 57.14% Conservativeness: 20
 Best Local Similarity: 40.34% Mismatches: 50
 Query Match: 31.68% Indels: 1
 DB: 4 Gaps: 1

US-09-690-825-34 (1-142) x US-09-738-946-3 (1-624)

QY 14 LeuLysAspHisArgIleSerThrPheLysAsnTrpProPheLeuGluGlyCysAlaCys 33
 Db 139 CTGGAACAGCATCGCGTGGAGAGCTCAAGAGTTGGCCCTTCCGGAGACCGCATCTGC 198
 QY 34 ThrProGluArgMetAlaGluAlaGlyPheIleHisCysProThrGluAsnGluProAsp 53
 Db 199 AGCATTTGAGAGTGGCGGAGCGGGATCTATTGGACGGGCACCAAGCGGGAACAGAC 258
 QY 54 LeuAlaGlnCysPhePheCysPheLysGluLeuGluGlyTrpGluProAspAspPro 73
 Db 259 ACTGCCACTTGTGTGTGCGGAAGACCCCTGGATGGCTGGGAGCCCGAAGATGATCG 318
 QY 74 IleGluGluHisLysLysHisSerSerGlyCysAlaPheLeuSerValLysLysGlnPhe 93
 Db 319 TGGNAGAGGACGTGAACATGACCCCAATGGAGTTCGCCAAGTATCGTGCCCGAA 378
 QY 94 GluGluLeuThrLeuGluGluPheLeuLysLeuAspArgGluArgAlaLysAsnLysIle 113
 Db 379 AGGAATTTAACCGTATCACAAATTTCTGGAATCTTGAACCTGTGAAGCGCATATA 438
 QY 114 AlalysGluThrAsnAsnLysLysLysGluPhe---GluGluThrAlalysLysVal 131
 Db 439 GAGAAACCTGCAAGCCCTTCAATCGAGCTTCGTCGGGAGAAATGAGAGCGGTCTA 495

RESULT 14
 US-09-283-144-1
 ; Sequence 1, Application US/09283144
 ; Patent No. 6346389
 ; GENERAL INFORMATION:
 ; APPLICANT: Yale University
 ; TITLE OF INVENTION: Method for Selectively Modulating the Interactions
 ; FILE REFERENCE: 44574-5033-US
 ; CURRENT APPLICATION NUMBER: US/09/283,144
 ; EARLIER FILING DATE: 1999-04-01
 ; EARLIER APPLICATION NUMBER: US 60/080,288
 ; EARLIER FILING DATE: 1998-04-01
 ; EARLIER APPLICATION NUMBER: US 08/975,080
 ; EARLIER FILING DATE: 1997-11-20
 ; EARLIER APPLICATION NUMBER: PCT/US97/21880
 ; EARLIER FILING DATE: 1997-11-20
 ; EARLIER APPLICATION NUMBER: US 60/031,435
 ; EARLIER FILING DATE: 1996-11-20
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1
 ; LENGTH: 417
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens

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 Pred. No.: 1.18e-09 Length: 5366
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 Best Local Similarity: 40.48% Mismatches: 29
 Query Match: 19.92% Indels: 6
 DB: 4 Gaps: 3

US-09-690-825-34 (1-142) x US-09-705-872-4 (1-5366)

QY 15 LysAspHisArgIleSerThrPheLysAsnTrpPhe---LeuGluGlyCysAlaCys 33
 Db 766 GAGGAGGCTAGCTTGCATCTTCAGAACTGGCCATTTATGTCCAAGG-----ATA 819
 QY 34 ThrProGluArgMetAlaGluAlaGlyPheIleHisCysProThrGluAsnGluProAsp 53
 Db 820 TCCCTTGTGTGCTCTCAGAGGCTGGCTTGTCTTT-----ACAGGTAACAGGAC 870

; FEATURE:
 ; OTHER INFORMATION: DNA sequence of proximal 5' flanking region of
 ; OTHER INFORMATION: Survivin gene
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (291)..(401)
 US-09-283-144-1

Alignment Scores:
 Pred. No.: 5,37e-20 Length: 417
 Score: 221.00 Matches: 38
 Percent Similarity: 92.86% Conservativeness: 1
 Best Local Similarity: 90.48% Mismatches: 3
 Query Match: 28.41% Indels: 0
 DB: 4 Gaps: 0

US-09-690-825-34 (1-142) x US-09-283-144-1 (1-417)

QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
 Db 231 ATGGTGGCCCGACGTTGCCCTTCTGGCAGCCCTTTCTCAAGGACCCACCGCATCTCT 350
 QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
 Db 351 ACATTCAGAACTGGCCCTTCTTGGAGGGCTGGCCCTGACCCCGAGCGGGTGAGACTG 410
 QY 41 AlaGly 42
 Db 411 CCCGGC 416

RESULT 15
 US-09-705-872-4
 ; Sequence 4, Application US/09705872
 ; Patent No. 6617429
 ; GENERAL INFORMATION:
 ; APPLICANT: Joh-E IKEDA
 ; APPLICANT: Kenji YAMAMOTO
 ; TITLE OF INVENTION: APOPTOSIS INHIBITORY PROTEIN, GENE ENCODING THE PROTEIN
 ; TITLE OF INVENTION: AND CDNA THEREOF
 ; FILE REFERENCE: 2000-1110/LC/00653
 ; CURRENT APPLICATION NUMBER: US/09/705,872
 ; CURRENT FILING DATE: 2000-11-06
 ; PRIOR APPLICATION NUMBER: 09/239,797
 ; PRIOR FILING DATE: 1999-01-29
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 4
 ; LENGTH: 5366
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (292)..(4176)
 US-09-705-872-4

GenCore version 5.1.6
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Run on: August 15, 2004, 23:26:29 ; Search time 509 Seconds
(without alignments)
1368.838 Million cell updates/sec

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Perfect score: 778
Sequence: 1 MGATLPPAWQFLKDRHS.....EFBETAKKVRRAQLAAMD 142

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3252727 seqs, 2453303834 residues

Total number of hits satisfying chosen parameters: 6451454

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blcsum62
-TRANS=human40.cdi -LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -MMAP=US09690845 @CNG 1 1 520 @runat_11082004_140953_13643
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Database : Published Applications NA:

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- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq*
- 6: /cgn2_6/ptodata/1/pubpna/PTCUS_PUBCOMB.seq*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq*
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- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq*
- 13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq*
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- 15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq*
- 16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq*
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- 18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq*
- 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Match Length DB ID Description

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2	778	100.0	1619	9	US-09-918-186A-97	Sequence 97, Appl
3	778	100.0	1619	13	US-10-342-868-566	Sequence 566, App
4	778	100.0	1619	13	US-10-172-118-566	Sequence 566, App
5	778	100.0	1619	13	US-10-181-316-97	Sequence 97, Appl
6	778	100.0	1619	13	US-10-388-360-324	Sequence 324, App
7	778	100.0	1619	17	US-10-283-975A-445	Sequence 445, App
8	778	100.0	2404	14	US-10-071-766-109	Sequence 109, App
9	778	100.0	2404	15	US-10-064-817-385	Sequence 285, App
10	721	92.7	740	16	US-10-305-720-918	Sequence 918, App
11	660	84.8	955	9	US-09-918-186A-10	Sequence 10, Appl
12	660	84.8	955	13	US-10-181-316-10	Sequence 3, Appli
13	382	49.1	14796	13	US-10-181-316-3	Sequence 973, App
14	382	49.1	14796	9	US-09-954-456-973	Sequence 1636, Ap
15	382	49.1	14796	9	US-09-954-456-1636	Sequence 3, Appli
16	382	49.1	14796	9	US-09-918-186A-3	Sequence 3421, Ap
17	382	49.1	14796	9	US-09-880-107-3421	Sequence 522, App
18	382	49.1	14796	12	US-09-968-007A-522	Sequence 35, Appl
19	382	49.1	14796	15	US-10-138-618-35	Sequence 1331, Ap
20	347	44.6	332	9	US-09-833-381-1331	Sequence 9972, Ap
21	298	38.3	555	15	US-10-029-386-9972	Sequence 33, Appl
22	233	29.9	121	15	US-10-179-730-33	Sequence 23672, A
23	216	27.8	120	15	US-10-029-386-23672	Sequence 2, Appli
24	214	27.5	1100	15	US-10-108-877-2	Sequence 1459, Ap
25	155	19.9	5502	17	US-10-641-643-1459	Sequence 1, Appli
26	155	19.9	5504	8	US-08-913-322-1	Sequence 21, Appl
27	155	19.9	5984	15	US-10-285-408-2	Sequence 2, Appl
28	155	19.9	6124	8	US-08-913-322-21	Sequence 16, Appl
29	155	19.9	6124	9	US-09-867-768A-184	Sequence 16, Appl
30	155	19.9	6133	8	US-08-913-322-2	Sequence 2, Appli
31	155	19.9	6228	8	US-08-913-322-23	Sequence 23, Appl
32	143	18.1	3773	15	US-10-041-859-1	Sequence 1, Appl
33	141	18.1	7339	10	US-09-764-861-16	Sequence 16, Appl
34	141	18.1	7339	13	US-09-764-861-16	Sequence 16, Appl
35	141	18.1	7339	13	US-10-103-313-71	Sequence 71, Appl
36	141	18.1	7339	15	US-10-115-928-16	Sequence 16, Appl
37	139.5	17.9	547	13	US-10-424-598-103666	Sequence 103666
38	138	17.7	1068	15	US-10-203-708-21	Sequence 21, Appl
39	138	17.7	5314	15	US-10-311-455-134	Sequence 134, App
40	138	17.7	5314	15	US-10-240-452-10	Sequence 10, Appl
41	137	17.6	1758	12	US-10-343-115-1	Sequence 1, Appli
42	136.5	17.5	843	15	US-10-244-586-2	Sequence 2, Appli
43	136.5	17.5	1168	16	US-10-188-646-12	Sequence 12, Appl
44	136.5	17.5	1260	16	US-10-188-646-4	Sequence 4, Appli
45	136.5	17.5	1337	15	US-10-235-026-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-10-665-975-1
; Sequence 1, Application US/10665975
; Publication No. US20040138119A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Tamm, Ingo
; TITLE OF INVENTION: USE OF HEPATITIS VIRUS B X-INTERACTING
; FILE REFERENCE: BURNHAM.005A
; CURRENT APPLICATION NUMBER: US/10/665,975
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: 60/412,109
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 429
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-665-975-1

Alignment Scores:

```

Pred. No.: 3.05e-95 Length: 429
Score: 778.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-09-690-825-34 (1-142) x US-10-665-975-1 (1-429)
QY 1 MetGlyAlaProThrLeuProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
DB 1 ATGGGTGCCCCGAGTTGGCCCCCTGCTGGAGCCCTTTCTCAAGGACCAACCGCACTCT 60
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 61 ACATTCAAGAACTGGCCCTTCTTGAGGGCTGCGCTGCACCCCGAGCGGATGGCGGAG 120
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPheCys 60
DB 121 GCTGCTTCATCCACTGCCCACTGAGAACGAGCCAGATGGCCCACTGTTCTTCTGTC 180
QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluHisLysLysHis 80
DB 181 TTCAAGGAGCTGGAGGCTGGAGCCAGATGACGACCCCATAGAGGAACATAAAAGCAT 240
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluThrLeuGlyGlu 100
DB 241 TCGTCCGGTTGCGCTTTCTTCTTCGTCAGAGGAGCTTTGAAGAAATTAACCTTTGGTGAA 300
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120
DB 301 TTTTGGAACTGGACAGAGGAGCCAGACCAAAATTCGAAAGGAAACCAACATATAG 360
QY 121 LysLysGluPheGluGluThrAlaLysLysValArgAlaIleGluGlnLeuAlaAla 140
DB 361 AAGAAAGAAATTTGAGAACTGCGAGAAAGTGGCGCTGCCATCGAGCAGCTGCTGCC 420
QY 141 MetAsp 142
DB 421 ATGGAT 426

RESULT 2
US-09-918-186A-97
; Sequence 97, Application US/09918186A
; Patent No. US20020137708A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Eric B. Swazey
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: ISPH-0585
; CURRENT APPLICATION NUMBER: US/09/918,186A
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 09/496,694
; PRIOR FILING DATE: 2000-02-02
; PRIOR APPLICATION NUMBER: 09/286,407
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 09/163,162
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 250
; SEQ ID NO 97
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-186A-97

Alignment Scores:
Pred. No.: 1.93e-94 Length: 1619
Score: 778.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DBs: 0

US-09-690-825-34 (1-142) x US-09-918-186A-97 (1-1619)
QY 1 MetGlyAlaProThrLeuProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
DB 50 ATGGGTGCCCCGAGCTTGGCCCCCTGCTGGAGCCCTTTCTCAAGGACCAACCGCACTCT 109
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 110 ACATTCAAGAACTGGCCCTTCTTGAGGGCTGCGCTGCACCCCGAGCGGATGGCGGAG 169
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPheCys 60
DB 170 GCTGCTTCATCCACTGCCCACTGAGAACGAGCCAGATGGCCCACTGTTCTTCTGTC 229
QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluHisLysLysHis 80
DB 230 TTCAAGGAGCTGGAGGCTGGAGCCAGATGACGACCCCATAGAGGAACATAAAAGCAT 289
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluThrLeuGlyGlu 100
DB 290 TCGTCCGGTTGCGCTTTCTTCTTCGTCAGAGGAGCTTTGAAGAAATTAACCTTTGGTGAA 349
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120
DB 350 TTTTGGAACTGGACAGAGGAGCCAGAAACAAATTCGAAAGGAAACCAACATATAG 409
QY 121 LysLysGluPheGluGluThrAlaLysLysValArgAlaIleGluGlnLeuAlaAla 140
DB 410 AAGAAAGAAATTTGAGAACTGCGAGAAAGTGGCGCTGCCATCGAGCAGCTGCTGCC 469
QY 141 MetAsp 142
DB 470 ATGGAT 475

RESULT 3
US-10-342-887-566
; Sequence 566, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 566
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-566

Alignment Scores:
Pred. No.: 1.93e-94 Length: 1619
Score: 778.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DBs: 13

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US-09-690-825-34 (1-142) x US-10-342-887-566 (1-1619)

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Qy 1 MetGlyAlaProThrLeuProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
Db 50 ATGGGTGCCCGACGCTTGGCCCTGCTGGCAGCCCTTTCTCAAGGACCCACCGCATCTCT 109
Qy 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
Db 110 ACATTTCAAGAACTGGCCCTTCTGGAGGCTGCGCTGCACCCCGGAGCGATGGCCGAG 169
Qy 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
Db 170 GTGTGCTTCATCCACTGCCCACTGAGAACGACGACACTTGGCCCACTGTTCTTCTGCG 229
Qy 61 PheLysGluLeuGluGlyTrpGluProAspLeuPheGlnPheGluGluHisLysHis 80
Db 230 TTCAAGGAGCTGGAAGCTGGGAGCGCAGATGACGACGACGACACTTGGCCCACTGTTCTTCTGCG 289
Qy 81 SerSerGlyCysAlaPheLeuSerValLysLysValArgAlaIleGluGluLeuGlu 100
Db 290 TGTGCGGTGGCTTCTTCTGTCAGAGAGCGAGTTGAGAGATTAACCCCTTGGTGAA 349
Qy 101 PheLeuLysLeuAspArgLysAlaLysLysLysLysLysLysLysLysLysLys 120
Db 350 TTTTGAAGCTGCAGAGAAAGCCCAAGAACAAATTGCAAGGAAACCAACAATAAG 409
Qy 121 LysLysGluPheGluGluThrAlaLysLysValArgAlaIleGluGluLeuAla 140
Db 410 AAGAAAGAAATTGAGGAAATCGGAAGAAAGTGCGCGCTGCATCGACGCTGGCTGCC 469
Qy 141 MetAsp 142
Db 470 ATGGAT 475
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RESULT 4

US-10-172-118-566
; Sequence 566, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 566
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_001168
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-566

Alignment Scores:
Pred. No.: 1,93e-94 Length: 1619
Score: 778.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-09-690-825-34 (1-142) x US-10-172-118-566 (1-1619)

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Qy 1 MetGlyAlaProThrLeuProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
Db 50 ATGGGTGCCCGACGCTTGGCCCTGCTGGCAGCCCTTTCTCAAGGACCCACCGCATCTCT 109
Qy 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
Db 110 ACATTTCAAGAACTGGCCCTTCTGGAGGCTGCGCTGCACCCCGGAGCGATGGCCGAG 169
Qy 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
Db 170 GTGTGCTTCATCCACTGCCCACTGAGAACGACGACACTTGGCCCACTGTTCTTCTGCG 229
Qy 61 PheLysGluLeuGluGlyTrpGluProAspLeuPheGlnPheGluGluHisLysHis 80
Db 230 TTCAAGGAGCTGGAAGCTGGGAGCGCAGATGACGACGACGACACTTGGCCCACTGTTCTTCTGCG 289
Qy 81 SerSerGlyCysAlaPheLeuSerValLysLysValArgAlaIleGluGluLeuGlu 100
Db 290 TGTGCGGTGGCTTCTTCTGTCAGAGAGCGAGTTGAGAGATTAACCCCTTGGTGAA 349
Qy 101 PheLeuLysLeuAspArgLysAlaLysLysLysLysLysLysLysLysLysLys 120
Db 350 TTTTGAAGCTGCAGAGAAAGCCCAAGAACAAATTGCAAGGAAACCAACAATAAG 409
Qy 121 LysLysGluPheGluGluThrAlaLysLysValArgAlaIleGluGluLeuAla 140
Db 410 AAGAAAGAAATTGAGGAAATCGGAAGAAAGTGCGCGCTGCATCGACGCTGGCTGCC 469
Qy 141 MetAsp 142
Db 470 ATGGAT 475
```

RESULT 5

US-10-181-316-97
; Sequence 97, Application US/10181316
; Publication No. US20030211607A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Eric B. Swayze
; APPLICANT: Lex M. Cowart
; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: ISPH-0650
; CURRENT APPLICATION NUMBER: US/10/181,316
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: PCT/US01/02939
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 09/496,694
; PRIOR FILING DATE: 2000-02-02
; PRIOR APPLICATION NUMBER: 09/286,407
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 09/163,162
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 249
; SEQ ID NO 97
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-181-316-97

Alignment Scores:
Pred. No.: 1,93e-94 Length: 1619
Score: 778.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-09-690-825-34 (1-142) x US-10-181-316-97 (1-1619)

```
Qy 1 MetGlyAlaProThrLeuProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
Db 50 ATGGGTGCCCGACGCTTGGCCCTGCTGGCAGCCCTTTCTCAAGGACCCACCGCATCTCT 109
```

Db 50 ATGGGTGCCCGACGTTGGCCCTGCTGGCAGCCCTTTCTCAAGACACACCGCATCTCT 109
 Qy 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
 Db 110 ACATTCAGAACTGGCCCTCTTGGAGGCTGGCCCTGCACCCCGGAGCGGATGGCCGAG 169
 Qy 41 AlaGlyPheLeuHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
 Db 170 GCTGGCTTCATCCACTGCCCTCTTGGAGGCTGGCCCTGCACCCCGGAGCGGATGGCCGAG 229
 Qy 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHisLysLysHis 80
 Db 230 TTCAGAGAGCTGGAGGCTGGAGCCAGATGACGCCCATAGAGGAACATAAAGCAT 289
 Qy 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
 Db 290 TCGTCGGTTCGGCTTTCCTTCTGTCAAGAGCAGTTTCAAGAAATTAACCTTGGTGAA 349
 Qy 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
 Db 350 TTTTGTGAACCTGGACAGAGAGAGCCCAAGAAATTCGAAAGGAACCAACAATAAG 409
 Qy 121 LysLysGluPheGluGluThrAlaLysLysValArgAlaIleGluGlnLeuAlaAla 140
 Db 410 AAGAAAGAAATTCAGGAACTGCGGAAAGTGGCCGTCGCATCGAGCAGCTGGCTGCC 469
 Qy 141 MetAsp 142
 Db 470 ATGGAT 475

RESULT 6

US-10-388-360-324
 ; Sequence 324, Application US/10388360
 ; Publication No. US2003022528A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GENOMIC HEALTH
 ; APPLICANT: Baker, Joffre B.
 ; APPLICANT: Cronin, Maureen T.
 ; APPLICANT: Kiefer, Michael C.
 ; APPLICANT: Shak, Steve
 ; APPLICANT: Walker, Michael Graham
 ; TITLE OF INVENTION: GENE EXPRESSION PROFILING IN BIOPSIED TUMOR TISSUES
 ; FILE REFERENCE: 39740-0001US
 ; CURRENT APPLICATION NUMBER: US/10/388,360
 ; PRIOR FILING DATE: 2003-03-12
 ; PRIOR APPLICATION NUMBER: US 60/412,049
 ; PRIOR FILING DATE: 2002-09-18
 ; PRIOR APPLICATION NUMBER: US 60/364,890
 ; PRIOR FILING DATE: 2002-03-13
 ; NUMBER OF SEQ ID NOS: 384
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 324
 ; LENGTH: 1619
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-388-360-324

Alignment Scores:

Pred. No.: 1.93e-94 Length: 1619
 Score: 778.00 Matches: 142
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 13 Gaps: 0

US-09-690-825-34 (1-142) x US-10-388-360-324 (1-1619)

Qy 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
 Db 50 ATGGGTGCCCGACGTTGGCCCTGCTGGCAGCCCTTTCTCAAGACACACCGCATCTCT 109
 Qy 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40

Db 110 ACATTCAGAACTGGCCCTCTTCTGGAGGCTGGCCCTGACCCCGGAGCGGATGGCCGAG 169
 Qy 41 AlaGlyPheLeuHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
 Db 170 GCTGGCTTCATCCACTGCCCTCTTGGAGGCTGGCCCTGCACCCCGGAGCGGATGGCCGAG 229
 Qy 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHisLysLysHis 80
 Db 230 TTCAGAGAGCTGGAGGCTGGAGCCAGATGACGCCCATAGAGGAACATAAAGCAT 289
 Qy 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
 Db 290 TCGTCGGTTCGGCTTTCCTTCTGTCAAGAGCAGTTTGAAGAAATTAACCTTGGTGAA 349
 Qy 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
 Db 350 TTTTGTGAACCTGGACAGAGAGAGCCCAAGAAATTCGAAAGGAACCAACAATAAG 409
 Qy 121 LysLysGluPheGluGluThrAlaLysLysValArgAlaIleGluGlnLeuAlaAla 140
 Db 410 AAGAAAGAAATTCAGGAACTGCGGAAAGTGGCCGTCGCATCGAGCAGCTGGCTGCC 469
 Qy 141 MetAsp 142
 Db 470 ATGGAT 475

RESULT 7

US-10-283-975A-445
 ; Sequence 445, Application US/10283975A
 ; Publication No. US20040110792A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ortho-Clinical Diagnostics, Inc.
 ; TITLE OF INVENTION: Methods For Assessing and Treating Leukemia
 ; FILE REFERENCE: CDS 233 FCT
 ; CURRENT APPLICATION NUMBER: US/10/283,975A
 ; PRIOR FILING DATE: 2002-10-30
 ; PRIOR APPLICATION NUMBER: 60/340,938
 ; PRIOR FILING DATE: 2001-10-30
 ; PRIOR APPLICATION NUMBER: 60/338,997
 ; PRIOR FILING DATE: 2001-10-30
 ; PRIOR APPLICATION NUMBER: 60/340,081
 ; PRIOR FILING DATE: 2001-10-30
 ; PRIOR APPLICATION NUMBER: 60/341,012
 ; PRIOR FILING DATE: 2001-10-30
 ; NUMBER OF SEQ ID NOS: 900
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 445
 ; LENGTH: 1619
 ; TYPE: DNA
 ; ORGANISM: HUMAN
 US-10-283-975A-445

Alignment Scores:

Pred. No.: 1.93e-94 Length: 1619
 Score: 778.00 Matches: 142
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 17 Gaps: 0

US-09-690-825-34 (1-142) x US-10-283-975A-445 (1-1619)

Qy 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
 Db 50 ATGGGTGCCCGACGTTGGCCCTGCTGGCAGCCCTTTCTCAAGACACACCGCATCTCT 109
 Qy 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
 Db 110 ACATTCAGAACTGGCCCTCTTCTGGAGGCTGGCCCTGACCCCGGAGCGGATGGCCGAG 169
 Qy 41 AlaGlyPheLeuHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
 Db 170 GCTGGCTTCATCCACTGCCCTCTTCTGGAGGCTGGCCCTGACCCCGGAGCGGATGGCCGAG 229

QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHisLysLysHis 80
DB 230 TTCAGGAGCTGGAGGCTGGAGCCAGATGACGACCCCATAGAGGACATATAAAGCAT 289
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
DB 290 TCGTCGGGTGGCTTTCCCTTCTCTCAAGAGCAGTGTGAAGAAATTAACCCCTTGGTGAA 349
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
DB 350 TTTTGAACCTGCAGAGAAAGACCAAGACAAATAATTCGAAGGAAACCAACATTAAG 409
QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAlaLa 140
DB 410 AAGAAAGAAATTTGAGAAACTGCGAAGAAAGTGGCGCGCATCGAGCAGCTGGCTGCC 469
QY 141 MetAsp 142
DB 470 ATGGAT 475
RESULT 8
US-10-071-766-109
; Sequence 109, Application US/10071766
; Publication No. US20020192678A1
; GENERAL INFORMATION:
; APPLICANT: Hwei-Mei Chen
; TITLE OF INVENTION: GENES EXPRESSED IN SENESENCE
; FILE REFERENCE: PA-0043 US
; CURRENT APPLICATION NUMBER: US/10/071,766
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: PERL Program
; SEQ ID NO 109
; LENGTH: 2404
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. US20020192678A1 251651.4
; LOCATION: 710, 717, 724, 982-1007
; OTHER INFORMATION: a, t, c, g, or other
US-10-071-766-109
Alignment Scores:
Pred. No.: 3,35e-94 Length: 2404
Score: 778.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-09-690-825-34 (1-142) x US-10-071-766-109 (1-2404)
QY 1 MetGlyAlaProThrLeuProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
DB 56 ATGGGTGCCCCGACGCTGGCCCTGCTGGCAGCCCTTCTCAAGGACCCCGCATCTCT 115
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 116 ACATTCAAGAACTGGCCCTTCTTGGAGGCTGGCCCTGCACCCCGGAGCGATGCCCGAG 175
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPheCys 60
DB 176 GCTGGTTCATCCACTGCCCTTCTTGGAGGCTGGCCCTGCACCCCGGAGCGATGCCCGAG 175
QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHisLysLysHis 80
DB 236 TTCAGGAGCTGGAGGCTGGAGCCAGATGACACCCCATAGAGGACATATAAAGCAT 295
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100

DB 296 TCGTCGGGTGGCTTTCCCTTCTGTCAAGAACAGCTTTGAAGAATTAACCCCTTGGTGAA 355
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
DB 356 TTTTGAACCTGCAGAGAAAGACCAAGACAAATAATTCGAAGGAAACCAACATTAAG 415
QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAlaLa 140
DB 416 AAGAAAGAAATTTGAGAAACTGCGAAGAAAGTGGCGCGCATCGAGCAGCTGGCTGCC 475
QY 141 MetAsp 142
DB 476 ATGGAT 481
RESULT 9
US-10-084-817-285
; Sequence 285, Application US/10084817
; Publication No. US20030119009A1
; GENERAL INFORMATION:
; APPLICANT: Susan Stuart
; APPLICANT: Jed G. Nuchtern
; APPLICANT: Sharon E. Pion
; APPLICANT: Jason M. Shohet
; TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION
; FILE REFERENCE: PA-0046 US
; CURRENT APPLICATION NUMBER: US/10/084,817
; CURRENT FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 60/270,784
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 365
; SOFTWARE: PERL Program
; SEQ ID NO 285
; LENGTH: 2404
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. US20030119009A1 251651.4
; NAME/KEY: unsure
; LOCATION: 710, 717, 724
; OTHER INFORMATION: a, t, c, g, or other
US-10-084-817-285
Alignment Scores:
Pred. No.: 3,35e-94 Length: 2404
Score: 778.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-09-690-825-34 (1-142) x US-10-084-817-285 (1-2404)
QY 1 MetGlyAlaProThrLeuProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
DB 56 ATGGGTGCCCCGACGCTGGCCCTGCTGGCAGCCCTTCTCAAGGACCCCGCATCTCT 115
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 116 ACATTCAAGAACTGGCCCTTCTTGGAGGCTGGCCCTGCACCCCGGAGCGATGCCCGAG 175
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPheCys 60
DB 176 GCTGGTTCATCCACTGCCCTTCTTGGAGGCTGGCCCTGCACCCCGGAGCGATGCCCGAG 175
QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHisLysLysHis 80
DB 236 TTCAGGAGCTGGAGGCTGGAGCCAGATGACACCCCATAGAGGACATATAAAGCAT 295
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
DB 296 TCGTCGGGTGGCTTTCCCTTCTGTCAAGAACAGCTTTGAAGAATTAACCCCTTGGTGAA 355

QY 101 PheLeuLysLeuAspArgGluThrAlaLysAsnLysIleAlaLysGluThrAsnLys 120
 Db 356 TTTTGAACCTGGACAGAGAAAGCCAAAGAAATTCGAAGGAAACCAACAATAAG 415
 QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAlaAla 140
 Db 416 AAGAAAGAAATTTGAGAAATTCGGAAGAAAGTGGCCGCTCCATCGAGCAGCTGGCTGCC 475
 QY 141 MetAsp 142
 Db 476 ATGGAT 481
 RESULT 10
 US-10-305-720-918
 ; Sequence 918, Application US/10305720
 ; Publication No. US20040010136A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
 ; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
 ; FILE REFERENCE: PA-0002-1 CON
 ; CURRENT APPLICATION NUMBER: US/10/305,720
 ; CURRENT FILING DATE: 2002-11-26
 ; PRIOR APPLICATION NUMBER: 09/016,434
 ; PRIOR FILING DATE: 1998-01-30
 ; NUMBER OF SEQ ID NOS: 1490
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 918
 ; LENGTH: 740
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. US20040010136A1 752848
 ; NAME/KEY: unsure
 ; LOCATION: (1) ... (740)
 ; OTHER INFORMATION: a, t, c, g, or other
 US-10-305-720-918
 Alignment Scores:
 Pred. No.: 3,15e-87 Length: 740
 Score: 721.00 Matches: 135
 Percent Similarity: 95.74% Conservative: 0
 Best Local Similarity: 95.74% Mismatches: 6
 Query Match: 92.67% Indels: 1
 DB: 16 Gaps: 0
 US-09-690-825-34 (1-142) x US-10-305-720-918 (1-740)
 QY 2 GlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSerThr 21
 Db 22 GGGTGGCGNCGTGGCCACT-GCGTGGCNCCTCTTCTCAAGGACCAACCGCATCTCTACA 80
 QY 22 PheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGluAla 41
 Db 81 TTCAAGAACTGGCCCTCTTGGAGGGCTGGCTGCACCCCGAGGGATGGCCGAGGT 140
 QY 42 GlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPheCysPhe 61
 Db 141 GGCTTCATCCACTGCCCACTGGANAACGAGCAGACTTGGCCCGAGTGTCTTCTGCTTC 200
 QY 62 LysGluLeuGluGlyTrpGluProAspAspProIleGluGluHisLysLysHisSer 81
 Db 201 AAGAGCTGAAGCTGGAGCCAGATGACAGCCCATAGAGGAACATATAAGCATTCG 260
 QY 82 SerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGluPhe 101
 Db 261 TCCGGTGGCTTCTCTCTCTGTCAGAACGAGTGTGAAGATTAACCTTGGTGAATTT 320
 QY 102 LeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLysLys 121
 Db 321 TTGAACCTGGACAGAGAAAGCCAAAGAAATTCGAAGGAAACCAACAATAAGAG 380

QY 122 LysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAlaAlaMet 141
 Db 381 AAGAATTTGAGAAACTGCGAAGAAAGTGGCCGCTGCATCGAGCAGCTGGCTGCCATG 440
 QY 142 Asp 142
 Db 441 GAT 443
 RESULT 11
 US-09-918-186A-10
 ; Sequence 10, Application US/09918186A
 ; Patent No. US20020137708A1
 ; GENERAL INFORMATION:
 ; APPLICANT: C. Frank Bennett
 ; APPLICANT: Elizabeth J. Ackermann
 ; APPLICANT: Eric E. Swayze
 ; APPLICANT: Lex M. Cowsett
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
 ; FILE REFERENCE: ISPH-0585
 ; CURRENT APPLICATION NUMBER: US/09/918,186A
 ; CURRENT FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: 09/496,694
 ; PRIOR FILING DATE: 2000-02-02
 ; PRIOR APPLICATION NUMBER: 09/286,407
 ; PRIOR FILING DATE: 1999-04-05
 ; PRIOR APPLICATION NUMBER: 09/163,162
 ; PRIOR FILING DATE: 1998-09-29
 ; NUMBER OF SEQ ID NOS: 250
 ; SEQ ID NO 10
 ; LENGTH: 955
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (109) ... (531)
 US-09-918-186A-10
 Alignment Scores:
 Pred. No.: 7,51e-79 Length: 955
 Score: 660.00 Matches: 118
 Percent Similarity: 92.86% Conservative: 12
 Best Local Similarity: 84.29% Mismatches: 10
 Query Match: 84.83% Indels: 0
 DB: 9 Gaps: 0
 US-09-690-825-34 (1-142) x US-09-918-186A-10 (1-955)
 QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
 Db 109 ATGGAGCTCCGGCGCTGCCAGATCTGGCAGCTGTACCTCAAGAACTACCGCATGCC 168
 QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
 Db 169 ACCCTCAAGAACTGGCCCTTCTCGAGGACTGCGCTGCACCCCGAGCGAATGGCGGAG 228
 QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPheCys 60
 Db 229 GCTGCTTCATCCACTGCCCTTACCAGAACGAGCTGATTTGGCCCACTGTTTCTTCG 288
 QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHisLysLysHis 80
 Db 289 TTTAAGGAATTTGAAGCTGGGAACCCGATGACAAACCCGATAGAGGAGCATAGAAGCAC 348
 QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
 Db 349 TCCCGTGGCTGGCTTCTCTCTGCTCAAGAGCAGATGGAAGAACTAACCCGTCAGTGAA 408
 QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120
 Db 409 TTCCTGAACCTGGACAGACAGAGACCAAGAAATTCGAAGGAGAGACCAACAAG 468
 QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAlaAla 140
 Db 141 TTTTGAACCTGGACAGAGAAAGCCAAAGAAATTCGAAGGAAACCAACAATAAGAG 380

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Db 469 CAAAAAGAGTTTGAGAGAGACTGCAAGAGACTACCCGTCAGTCAATTGAGCAGCTGGCTGCC 528
RESULT 12
US-10-181-316-10
; Sequence 10, Application US/10181316
; Publication No. US20030211607A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Eric E. Swayze
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: ISPH-0650
; CURRENT APPLICATION NUMBER: US/10/181,316
; PRIOR FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: PCT/US01/02939
; PRIOR FILING DATE: 2000-02-02
; PRIOR APPLICATION NUMBER: 09/496,694
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 09/286,407
; PRIOR FILING DATE: 2000-02-02
; PRIOR APPLICATION NUMBER: 09/286,407
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 09/163,162
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 249
; SEQ ID NO 10
; LENGTH: 955
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (109)...(531)
US-10-181-316-10
Alignment Scores:
Pred. No.: 7,51e-79 Length: 955
Score: 660.00 Matches: 118
Percent Similarity: 92.86% Conservative: 12
Best Local Similarity: 84.29% Mismatches: 10
Query Match: 84.83% Indels: 0
DB: 13 Gaps: 0
US-09-690-825-34 (1-142) x US-10-181-316-10 (1-955)
QY 1 MetGlyAlaProThrLeuProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
Db 109 ATGGGAGCTCCGGCGCTGCCAGATCTGGCAGCTGTACCTCAAGAATACCGCATCGCC 169
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
Db 169 ACCTTCAGAACTGGCCCTTCTGGAGGACTCGGCTGCACCCAGAGCGAATGGCGGAG 228
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
Db 229 GTGGCTTCATCCACTGCCCTACCGAGAACGAGCCCTGATTGGCCAGTGTTTTCTGCG 288
QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHisLysLysHis 80
Db 289 TTTAAGGAATTGGAAGCTGGGAACCCGATGACACCCGATAGAGAGGACATGAAGCAC 348
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluLeuThrLeuGlyGlu 100
Db 349 TCCCTCGGCTGGCCCTTCTCACTGTCAAGAAGCAGATGGAAGAACTAACCGTCAGTGAA 408
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
Db 409 TTCTTGAAACTGGACAGACAGAGAGCCAAAGACAAAATTGCAAGAGAGCCACACACAG 468
QY 121 LysLysGluPheGluGluThrAlaLysLysValArgAlaIleGluGlnLeuAla 140
Db 469 CAAAAAGAGTTTGAGAGAGACTGCAAGAGACTACCCGTCAGTCAATTGAGCAGCTGGCTGCC 528
RESULT 13
US-10-181-316-3
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; Sequence 3, Application US/10181316
; Publication No. US20030211607A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Eric E. Swayze
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: ISPH-0650
; CURRENT APPLICATION NUMBER: US/10/181,316
; PRIOR FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: PCT/US01/02939
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 09/496,694
; PRIOR FILING DATE: 2000-02-02
; PRIOR APPLICATION NUMBER: 09/286,407
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 09/163,162
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 249
; SEQ ID NO 3
; LENGTH: 14795
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2811)...(2921)
; NAME/KEY: CDS
; LOCATION: (3174)...(3283)
; NAME/KEY: CDS
; LOCATION: (5158)...(5275)
; NAME/KEY: CDS
; LOCATION: (11955)...(12044)
US-10-181-316-3
Alignment Scores:
Pred. No.: 1.02e-39 Length: 14795
Score: 382.00 Matches: 73
Percent Similarity: 46.84% Conservative: 1
Best Local Similarity: 46.20% Mismatches: 0
Query Match: 49.10% Indels: 84
DB: 13 Gaps: 1
US-09-690-825-34 (1-142) x US-10-181-316-3 (1-14795)
QY 1 MetGlyAlaProThrLeuProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
Db 2811 ATGGGTGCCCGAGCTTGGCCCTGCTGGCAGCCCTTCTCAAGGACCAACCGCATCTCT 2870
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArg 37
Db 2871 ACATTCAAGAACTGGCCCTTCTTGGAGGGCTGCCTGCACCCCGGAGCGGTGAGACTG 2930
QY 37 ----- 37
Db 2931 CCGGGCTCTCTGGGTCCCCACGCCGCTTGCCTGTCTCTAGCGAGGCCACTGTGAC 2990
QY 37 ----- 37
Db 2991 TGGGCTTCGGGGGTACAAGCCGCTTCCCTCCCGTCTGTCCCGAGCGGCACTGT 3050
QY 37 ----- 37
Db 3051 GGCTGGGCCCTTGGGTTCAGGCCGGGCTCCCTCCCTGCTGTTTGTCCCATCGAGGCCTT 3110
QY 37 ----- 37
Db 3111 TGTGGCTGGGCCCTCGGGGTTCCGGGGTGCACGCTGCACACTCAGCAGCTGTCTGTCCTTG 3170
QY 38 ---MetAlaGluAlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGln 56
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Db 3171 CAGATGCCGAGGCTGCTTCACTCCACCTGAGACGAGGACAGACTGGCCGAG 3230
Qy 57 CysPhePheCysPheLysGluLeuGluGlyTTPGluProAspAspProlle 74
Db 3231 TGTTCCTCTCTTCAAGGAGCTGGAAGGCTGGAGGCTGGAGGACAGATGACGACCCCATG 3284

RESULT 14
US-09-954-456-973
; Sequence 973, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 973
; LENGTH: 14796
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-973

Alignment Scores:
Pred. No.: 1,02e-39 Length: 14796
Score: 382.00 Matches: 73
Percent Similarity: 46.84% Conservative: 1
Best Local Similarity: 46.20% Mismatches: 0
Query Match: 49.10% Indels: 84
DB: 9 Gaps: 1

US-09-690-825-34 (1-142) x US-09-954-456-973 (1-14796)
Qy 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
Db 2811 ATGGGTGCCCGGACGCTTCCCTGCGGAGGCGCTTCTCAAGGACCCACCGCATCTCT 2870
Qy 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArg----- 37
Db 2871 ACATTCAAGAACTGGCCCTTCTTGAGGGGCTGCGCTGCACCCCGGAGCGGTGAGACTG 2930
Qy 37 ----- 37
Db 2931 CCGGCGCTCTGGGTGCCCGCCACGCGCCCTTGCCCTTGCCCTAGCGAGGCCACTGTGAC 2990
Qy 37 ----- 37
Db 2991 TGGGCTCGGGGTACAAGCGCGCTCCCTCCCGTCTCTGTCGCCAGCGGACCACTGT 3050
Qy 37 ----- 37
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Db 3051 GGCTGGGCCCCCTTGGGTCCAGGCGCGCTCCCTCCCTGCTTGTCCCATCGAGGCTT 3110
Qy 37 ----- 37
Db 3111 TGTGGCTGGGCTCGGGGTTCGGGCTGCCACGTCCTCACTCAGAGCTGTGCTGTCCCTTG 3170
Qy 38 ---MetalAlaGluAlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGln 56
Db 3171 CAGATGCCGAGGCTGGCTTTCATCCACTGCCCCACTGAGAACGAGCCAGACTTGGCCGAG 3230
Qy 57 CysPhePheCysPheLysGluLeuGluGlyTTPGluProAspAspProlle 74
Db 3231 TGTTCCTCTCTTCAAGGAGCTGGAAGGCTGGAGGCTGGAGGACAGATGACGACCCCATG 3284

RESULT 15
US-09-954-456-1636
; Sequence 1636, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1636
; LENGTH: 14796
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-1636

Alignment Scores:
Pred. No.: 1,02e-39 Length: 14796
Score: 382.00 Matches: 73
Percent Similarity: 46.84% Conservative: 1
Best Local Similarity: 46.20% Mismatches: 0
Query Match: 49.10% Indels: 84
DB: 9 Gaps: 1

US-09-690-825-34 (1-142) x US-09-954-456-1636 (1-14796)
Qy 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
Db 2811 ATGGGTGCCCGGACGCTTCCCTGCGGAGGCGCTTCTCAAGGACCCACCGCATCTCT 2870
Qy 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArg----- 37
Db 2871 ACATTCAAGAACTGGCCCTTCTTGAGGGGCTGCGCTGCACCCCGGAGCGGTGAGACTG 2930
Qy 37 ----- 37
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Db 2931 CCCGGCTCCTGGGGTCCCCACGCCGCTTGCCCTGTCCCTAGCGAGCCACTGTGAC 2990
QY 37 ----- 37
Db 2991 TGGGCTCGGGGTACAGCCGCCCTCCCTCCCGTCTGTCCCGAGGCGCACTGT 3050
QY 37 ----- 37
Db 3051 GGCTGGGCCCTTGGGTCCAGGCCGCTCCCTCCCTGTCTTGTCCCATCGAGGCCTT 3110
QY 37 ----- 37
Db 3111 TGTGCTGGGCTCGGGGTCCGGCTGCCAGTCCACTCAGAGCTGTGTCCCTTG 3170
QY 38 ---MetAlaGluAlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGln 56
Db 3171 CAGATGGCGAGGCTGGCTTCATCCACTGCCCACTGAGACGAGCCAGACTTGGCCAG 3230
QY 57 CysPhePheCysPheLysGluLeuGlyTrpGluProAspAspProile 74
Db 3231 TGTTCCTTCTGCTTCAGGAGCTGGAGGCTGGGAGCCAGATGACGCCCATG 3294
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Search completed: August 16, 2004, 01:27:36
Job time : 518 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 11, 2004, 14:21:52 ; Search time 16 Seconds

(without alignments)
853.700 Million cell updates/sec

Title: US-09-690-825-34

Perfect score: 142

Sequence: 1 MGAPLPPAWQFFLKDHRS.....EFETAKKVRRAIEQLAAMD 142

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : PIR 78:*

1: Pir1:*

2: Pir2:*

3: Pir3:*

4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	5.6	706	2 S74610	hypothetical prote
2	8	5.6	875	2 T27495	hypothetical prote
3	8	5.6	1822	2 S33441	EF protein - Strep
4	7	4.9	130	2 T15642	hypothetical prote
5	7	4.9	140	2 A57544	BM88 antigen - pig
6	7	4.9	152	2 AD1071	conserved hypotet
7	7	4.9	179	2 AD1597	20S proteasome bet
8	7	4.9	179	2 AF1234	20S proteasome bet
9	7	4.9	199	2 H71927	cag island protein
10	7	4.9	199	2 F64585	cag pathogenicity
11	7	4.9	228	2 D75048	aspartate racemase
12	7	4.9	228	2 G71112	probable aspartate
13	7	4.9	248	2 T13126	protein gp40 - pha
14	7	4.9	253	2 A96028	probable protocate
15	7	4.9	271	2 G69462	conserved hypotet
16	7	4.9	343	2 T40306	hypothetical prote
17	7	4.9	374	2 G88955	protein K04F1.6 [i
18	7	4.9	379	2 E83387	conserved hypotet
19	7	4.9	393	2 C83387	iron-sulfur cofact
20	7	4.9	427	2 T46148	hypothetical prote
21	7	4.9	442	2 A45529	heat shock protein
22	7	4.9	525	2 F97305	spore germination
23	7	4.9	662	2 T16845	hypothetical prote
24	7	4.9	698	2 AC0016	4-alpha-glucanotra
25	7	4.9	744	2 S64292	hypothetical prote
26	7	4.9	885	2 S76357	penicillin-binding
27	7	4.9	932	2 T04443	hypothetical prote
28	7	4.9	997	2 T43523	cut17 protein - fi
29	7	4.9	1098	2 T28816	hypothetical prote

30	7	4.9	2010	2 B71616	phosphatase (acid
31	7	4.9	2116	2 A26655	myosin heavy chain
32	7	4.9	2212	2 T28157	erythrocyte membra
33	7	4.9	2285	2 T12796	probable transglyc
34	7	4.9	2647	2 T28161	hypothetical prote
35	6	4.2	35	2 B95898	hypothetical prote
36	6	4.2	52	2 S77666	probable ornithine
37	6	4.2	62	2 S65922	homeotic protein e
38	6	4.2	62	2 S49558	hypothetical prote
39	6	4.2	68	2 H98098	hypothetical prote
40	6	4.2	73	2 AB1413	hypothetical prote
41	6	4.2	73	2 A11788	hypothetical prote
42	6	4.2	75	2 S75054	hypothetical prote
43	6	4.2	80	2 AH2420	hypothetical prote
44	6	4.2	82	1 VCBPRK	coat protein B pre
45	6	4.2	87	2 B36907	pyocin S1 SII subu
46	6	4.2	87	2 D36907	pyocin S2 immunity
47	6	4.2	98	2 H96585	hypothetical prote
48	6	4.2	100	2 B71567	hypothetical prote
49	6	4.2	103	2 F71137	probable membrane
50	6	4.2	107	2 S53575	probable anti-sigm
51	6	4.2	108	2 A71353	probable Spbeta ph
52	6	4.2	108	2 T12829	hypothetical prote
53	6	4.2	108	2 F71158	hypothetical prote
54	6	4.2	115	2 T30042	hypothetical prote
55	6	4.2	116	2 C72265	hypothetical prote
56	6	4.2	121	2 B96847	hypothetical prote
57	6	4.2	122	2 AC2545	MobB protein limpo
58	6	4.2	131	2 D69145	conserved hypotet
59	6	4.2	133	2 AB3465	hypothetical prote
60	6	4.2	134	2 T35557	ribosomal protein
61	6	4.2	134	2 B75037	hypothetical prote
62	6	4.2	135	2 C71126	hypothetical prote
63	6	4.2	136	1 H64306	conserved hypotet
64	6	4.2	141	2 B64670	ribosomal protein
65	6	4.2	142	2 C72430	hypothetical prote
66	6	4.2	142	2 AF1517	hypothetical prote
67	6	4.2	145	2 B56150	probable general s
68	6	4.2	145	2 AB1277	transcription regu
69	6	4.2	149	2 H71205	hypothetical prote
70	6	4.2	150	2 AB1265	hypothetical prote
71	6	4.2	151	2 S43727	hypothetical prote
72	6	4.2	152	2 A87707	conserved hypotet
73	6	4.2	156	1 R3TW7	ribosomal protein
74	6	4.2	156	2 D75536	ribosomal protein
75	6	4.2	158	2 D82044	rRNA methylase, Sp
76	6	4.2	163	2 A72530	probable isosinol
77	6	4.2	168	2 A41547	ubiquitin-conjugat
78	6	4.2	170	2 B71864	hypothetical prote
79	6	4.2	172	2 E70057	hypothetical prote
80	6	4.2	172	2 E83886	hypothetical prote
81	6	4.2	172	2 A12268	hypothetical prote
82	6	4.2	173	2 A90397	hypothetical prote
83	6	4.2	174	2 A10013	heat shock protein
84	6	4.2	176	1 FWEC	inorganic diphosph
85	6	4.2	176	2 D91279	inorganic pyrophos
86	6	4.2	176	2 D86120	inorganic pyrophos
87	6	4.2	177	2 C87308	hypothetical prote
88	6	4.2	177	2 D83015	heat shock protein
89	6	4.2	178	2 S64257	hypothetical prote
90	6	4.2	182	2 F64589	hypothetical prote
91	6	4.2	188	2 T39211	hypothetical prote
92	6	4.2	196	2 PN0478	vancomycin resista
93	6	4.2	198	2 S50710	hypothetical prote
94	6	4.2	201	2 A31484	tropoin I, fast s
95	6	4.2	201	2 F70468	conserved hypotet
96	6	4.2	202	2 C87353	hypothetical prote
97	6	4.2	205	2 F83261	hypothetical prote
98	6	4.2	205	2 B97302	transcription regu
99	6	4.2	207	1 D64601	phosphoserine phos
100	6	4.2	207	2 B83523	hypothetical prote

ALIGNMENTS

RESULT 1

S74610
 hypothetical protein slr1103 - *Synechocystis* sp. (strain PCC 6803)
 C:Species: *Synechocystis* sp.
 A:Variety: PCC 6803
 C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 17-Feb-2003
 R:Accession: S74610
 R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
 A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* s.

A:Reference number: S74322; MUID:97061201; PMID:8905231
 A:Accession: S74610
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-706 <XAN>
 A:Cross-references: EMBL:D90900; GB:A3001339; NID:gl651768; PIDN:BAA16762.1; PID:gl65183
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
 C:Superfamily: signal transduction protein with FHA, Fas, GDEF, EAL domains

Query Match 5.6%; Score 8; DB 2; Length 706;
 Best Local Similarity 100.0%; Pred. No. 5;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 RRAIEQLA 139
 |||||
 Db 585 RRAIEQLA 592

RESULT 2

T27495
 hypothetical protein ZC15.1 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T27495
 R: Basham, V.
 submitted to the EMBL Data Library, March 1997
 A:Reference number: Z20377
 A:Accession: T27495
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-875 <WIL>
 A:Cross-references: EMBL:Z93396; NID:gl188462; PIDN:CAB07709.1; GSPDB:GN000023; CESP:ZC15
 A:Experimental source: clone ZC15
 C:Genetics:
 A:Gene: CESP:ZC15.1
 A:Map position: 5
 A:Introns: 345/3; 380/3; 426/3; 669/2

Query Match 5.6%; Score 8; DB 2; Length 875;
 Best Local Similarity 100.0%; Pred. No. 6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAPTLPQA 9
 |||||
 Db 433 GAPTLPQA 440

RESULT 3

S33441
 EF protein - *Streptococcus suis*
 C:Species: *Streptococcus suis*
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 15-Oct-1999
 R:Smith, H.E.; Reek, F.H.; Veicht, U.; Gielkens, A.L.J.; Smits, M.A.
 submitted to the EMBL Data Library, May 1993
 A:Description: Repeats in an extracellular protein of weak-pathogenic strains are absent
 A:Reference number: S33441
 A:Accession: S33441

A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1822 <SMI>
 A:Cross-references: EMBL:X71980; NID:G298031; PIDN:CAA50714.1; PID:G298032

Query Match 5.6%; Score 8; DB 2; Length 1822;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 AKNKIAKE 116
 |||||
 Db 1057 AKNKIAKE 1064

RESULT 4

T15642
 hypothetical protein C26F1.4 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 24-Nov-1999
 C:Accession: T15642
 R:Geisel, C.; Stellyes, L.; Bradshaw, H.
 submitted to the EMBL Data Library, March 1996
 A:Description: The sequence of *C. elegans* cosmid C26F1.
 A:Reference number: Z18381
 A:Accession: T15642
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-130 <GEI>
 A:Cross-references: EMBL:U53148; NID:gl255375; PID:gl255381; PIDN:AAB37076.1; GSPDB:GN000
 A:Experimental source: strain Bristol N2; clone C26F1
 C:Genetics:
 A:Gene: CESP:C26F1.4
 A:Map position: 5
 A:Introns: 27/3; 71/1
 C:Superfamily: unassigned ubiquitin-related proteins; ubiquitin homology

Query Match 4.9%; Score 7; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 94 BELTLE 100
 |||||
 Db 47 BELTLE 53

RESULT 5

A57544
 BM88 antigen - pig
 C:Species: *Sus scrofa domestica* (domestic pig)
 C:Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 05-Nov-1999
 C:Accession: A57544; S49384
 R:Mamalak, A.; Boutou, E.; Hurel, C.; Patsavoudi, E.; Tzartos, S.; Matsas, R.
 J. Biol. Chem. 270, 14201-14208, 1995
 A:Title: The BM88 antigen, a novel neuron-specific molecule, enhances the differentiation
 A:Reference number: A57544; MUID:95294030; PMID:7775480
 A:Accession: A57544
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-140 <MAM>
 A:Cross-references: EMBL:X82027; NID:G557672; PIDN:CAA57549.1; PID:G557673
 C:Superfamily: pig BM88 antigen
 C:Keywords: phosphoprotein; transmembrane protein

Query Match 4.9%; Score 7; DB 2; Length 140;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 APTLPQA 9
 |||||
 Db 50 APTLPQA 56

RESULT 6

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AD1071
conserved hypothetical protein SRY4902 [imported] - Salmonella enterica subsp. enterica
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AD1071
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerthon, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AD1071
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-152 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD03387.1; PID:GI6505656; GSPDB:GN00176
C:Genetics:
A:Gene: SRY4902

Query Match 4.9%; Score 7; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 TPERMAE 40
Db 135-TPERMAE 141

RESULT 7
20S proteasome beta-type chain homolog clpQ [imported] - Listeria innocua (strain Clp11
AD1597
C:Species: Listeria innocua
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C:Accession: AD1597
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluster, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AD1597
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-179 <GLA>
A:Cross-references: GB:AL592022; PIDN:CAC96548.1; PID:GI6413790; GSPDB:GN00178
A:Experimental source: strain Clp11262
C:Genetics:
A:Gene: clpQ

Query Match 4.9%; Score 7; DB 2; Length 179;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 TAKKVR 133
Db 36 TAKKVR 42

RESULT 8
20S proteasome beta-type chain homolog clpQ [imported] - Listeria monocytogenes (strain
AF1234
C:Species: Listeria monocytogenes
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C:Accession: AF1234
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma

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ok, C.; Schluster, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AF1234
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-179 <GLA>
A:Cross-references: GB:NC_003210; PIDN:CAC99356.1; PID:GI6410694; GSPDB:GN00177
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: clpQ

Query Match 4.9%; Score 7; DB 2; Length 179;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 TAKKVR 133
Db 36 TAKKVR 42

RESULT 9
H71927
cag island protein - Helicobacter pylori (strain J99)
C:Species: Helicobacter pylori
A:Variety: strain J99
C>Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
C:Accession: H71927
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
Ives, C.; Gibson, R.; Merberg, D.; Millis, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; J
Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric patho
A:Reference number: A71800; MUID:99120557; PMID:9923682
A:Accession: H71927
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-199 <ARN>
A:Cross-references: GB:AB001481; GB:AB001439; MID:94155005; PIDN:AAD06046.1; PID:G4155006
A:Experimental source: strain J99
C:Genetics:
A:Gene: orf12

Query Match 4.9%; Score 7; DB 2; Length 199;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 ELTLGEF 101
Db 98 ELTLGEF 104

RESULT 10
F64585
cag pathogenicity island protein cagE - Helicobacter pylori (strain 26695)
C:Species: Helicobacter pylori
C>Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
C:Accession: F64585
R:Tomb, J.F.; White, O.; Kervavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.N
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; MUID:9794467; PMID:9252185
A:Accession: F64585
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-199 <TOM>
A:Cross-references: GB:AB000566; GB:AB000511; MID:92313628; PIDN:AAD07593.1; PID:G2313664

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Query Match 4.9%; Score 7; DB 2; Length 199;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 95 ETLTGEF 101
 |||||
 Db 98 ETLTGEF 104

RESULT 11

D75048

aspartate racemase PAB0912 - Pyrococcus abyssi (strain Orsay)

C:Species: Pyrococcus abyssi

C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000

C:Accession: D75048

R:Anonymous, Genoscope

submitted to the EMBL Data Library, July 1999

A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure

A:Reference number: A75001

A:Accession: D75048

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-228 <KAW>

A:Cross-references: GB:A0248287; GB:AL096836; NID:G5458657; PIDN:CAB50281.1; PID:G545879

A:Experimental source: strain Orsay

C:Genetics:

A:Gene: racD-1; PAB0912

C:Superfamily: Escherichia coli hypothetical 25.2K (lysR-araE intergenic region)

Query Match

Best Local Similarity 4.9%; Score 7; DB 2; Length 228;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 BETAKKV 131

|||||

Db 105 BETAKKV 111

RESULT 12

G71112

probable aspartate racemase - Pyrococcus horikoshii

C:Species: Pyrococcus horikoshii

C>Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000

C:Accession: G71112

R:Kawababayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin

M.; Ohtoku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi

DNA Res. 5, 55-76, 1998

A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a

A:Reference number: A71000; MUID:9834137; PMID:9679194

A:Accession: G71112

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-228 <KAW>

A:Cross-references: GB:AP000003; NID:G3236130; PIDN:BAA29761.1; PID:G3257078

A:Experimental source: strain OT3

A:Note: this accession replaces an interim accession for a sequence replaced by GenBank

C:Genetics:

A:Gene: PH0670

C:Superfamily: Escherichia coli hypothetical 25.2K (lysR-araE intergenic region)

Query Match

Best Local Similarity 4.9%; Score 7; DB 2; Length 228;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 BETAKKV 131

|||||

Db 105 BETAKKV 111

RESULT 13

T13126

protein gp40 - phage N15

C:Species: phage N15

C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 03-Nov-2003

C:Accession: T13126

R:Hendrix, R.W.; Ravin, V.K.; Casjens, S.R.; Ford, M.E.; Ravin, N.V.; Smirnov, I.K.

submitted to the EMBL Data Library, May 1998

A:Reference number: Z17603

A:Accession: T13126

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-248 <HEN>

A:Cross-references: EMBL:AF064539; NID:G3192683; PID:G3192714; PIDN:AAC19067.1

C:Genetics:

A:Note: Gene 40

C:Superfamily: antitermination protein Q

Query Match

Best Local Similarity 4.9%; Score 7; DB 2; Length 248;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 RRAIEQL 138

|||||

Db 91 RRAIEQL 97

RESULT 14

A96028

probable protocatechuate 3,4-dioxygenase (EC 1.13.11.3) beta chain [imported] - Sinorhizobium meliloti

C:Species: Sinorhizobium meliloti

C>Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 20-Jan-2003

C:Accession: A96028

R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernand

Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001

A:Title: The complete sequence of the 1,683-Kb pSymb megaplasmid from the N2-fixing endo

A:Reference number: A95842; MUID:21396508; PMID:11481431

A:Accession: A96028

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-253 <KUR>

A:Cross-references: GB:AL591985; PIDN:CAC49889.1; PID:G15141377; GSPDB:GN00167

A:Experimental source: strain 1021, megaplasmid pSymb

R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,

pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;

L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,

hebaud, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.C

A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A:Reference number: A96039; MUID:21368234; PMID:11474104

A:Contents: annotation

C:Genetics:

A:Gene: pcaH; SMD20577

A:Genome: plasmid

C:Superfamily: protocatechuate 3,4-dioxygenase beta chain

C:Keywords: oxidoreductase

Query Match

Best Local Similarity 4.9%; Score 7; DB 2; Length 253;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 RRAIEQL 138

|||||

Db 209 RRAIEQL 215

RESULT 15

G69462

conserved hypothetical protein AF1704 - Archaeoglobus fulgidus

C:Species: Archaeoglobus fulgidus

C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 29-Sep-1999

C:Accession: G69462

R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson,

F.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.;

Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997

A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artisch, P.; Kaine, B.P.; Sykes, S.P

Smith, H.O.; Woese, C.R.; Venter, J.C.

A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo

A:Reference number: A69250; MUID:98049343; PMID:9389475
A:Accession: G69462
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-271 <NLE>
A:Cross-references: GB:AA000986; GB:AE000782; NID:G2689309; PIDN:AA889546.1; PID:G264885
C:Superfamily: hypothetical protein HP0152

Query Match 4.9%; Score 7; DB 2; Length 271;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 LDRERAK 110
|||||
Db 220 LDRERAK 226

RESULT 16
T40306
hypothetical protein SPBC36.11 - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T40306
R:Lyne, M.; Wood, V.; Rajandream, M.A.; Barrell, B.G.; Hilbert, H.; Moestl, D.; Duesterh
submitted to the EMBL Data Library, May 1998
A:Reference number: Z11919
A:Accession: T40306
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-343 <LYN>
A:Cross-references: EMBL:AL023589; PIDN:CAA19059.1; GSPDB:GN00067; SPDB:SPBC36.11
A:Experimental source: strain 972h-; cosmid c36
C:Genetics:
A:Gene: SPDB:SPBC36.11
A:Map position: 2

Query Match 4.9%; Score 7; DB 2; Length 343;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 EEKKGHS 81
|||||
Db 330 EEKKGHS 336

RESULT 17
G88955
protein K04F1.6 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C:Accession: G88955
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C_ele
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: G88955
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-374 <STO>
A:Cross-references: GB:chr_V; PIDN:AACT8165.1; PID:G3886012; GSPDB:GN00023; CESP:K04F1.6
C:Genetics:
A:Gene: K04F1.6
A:Map position: 5

Query Match 4.9%; Score 7; DB 2; Length 374;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 QFEELTL 98
|||||
Db 236 QFEELTL 242

RESULT 18

E75364
conserved hypothetical protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C:Accession: E75364
R:White, O.; Eisen, J.A.; Heideberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; I
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: E75364
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-379 <WHI>
A:Cross-references: GB:AE002011; GB:AE000513; NID:G6459461; PIDN:AAF11251.1; PID:G6459461
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR1694
A:Map position: 1
C:Superfamily: probable methyltransferase b0967

Query Match 4.9%; Score 7; DB 2; Length 379;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 AIEQLAA 140
|||||
Db 262 AIEQLAA 268

RESULT 19

iron-sulfur cofactor synthesis protein PA2062 [similarity] - Pseudomonas aeruginosa (stra
C:Accession: C83387
N:Contains: L-cysteine sulfintransferase (EC 2.8.1.-)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: C83387
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Bri
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:2043737; PMID:10984043
A:Accession: C83387
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-393 <STO>
A:Cross-references: GB:AE004633; GB:AE004091; NID:G9948070; PIDN:AA05450.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA2062
C:Superfamily: nitrogen fixation protein nifs
C:Keywords: phosphoprotein; pyridoxal phosphate; sulfotransferase
F:206/Binding site: pyridoxal phosphate (lys) (covalent) #status predicted
F:327/Active site: Cys (cysteine persulfide intermediate) #status predicted

Query Match 4.9%; Score 7; DB 2; Length 393;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PAWQPFL 14
|||||
Db 381 PAWQPFL 387

RESULT 20

T46148
hypothetical protein T3A5.90 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)

C>Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
 C:Accession: T46148
 R:Bloeker, H.; Mewes, H.W.; Mayer, K.F.X.; Lemcke, K.; Schueller, C.; Quetier, F.; Sala
 submitted to the Protein Sequence Database, December 1999
 A:Reference number: Z23024
 A:Accession: T46148
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-427 <BLO>
 A:Cross-references: EMBL:AL132979
 A:Experimental source: cultivar Columbia; BAC clone T3A5
 C:Genetics:
 A:Map position: 3
 A:Introns: 286/3; 329/3
 A:Note: T3A5.90

Query Match 4.9%; Score 7; DB 2; Length 427;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 71 DDPIEEH 77
 |||||
 Db 339 DDPIEEH 345

RESULT 21
 A45529
 heat shock protein 86 - fluke (Schistosoma mansoni) (fragment)
 C:Species: Schistosoma mansoni
 C>Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 20-Aug-1999
 C:Accession: A45529
 R:Johnson, K.S.; Wells, K.; Bock, J.V.; Nene, V.; Taylor, D.W.; Cordingley, J.S.
 Mol. Biochem. Parasitol. 36, 19-28, 1989
 A:Title: The 86-kilodalton antigen from Schistosoma mansoni is a heat-shock protein homolog
 A:Reference number: A45529; MUID:90043865; PMID:2509907
 A:Accession: A45529
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-442 <JOH>
 A:Cross-references: GB:J04017; NID:G161027; PIDN:AAA29899.1; PID:G161028
 C:Superfamily: heat shock protein 90

Query Match 4.9%; Score 7; DB 2; Length 442;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 90 KKQPEEL 96
 |||||
 Db 269 KKQPEEL 275

RESULT 22
 F97305
 spore germination protein GerKA, membrane protein [imported] - Clostridium acetobutylicum
 C:Species: Clostridium acetobutylicum
 C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001
 C:Accession: F97305
 R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
 ; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
 J. Bacteriol. 183, 4823-4838, 2001
 A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
 A:Reference number: A96900; MUID:21359325; PMID:21359325
 A:Accession: F97305
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-525 <KUR>
 A:Cross-references: GB:AE001437; PIDN:AK81233.1; PID:G15026379; GSPDB:GN00168
 A:Experimental source: Clostridium acetobutylicum ATCC824
 C:Genetics:
 A:Gene: CAC3300
 C:Superfamily: spore germination protein gerBA

Query Match 4.9%; Score 7; DB 2; Length 525;

Best Local Similarity 100.0%; Pred. No. 43;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 94 BELTIGE 100
 |||||
 Db 183 BELTIGE 189

RESULT 23
 T16845
 hypothetical protein T10F2.3 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
 C:Accession: T16845
 R:Miller, N.
 submitted to the EMBL Data Library, March 1995
 A:Description: The sequence of C. elegans cosmid T10F2.
 A:Reference number: Z18589
 A:Accession: T16845
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-662 <MIL>
 A:Cross-references: EMBL:U23412; NID:G727446; PID:G727449; PIDN:AAA64293.1; CESP:T10F2.3
 A:Experimental source: strain Bristol N2
 C:Genetics:
 A:Gene: CESP:T10F2.3
 A:Introns: 17/1; 51/1; 96/3; 197/3; 291/3; 342/3; 375/2; 619/2; 645/3; 649/1

Query Match 4.9%; Score 7; DB 2; Length 662;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 108 RAKNKIA 114
 |||||
 Db 339 RAKNKIA 345

RESULT 24
 AC0016
 4-alpha-glucanotransferase (EC 2.4.1.25) [imported] - Yersinia pestis (strain CO92)
 C:Species: Yersinia pestis
 C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
 C:Accession: AC0016
 R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
 deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; H
 il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, B
 Nature 413, 523-527, 2001
 A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
 A:Reference number: AB0001; MUID:21470413; PMID:11586360
 A:Accession: AC0016
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-698 <KUR>
 A:Cross-references: GB:AL590842; PIDN:CAC89898.1; PID:G15978231; GSPDB:GN00175
 C:Genetics:
 A:Gene: malQ
 C:Superfamily: 4-alpha-glucanotransferase
 C:Keywords: Glycosyltransferase; hexosyltransferase

Query Match 4.9%; Score 7; DB 2; Length 698;
 Best Local Similarity 100.0%; Pred. No. 55;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 LDRERAK 110
 |||||
 Db 586 LDRERAK 592

RESULT 25
 S64292
 hypothetical protein YGR003w - yeast (Saccharomyces cerevisiae)
 N:Alternate names: hypothetical protein G3843
 C:Species: Saccharomyces cerevisiae

C>Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 19-Apr-2002
C/Accession: S64292
R/Hebling, U.; Hofmann, B.; Delius, H.
submitted to the Protein Sequence Database, May 1996
A/Reference number: S64003
A/Accession: S64292
A/Molecule type: DNA
A/Residues: 1-744 <HEB>
A/Cross-references: EMBL:Z72788; NID:gl322956; PID:e243365; PID:gl322957; GSPDB:GN00007;
A/Experimental source: strain S288C
C/Genetics:
A/Gene: MIPS:YGR003w
A/Cross-references: SGD:S0003235
A/Map position: 7R

Query Match 4.9%; Score 7; DB 2; Length 744;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 94 BELTLGE 100
|||||
Db 587 BELTLGE 593

RESULT 26

S76357
penicillin-binding protein 1A - *Synechocystis* sp. (strain PCC 6803)
N/Alternate names: protein sl1002
C/Species: *Synechocystis* sp.
A/Variety: PCC 6803
C/Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 01-Mar-2002
C/Accession: S76357
R/Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A/Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*
s.
A/Reference number: S74322; MUID:97061201; PMID:8905231
A/Accession: S76357
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-885 <KAN>
A/Cross-references: EMBL:D64000; GB:AB001339; NID:gl001484; PID:BAAL0209.1; PID:dl01086
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C/Genetics:
A/Gene: ponA
A/Start codon: GTG
C/Superfamily: penicillin-binding protein

Query Match 4.9%; Score 7; DB 2; Length 885;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 94 BELTLGE 100
|||||
Db 370 BELTLGE 376

RESULT 27

T04443
hypothetical protein T18B16.190 - *Arabidopsis thaliana*
C/Species: *Arabidopsis thaliana* (mouse-ear cress)
C/Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 30-Apr-1999
C/Accession: T04443
R/Bavan, M.; Benes, V.; Rechmann, S.; Borkova, D.; Ansoorge, W.; Bancroft, I.; Mewes, H.W.
submitted to the Protein Sequence Database, April 1998
A/Reference number: Z15359
A/Accession: T04443
A/Molecule type: DNA
A/Residues: 1-932 <BEV>
A/Cross-references: EMBL:AL021687
A/Experimental source: cultivar Columbia; BAC clone T18B16
C/Genetics:

A/Map position: 4
A/Introns: 527/2
A/Note: T18B16.190

Query Match 4.9%; Score 7; DB 2; Length 932;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 94 BELTLGE 100
|||||
Db 303 BELTLGE 309

RESULT 28

T43523
cut17 protein - fission yeast (*Schizosaccharomyces pombe*)
C/Species: *Schizosaccharomyces pombe*
C/Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 02-Jun-2000
C/Accession: T43523; T41649; T41700
R/Morishita, J.; Matsusaka, T.; Yanagida, M.
submitted to the EMBL Data Library, August 1999
A/Description: Fission yeast cut17 is required for chromosome segregation.
A/Reference number: Z22536
A/Accession: T43523
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-997 <MOR>
A/Cross-references: EMBL:AB031034; PIDN:BAAB3415.1
R/Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, August 1998
A/Reference number: Z22007
A/Accession: T41649
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-997 <HAR>
A/Cross-references: EMBL:AL031323; PIDN:CAA20434.1; GSPDB:GN00068; SPDB:SPCC962.02c
A/Experimental source: strain 972h-; cosmid c962
R/Wedler, H.; Duesterhoeft, A.; Mbougall, R.C.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, October 1999
A/Reference number: Z22010
A/Accession: T41700
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 932-997 <WED>
A/Cross-references: EMBL:AL121859; PIDN:CAB58376.1; GSPDB:GN00068; SPDB:SPCP31B10.10c
C/Genetics:
A/Gene: cut17; SPCC962.02c; SPDB:SPCP31B10.10c
A/Map position: 3L
A/Introns: 43/3

Query Match 4.9%; Score 7; DB 2; Length 997;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 WEPPDDP 73
|||||
Db 173 WEPPDDP 179

RESULT 29

T28816
hypothetical protein F07C3.4 - *Caenorhabditis elegans*
C/Species: *Caenorhabditis elegans*
C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C/Accession: T28816
R/Favella, A.; Gattung, S.
submitted to the EMBL Data Library, March 1996
A/Description: The sequence of *C. elegans* cosmid F07C3.
A/Reference number: Z20528
A/Accession: T28816
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1098 <FAV>

A;Cross-references: EMBL:U50308; PIDN:AAC48003.1; CSPDB:GN00023; CESP:F07C3.4
 A;Experimental source: strain Bristol N2; clone F07C3
 C;Genetics:
 A;Gene: CESP:F07C3.4
 A;Map position: 5
 A;Introns: 70/3; 122/2; 192/3; 214/3; 259/2; 326/3; 444/1; 471/3; 526/3; 788/1; 1047/3

Query Match 4.9%; Score 7; DB 2; Length 1098;
 Best Local Similarity 100.0%; Pred. No. 81;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CAPTLPP 8
 |||||
 DB 458 CAPTLPP 464

RESULT 30

B71616
 Phosphatase (acid phosphatase family) PFB0380c - malaria parasite (Plasmodium falciparum)
 C;Species: Plasmodium falciparum
 C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
 C;Accession: B71616
 R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
 ; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.
 Science 282, 1126-1132, 1998
 A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
 A;Reference number: A71600; MUID:99021743; PMID:9804551
 A;Accession: B71616
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-2010 <GAR>
 A;Cross-references: GB:AB001391; GB:AB001362; NID:G3845168; PIDN:AAC71865.1; PID:G384516
 A;Experimental source: clone 3D7
 C;Genetics:
 A;Gene: PFB0380c

Query Match 4.9%; Score 7; DB 2; Length 2010;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 117 TNNKKKE 123
 |||||
 DB 427 TNNKKKE 433

RESULT 31

A26655
 myosin heavy chain [similarity] - slime mold (Dictyostelium discoideum)
 N;Contains: myosin ATPase (EC 3.6.4.1)
 C;Species: Dictyostelium discoideum
 C;Date: 05-Oct-1988 #sequence_revision 05-Oct-1988 #text_change 19-Apr-2002
 C;Accession: A26655; A24728; S00250
 R;Warick, H.M.; De Lozanne, A.; Leinwand, L.A.; Spudich, J.A.
 Proc. Natl. Acad. Sci. U.S.A. 85, 9433-9437, 1988
 A;Title: Conserved protein domains in a myosin heavy chain gene from Dictyostelium disc
 A;Reference number: A26655; MUID:87092266; PMID:3540939
 A;Accession: A26655
 A;Molecule type: DNA
 A;Residues: 1-2116 <WAR>
 A;Cross-references: GB:M14628; GB:M11938; NID:G157834; PIDN:AAA33227.1; PID:G167835
 R;DeLozanne, A.; Lewis, M.; Spudich, J.A.; Leinwand, L.A.
 Proc. Natl. Acad. Sci. U.S.A. 85, 8807-8810, 1988
 A;Reference number: A24728; MUID:86016788; PMID:3901008
 A;Accession: A24728
 A;Molecule type: mRNA
 A;Residues: 2035-2116
 R;Wagle, G.; Noegel, A.; Scheel, J.; Gerisch, G.
 FEBS Lett. 227, 71-75, 1988
 A;Title: Phosphorylation of threonine residues on cloned fragments of the Dictyostelium
 A;Reference number: S00250; MUID:88112226; PMID:2828113
 A;Accession: S00250
 A;Status: nucleic acid sequence not shown
 A;Molecule type: DNA

A;Residues: 1734-1993 <WAG>
 C;Comment: The rod domain is highly periodic, containing a pattern of 7-residue repeats
 C;Superfamily: myosin heavy chain; myosin motor domain homology
 C;Keywords: actin binding; ATP; coiled coil; hydrolase; nucleotide binding; P-loop; phosph
 F;1-818/Domain: globular head <HED>
 F;89-747/Domain: myosin motor domain homology <MMOT>
 F;179-186/Region: nucleotide-binding motif A (P-loop)
 F;819-2116/Domain: alpha-helical rod <ROD>

Query Match 4.9%; Score 7; DB 2; Length 2116;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EETAKKV 131
 |||||
 DB 1413 EETAKKV 1419

RESULT 32

T28157
 erythrocyte membrane protein 1 - malaria parasite (Plasmodium falciparum)
 C;Species: Plasmodium falciparum
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000
 C;Accession: T28157
 R;Yang, S.Q.; Wollish, W.S.; Gut, J.; Wu, J.; Ahn, J.; Petersen, C.; Fujioka, H.; Aikawa,
 submitted to the EMBL Data Library, July 1995
 A;Description: The molecular cloning and DNA sequence analysis of Plasmodium falciparum
 A;Reference number: Z20479
 A;Accession: T28157
 A;Status: preliminary; translated from GB/EMBL/DBDJ
 A;Molecule type: DNA
 A;Residues: 1-2212 <YAN>
 A;Cross-references: EMBL:U31083; NID:G1517813; PID:G1517814; PIDN:AAB06961.1
 C;Genetics:
 A;Gene: EMP1

Query Match 4.9%; Score 7; DB 2; Length 2212;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 119 NKKKKE 125
 |||||
 DB 382 NKKKKE 388

RESULT 33

T12796
 Probable transglycosylase - Bacillus subtilis phage SPBc2
 C;Species: Bacillus subtilis phage SPBc2
 C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 15-Oct-1999
 C;Accession: T12796; A69911
 R;Lazarevic, V.; Duesterhoeft, A.; Soldo, B.; Hilbert, H.; Maue, C.; Karamata, D.
 submitted to the EMBL Data Library, August 1997
 A;Description: The complete nucleotide sequence of the Bacillus subtilis SPBc2 prophag
 A;Reference number: Z17583
 A;Accession: T12796
 A;Status: translated from GB/EMBL/DBDJ
 A;Molecule type: DNA
 A;Residues: 1-2285 <LAZ>
 A;Cross-references: EMBL:AF020713; NID:G3025478; PID:G3025510; PIDN:AAC13005.1
 R;Kunst, F.; Ogasawara, N.; Moser, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berteri
 C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi
 A.; Ehrlich, S.D.; Emmerich, P.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
 Nature 390, 249-256, 1997
 A;Authors: Foulger, D.; Fritz, C.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallerc
 iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.;
 Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
 A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue,
 Y., M.; Ogasawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle,
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
 A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sero,
 akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpatra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.

A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
 A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
 A:Reference number: A69580; MUID:198044033; PMID:9384377
 A:Accession: A69911
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-2285 <KUN>
 A:Cross-references: GB:Z299115; GB:AL009126; NID:g2634479; PIDN:CAB14053.1; PID:e1183582;
 A:Experimental source: strain 168
 C:Genetics:
 A:Gene: yomI

Query Match 4.9%; Score 7; DB 2; Length 2285;

Best Local Similarity 100.0%; Pred. No. 1.5e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0;

QY 132 RRAIEQL 138

DB 184 RRAIEQL 190

RESULT 34

T28161
 hypothetical protein FCR3-varT11-1 - malaria parasite (*Plasmodium falciparum*) (fragments
 C:Species: *Plasmodium falciparum*

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000

A:Accession: T28161

R:R Hernandez-Rivas, R.; Mattei, D.; Sterkers, Y.; Peterson, D.S.; Wellem, T.E.; Scherf, Mol. Cell. Biol. 17, 604-611, 1997

A:Title: Expressed var genes are found in *Plasmodium falciparum* subtelomeric regions.

A:Reference number: Z20483; MUID:97154495; PMID:9001213

A:Accession: T28161

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-2847 <HER>

A:Cross-references: EMBL:U67959; NID:G1794255; PID:G1809295; PIDN:AAC47438.1

A:Experimental source: strain FCQ27/PNG

C:Genetics:

A:Introns: 2158/3

A:Note: FCR3-varT11-1

Query Match

Best Local Similarity 100.0%; Pred. No. 1.7e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 119 NKKKEPE 125

DB 382 NKKKEPE 388

RESULT 35

E95098
 hypothetical protein SP0853 [imported] - *Streptococcus pneumoniae* (strain TIGR4)

C:Species: *Streptococcus pneumoniae*

C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001

A:Accession: E95098

R:Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heidson, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E.

Science 293, 498-506, 2001

A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A:Title: Complete Genome Sequence of a virulent isolate of *Streptococcus pneumoniae*.

A:Reference number: A95000; MUID:21357209; PMID:11463916

A:Accession: E95098

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-35 <KUR>

A:Cross-references: GB:AE005672; PIDN:AAK74982.1; PID:G14972326; GSPDB:GN00164; TIGR:SP4

A:Experimental source: strain TIGR4

C:Genetics:

A:Gene: SP0853

Query Match

4.2%; Score 6; DB 2; Length 35;

Best Local Similarity 100.0%; Pred. No. 44;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 89 VKKQFE 94

DB 20 VKKQFE 25

RESULT 36

S77766
 probable ornithine carbamoyltransferase (EC 2.1.3.3) - *Mycoplasma capricolium* (fragment)

N:Alternate names: protein MC419

C:Species: *Mycoplasma capricolium*

C>Date: 09-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 07-Dec-1999

A:Accession: S77766

R:Bork, P.; Ouzounis, C.; Casari, G.; Schneider, R.; Sander, C.; Dolan, M.; Gilbert, W.; Mol. Microbiol. 16, 955-967, 1995

A:Title: Exploring the *Mycoplasma capricolium* genome: a minimal cell reveals its physiology

A:Reference number: S77739; MUID:96059641; PMID:7476192

A:Accession: S77766

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-52 <BOR>

A:Cross-references: EMBL:Z23311; NID:G514486; PIDN:CAA83833.1; PID:G530484

A:Experimental source: ATCC 27343

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994

C:Genetics:

A:Genetic code: SGC3

C:Function:

A>Description: catalyzes the conversion of ornithine and carbamoyl phosphate to citrullin
 A:Pathway: amino acid metabolism; arginine biosynthesis
 A:Note: evolutionary related to aspartate carbamoyltransferase (EC 2.1.3.2)

C:Superfamily: ornithine carbamoyltransferase; aspartate/ornithine carbamoyltransferase

C:Keywords: arginine biosynthesis; transferase

F:1-52/Domain: aspartate/ornithine carbamoyltransferase homology (fragment) <ACT>

Query Match

4.2%; Score 6; DB 2; Length 52;

Best Local Similarity 100.0%; Pred. No. 63;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 IAKETN 118

DB 18 IAKETN 23

RESULT 37

S65922

homeotic protein engrailed homolog A - *Nautilus pompilius* (fragment)

C:Species: *Nautilus pompilius*

C>Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 17-Mar-1999

A:Accession: S65922

R:Wray, C.G.; Jacobs, D.K.; Kostriken, R.; Vogler, A.P.; Baker, R.; Desallie, R.

FEBS Lett. 365, 71-74, 1995

A:Title: Homologues of the engrailed gene from five molluscan classes.

A:Reference number: S65916; MUID:95293128; PMID:7774719

A:Accession: S65922

A:Molecule type: DNA

A:Residues: 1-62 <WRA>

A:Cross-references: EMBL:U23431

C:Superfamily: unassigned homeobox proteins; homeobox homology

C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

F:1-50/Domain: homeobox homology (fragment) <HOX>

Query Match

4.2%; Score 6; DB 2; Length 62;

Best Local Similarity 100.0%; Pred. No. 73;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 KKEEEE 126

DB 9 KKEEEE 14

RESULT 38

S49558
 Hypothetical protein 4 - Clostridium perfringens
 C:Species: Clostridium perfringens
 C:Date: 29-Nov-1995 #sequence_revision 01-Mar-1996 #text_change 15-Oct-1999
 C:Accession: S49558
 R:Lyristis, M.; Bryant, A.E.; Sloan, J.; Awad, M.M.; Nisbet, I.T.; Stevens, D.L.; Rood, M.J. Microbiol. 12, 761-777, 1994
 A:Title: Identification and molecular analysis of a locus that regulates extracellular proteolysis
 A:Reference number: S49552; MUID:94328928; PMID:8052128
 A:Accession: S49558
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-62 <LYR>
 A:Cross-references: ENBL:U04966; NID:9498837; PIDN:AA458952.1; PID:G498844
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1994

Query Match 4.2%; Score 6; DB 2; Length 62;
 Best Local Similarity 100.0%; Pred. No. 73;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 FLSVKK 91
 DB 39 FLSVKK 44
 |||||

RESULT 39
 H98098
 Hypothetical protein spr18 [imported] - Streptococcus pneumoniae (strain R6)
 C:Species: Streptococcus pneumoniae
 C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001
 C:Accession: H98098
 R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; Eber, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M.Y.; P.; Sun, P.M.; Winkler, M.E.
 J. Bacteriol. 183, 5709-5717, 2001
 A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
 A:Reference number: A97872; MUID:21429245; PMID:11544234
 A:Accession: H98098
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-68 <KUR>
 A:Cross-references: GB:AE007317; PIDN:AAL00621.1; PID:G15459505; GSPDB:GN00174
 C:Genetics:
 A:Gene: spr1818

Query Match 4.2%; Score 6; DB 2; Length 68;
 Best Local Similarity 100.0%; Pred. No. 79;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 KKEFEE 126
 DB 63 KKEFEE 68
 |||||

RESULT 40
 AB1413
 Hypothetical protein lmo2707 [imported] - Listeria monocytogenes (strain EGD-e)
 C:Species: Listeria monocytogenes
 C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
 C:Accession: AB1413
 R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; D.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; M.; Ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A:Title: Comparative genomics of Listeria species.
 A:Reference number: AB1077; MUID:21537279; PMID:11679669
 A:Accession: AB1413
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-73 <GLA>

A:Cross-references: GB:NC_003210; PIDN:CAD00920.1; PID:G16412207; GSPDB:GN00177
 A:Experimental source: strain EGD-e
 C:Genetics:
 A:Gene: lmo2707

Query Match 4.2%; Score 6; DB 2; Length 73;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 112 KIARET 117
 DB 51 KIARET 56
 |||||

RESULT 41
 A11788
 Hypothetical protein lin2855 [imported] - Listeria innocua (strain Clip11262)
 C:Species: Listeria innocua
 C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
 C:Accession: A11788
 R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; D.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; M.; Ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A:Title: Comparative genomics of Listeria species.
 A:Reference number: AB1077; MUID:21537279; PMID:11679669
 A:Accession: A11788
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-73 <GLA>
 A:Cross-references: GB:AL592022; PIDN:CAC98081.1; PID:G16415390; GSPDB:GN00178
 A:Experimental source: strain Clip11262
 C:Genetics:
 A:Gene: lin2855

Query Match 4.2%; Score 6; DB 2; Length 73;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 112 KIARET 117
 DB 51 KIARET 56
 |||||

RESULT 42
 S75054
 Hypothetical protein ssl127 - Synecocystis sp. (strain PCC 6803)
 C:Species: Synecocystis sp.
 A:Variety: PCC 6803
 C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
 C:Accession: S75054
 R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DNA Res. 3, 109-136, 1996
 A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocystis s.
 A:Reference number: S74322; MUID:97061201; PMID:8905231
 A:Accession: S75054
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-75 <KAN>
 A:Cross-references: ENBL:D90910; GB:AB001339; NID:G1652956; PIDN:BA17916.1; PID:dl018664
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
 C:Genetics:
 A:Start codon: GTG

Query Match 4.2%; Score 6; DB 2; Length 75;
 Best Local Similarity 100.0%; Pred. No. 86;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 94 BELTIG 99

Db 69 EELTLG 74

RESULT 43

AH2420
 C:Species: Nostoc sp. PCC 7120
 A:Notes: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
 C:Accession: AH2420
 R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriiguchi, Nakazaki, M.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001
 A>Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
 A:Reference number: AB1807; MUID:21595285; PMID:11759840
 A:Accession: AH2420
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-80 <KUR>
 A:Cross-references: GB:BA000019; PIDN:BA076619.1; PID:gl7134058; GSPDB:GN00179
 A:Experimental source: strain PCC 7120
 C:Genetics:
 A:Gene: asr4920

Query Match 4.2%; Score 6; DB 2; Length 80;

Best Local Similarity 100.0%; Pred. No. 91;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 136 EQLAAM 141

Db 50 EQLAAM 55

RESULT 44

VCBPIX
 coat protein B precursor - phage Iike
 N:Alternate names: gene viii protein
 C:Species: phage Iike
 A:Note: host Escherichia coli
 C>Date: 29-Jul-1981 #sequence_revision 28-May-1986 #text_change 28-Jul-2000
 R:Peeters, B.P.H.; Peters, R.M.; Schoenmakers, J.G.G.; Konings, R.N.H.
 J. Mol. Biol. 131, 27-39, 1985
 A>Title: Nucleotide sequence and genetic organization of the genome of the N-specific filamentous bacteriophage phi 80
 A:Reference number: A92912; MUID:85160831; PMID:3981635
 A:Accession: A92912
 A:Molecule type: DNA
 A:Residues: 1-82 <PEE>
 A:Cross-references: GB:K02750; NID:gl4942; PIDN:CAA36072.1; PID:gl4948
 R:Nakashima, Y.; Frangione, B.; Wiseman, R.L.; Konigsberg, W.H.
 J. Biol. Chem. 256, 5792-5797, 1981
 A>Title: Primary structure of the major coat protein of the filamentous bacterial virus phi 30-82
 A:Reference number: A92326; MUID:81215498; PMID:7240173
 A:Accession: A92326
 A:Molecule type: protein
 A:Residues: 30-82 <NAK>
 A:Note: coat protein B is the major coat protein of the virion
 C:Genetics:
 A:Gene: viii
 C:Superfamily: filamentous phage coat protein B

F:1-29/Domain: signal sequence #status predicted <SIG>

F:30-82/Product: coat protein B #status experimental <CPB>

Query Match 4.2%; Score 6; DB 1; Length 82;

Best Local Similarity 100.0%; Pred. No. 93;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 109 AKNKIA 114

Db 10 AKNKIA 15

RESULT 45

B36907
 Pyocin S1 S1I subunit - Pseudomonas aeruginosa
 C:Species: Pseudomonas aeruginosa
 C>Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
 C:Accession: B36907
 R:Sano, Y.; Matsui, H.; Kobayashi, M.; Kageyama, M.
 J. Bacteriol. 175, 2907-2916, 1993
 A>Title: Molecular structures and functions of pyocins S1 and S2 in Pseudomonas aeruginosa
 A:Reference number: A36907; MUID:93259934; PMID:8491711
 A:Accession: B36907
 A>Status: preliminary
 A:Molecule type: DNA; protein
 A:Residues: 1-87 <SAN>
 A:Cross-references: GB:D12707; NID:G286179; PIDN:BAA02202.1; PID:G286181
 A:Note: sequence extracted from NCBI backbone (NCBIN:131814, NCBIP:131817)
 C:Superfamily: immunity protein E2
 C:Keywords: bacteriocin immunity

Query Match 4.2%; Score 6; DB 2; Length 87;

Best Local Similarity 100.0%; Pred. No. 98;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 117 TNNKKK 122

Db 22 TNNKKK 27

RESULT 46

D36907
 Pyocin S2 immunity protein S2I chain - Pseudomonas aeruginosa
 C:Species: Pseudomonas aeruginosa
 C>Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 31-Dec-2000
 C:Accession: D36907; E83501
 R:Sano, Y.; Matsui, H.; Kobayashi, M.; Kageyama, M.
 J. Bacteriol. 175, 2907-2916, 1993
 A>Title: Molecular structures and functions of pyocins S1 and S2 in Pseudomonas aeruginosa
 A:Reference number: A36907; MUID:93259934; PMID:8491711
 A:Accession: D36907
 A>Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-87 <SAN>
 A:Cross-references: GB:D12708; NID:G286182; PIDN:BAA02204.1; PID:G286184
 A:Note: sequence extracted from NCBI backbone (NCBIP:131820)
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Brj adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A>Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
 A:Reference number: A82950; MUID:20437337; PMID:10984043
 A:Accession: E83501
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-87 <STO>
 A:Cross-references: GB:AE004545; GB:AE004091; NID:g9947070; PIDN:AAG04540.1; GSPDB:GN001;
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: imm2; PA1151
 C:Superfamily: immunity protein E2
 C:Keywords: bacteriocin immunity

Query Match 4.2%; Score 6; DB 2; Length 87;

Best Local Similarity 100.0%; Pred. No. 98;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 117 TNNKKK 122

Db 22 TNNKKK 27

RESULT 47

H96585

hypothetical protein F20D21.23 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C:Accession: H96585
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chn, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Hansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: H96585
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-98 <STO>
 A:Cross-references: GB:AF005173; NID:94585983; PIDN:AAD25619.1; GSPDB:GN00141
 C:Genetics:
 A:Map position: 1

Query Match 4.2%; Score 6; DB 2; Length 98;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 EEKKH 80
 |||||
 DB 27 EEKKH 32

RESULT 48
 B71567
 hypothetical protein CT031 - Chlamydia trachomatis (serotype D, strain UW3/Cx)
 C:Species: Chlamydia trachomatis
 C:Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 18-Aug-2000
 C:Accession: B71567
 R:Stephens, R.S.; Kaiman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998
 A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis.
 A:Reference number: A71570; MUID:99000809; PMID:9784136
 A:Accession: B71567
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-100 <ARN>
 A:Cross-references: GB:AE001277; GB:AE001273; NID:93328408; PIDN:AAC67621.1; PID:9332842
 A:Experimental source: serotype D, strain UW-3/Cx
 C:Genetics:
 A:Gene: CT031
 C:Superfamily: conserved hypothetical protein TC0300

Query Match 4.2%; Score 6; DB 2; Length 100;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 AKNKIA 114
 |||||
 DB 30 AKNKIA 35

RESULT 49
 F71137
 hypothetical protein PH0866 - Pyrococcus horikoshii
 C:Species: Pyrococcus horikoshii
 C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 21-Jul-2000
 C:Accession: F71137
 R:Kawarayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekiri, M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi, DNA Res. 5, 55-76, 1998
 A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic archaeon.
 A:Reference number: A71000; MUID:98344137; PMID:9679194

A:Accession: F71137
 A:Status: Preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-103 <KAW>
 A:Cross-references: GB:AF000003; NID:93236130; PIDN:BAA29960.1; PID:93257277
 A:Experimental source: strain OT3
 A:Note: This accession replaces an interim accession for a sequence replaced by GenBank C:Genetics:
 A:Gene: PH0866
 C:Superfamily: Pyrococcus horikoshii hypothetical protein PH0866

Query Match 4.2%; Score 6; DB 2; Length 103;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 KHSQC 84
 |||||
 DB 53 KHSQC 58

RESULT 50
 S53575
 probable membrane protein YIR023c-a - Yeast (Saccharomyces cerevisiae)
 C:Species: Saccharomyces cerevisiae
 C:Date: 06-May-1995 #sequence_revision 19-Oct-1995 #text_change 05-Nov-1999
 C:Accession: S53575
 R:Rowley, K.
 submitted to the EMBL Data Library, October 1994
 A:Reference number: S48478
 A:Accession: S53575
 A:Molecule type: DNA
 A:Residues: 1-107 <ROW>
 A:Cross-references: EMBL:Z38061; GSPDB:GN00009; MIPS:YIR023c-a
 C:Genetics:
 A:Gene: MIPS:YIR023c-a
 A:Map position: 9R
 C:Superfamily: Saccharomyces probable membrane protein YIR023c-a
 C:Keywords: transmembrane protein
 F10-26/Domain: transmembrane #status predicted <TW1>
 F180-96/Domain: transmembrane #status predicted <TW2>

Query Match 4.2%; Score 6; DB 2; Length 107;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 BLTIGE 100
 |||||
 DB 92 BLTIGE 97

RESULT 51
 A71353
 probable anti-sigma F factor antagonist (spoIIIA-1) - syphilis spirochete
 C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
 C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999
 C:Accession: A71353
 R:Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin, rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDo, they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
 Science 281, 375-388, 1998
 A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
 A:Reference number: A71250; MUID:98332770; PMID:9665876
 A:Accession: A71353
 A:Status: Preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-108 <COL>
 A:Cross-references: GB:AE001203; GB:AE000520; NID:93322476; PIDN:AAC65207.1; PID:93322487
 A:Experimental source: strain Nichols
 C:Genetics:
 A:Gene: TP0220
 C:Superfamily: sporulation protein stage II

Query Match 4.2%; Score 6; DB 2; Length 108;

Best Local Similarity 100.0%; Pred. No. 1.2e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 VRRATE 136
|||||

Db 85 VRRATE 90

RESULT 52
T12829
probable SPbeta phage repressor - Bacillus subtilis phage SPBc2
N/Alternate names: transcription regulator phage-related yonR
C/Species: Bacillus subtilis phage SPBc2
C/Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 20-Jun-2000
C/Accession: T12829; A69315
R/Lazarevic, V.; Duesterhoeft, A.; Soldo, B.; Hilbert, H.; Muel, C.; Karamata, D.
submitted to the EMBL Data Library, August 1997
A/Description: The complete nucleotide sequence of the Bacillus subtilis SPbetac2 prophage
A/Reference number: Z17583
A/Accession: T12829
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-108 <LAZ>
A/Cross-references: EMBL:AF020713; NID:G3025478; PID:G3025543; PIDN:AAC13038.1
R/Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
C.; Bron, S.; Brouillet, C.V.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A/Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Hoisappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A/Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A/Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
A/Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A/Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A/Reference number: A69580; MUID:98044033; PMID:9384377
A/Accession: A69915
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-108 <KUN>
A/Cross-references: GB:Z99115; GB:AL009126; NID:G2634478; PIDN:CAB14020.1; PID:G2634522
A/Experimental source: strain 168
C/Genetics:
A/Genes: yonR
C/Superfamily: probable transcription repressor yonR

Query Match 4.2%; Score 6; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 KKEFEE 126
|||||

Db 102 KKEFEE 107

RESULT 53
F71158
hypothetical protein PH0468 - Pyrococcus horikoshii
C/Species: Pyrococcus horikoshii
C/Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
C/Accession: F71158
R/Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kishida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A/Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A/Reference number: A71000; MUID:98344137; PMID:9679194
A/Accession: F71158
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA

A/Residues: 1-108 <KAW>
A/Cross-references: GB:AP000002; NID:G3236129; PIDN:BAA29555.1; PID:G3256872
A/Experimental source: strain OT3
A/Note: this accession replaces an interim accession for a sequence replaced by GenBank
C/Genetics:
A/Genes: PH0468

Query Match 4.2%; Score 6; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 RERAKN 111
|||||

Db 57 RERAKN 62

RESULT 54
T30042
hypothetical protein F20A1.10 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
C/Accession: T30042
R/Gattung, S.; Wu, X.
submitted to the EMBL Data Library, March 1996
A/Description: The sequence of C. elegans cosmid F20A1.
A/Reference number: Z20726
A/Accession: T30042
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-115 <GAT>
A/Cross-references: EMBL:U53150; PIDN:AAA96132.1; GSPDB:GN00023; CESP:F20A1.10
A/Experimental source: strain Bristol N2; clone F20A1
C/Genetics:
A/Genes: CESP:F20A1.10
A/Map position: 5
A/Map position: 25/1
C/Superfamily: Caenorhabditis elegans hypothetical protein F57E7.1

Query Match 4.2%; Score 6; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 120 KXKEFE 125
|||||

Db 102 KXKEFE 107

RESULT 55
C72265
hypothetical protein - Thermotoga maritima (strain MSB8)
C/Species: Thermotoga maritima
C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C/Accession: C72265
R/Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey,
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.

Query Match 4.2%; Score 6; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 VRRATE 136

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Db      111 VRRRAIE 116
|||||
RESULT 56
hypothetical protein F19K23.2 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: B96647
R:Theologias, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
anssen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: B96647
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-121 <STO>
A:Cross-references: GB:AE005173; NID:g2160134; PIDN:AAB60756.1; GSPDB:GN00141
C:Genetics:
A:Gene: F19K23.2
A:Map position: 1

Query Match      4.2%; Score 6; DB 2; Length 121;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 PTLPPA 9
|||||
Db      56 PTLPPA 61

RESULT 57
McbB protein [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120beta
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C:Accession: AC2545
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriiguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AC2545
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-122 <KUR>
A:Cross-references: GB:AP003602; PIDN:BA877289.1; PID:g17134731; GSPDB:GN00181
C:Genetics:
A:Gene: alr7646
A:Genome: plasmid

Query Match      4.2%; Score 6; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      114 AKETNN 119
|||||
Db      81 AKETNN 86

RESULT 58
conserved hypothetical protein MTH352 - Methanobacterium thermoautotrophicum (strain Del
D69145
C:Species: Methanobacterium thermoautotrophicum
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 24-Sep-1999
C:Accession: D69145
R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; I
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwan, N.;
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: functi
A:Reference number: A69000; MUID:98037514; PMID:9371463
A:Accession: D69145
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-131 <MTH>
A:Cross-references: GB:AE000820; GB:AE000666; NID:g2621405; PIDN:AAB84858.1; PID:g262141(
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH352
C:Superfamily: hypothetical protein MJ1618

Query Match      4.2%; Score 6; DB 2; Length 131;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      87 LSVKKQ 92
|||||
Db      123 LSVKKQ 128

RESULT 59
AB3465
hypothetical protein BMEI1704 [imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C:Accession: AB3465
R:DeIvecchio, V.G.; Kaputal, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, N.
; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensi
A:Reference number: AD3252; PMID:11756688
A:Accession: AB3465
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-133 <KUR>
A:Cross-references: GB:AE008917; PIDN:AAL52885.1; PID:g17983729; GSPDB:GN00190
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BMEI1704
A:Map position: 1

Query Match      4.2%; Score 6; DB 2; Length 133;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      38 MAEAGF 43
|||||
Db      65 MAEAGF 70

RESULT 60
T35557
ribosomal protein S11 - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 12-Jun-2003
C:Accession: T35557
R:Saunders, D.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, August 1998
A:Reference number: Z21583
A:Accession: T35557
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-134 <SAU>
A:Cross-references: EMBL:AL031317; PIDN:CAA20384.1; GSPDB:GN00070; SCOEDB:SC6G4.06
A:Experimental source: strain A3(2)

```

```

C:Genetics:
A:Gene: rpsK; SCOE:DB:SC6G4.06
C:Superfamily: ribosomal protein S11/S14

Query Match      4.2%; Score 6; DB 2; Length 134;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 128 AKKVR 133
Db 10 AKKVR 15

RESULT 61
B75037
Hypothetical protein PAB0847 - Pyrococcus abyssi (strain Orsay)
C:Species: Pyrococcus abyssi
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C:Accession: B75037
R:anonymous, Genoscope
Submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A:Reference number: A75001
A:Accession: B75037
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-134 <KAW>
A:Cross-references: GB:AJ248287; GB:AL096836; NID:g5458657; PIDN:CAB50191.1; PID:g545870
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: PAB0847

Query Match      4.2%; Score 6; DB 2; Length 134;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 64 LEGWEP 69
Db 42 LEGWEP 47

RESULT 62
C71126
Hypothetical protein PH0777 - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
C:Accession: C71126
R:Kawarayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A:Reference number: A71000; MUID:98344137; PMID:9679194
A:Accession: C71126
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-135 <KAW>
A:Cross-references: GB:AP000003; NID:g3236130; PIDN:BA29869.1; PID:g3257186
A:Experimental source: strain OT3
A:Note: this accession replaces an interim accession for a sequence replaced by GenBank
C:Genetics:
A:Gene: PH0777

Query Match      4.2%; Score 6; DB 2; Length 135;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 64 LEGWEP 69
Db 40 LEGWEP 45

RESULT 63
H64306
conserved hypothetical protein MJ0056 - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C:Accession: H64306
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, C.
ison, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.
A:Reference number: A64300; MUID:96337999; PMID:8688087
A:Accession: H64306
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-136 <BUL>
A:Cross-references: GB:U67463; GB:L77117; NID:g1590846; PIDN:AAB98036.1; PID:g1590850; TJ
C:Genetics:
A:Map position: REV56166-55756
A:Start codon: TTG
C:Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0056

Query Match      4.2%; Score 6; DB 1; Length 136;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 102 LKLDRE 107
Db 46 LKLDRE 51

RESULT 64
B64670
ribosomal protein L11 - Helicobacter pylori
C:Species: Helicobacter pylori
A:Variety: strains J99, 26895
C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 24-Sep-1999
C:Accession: B64670; F71846
R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Wathley, L.
Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.N
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; MUID:97394467; PMID:9252185
A:Accession: B64670
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-141 <TCM>
A:Cross-references: GB:AE000626; GB:AE000511; NID:g2314360; PIDN:AAD08248.1; PID:g2314364
A:Experimental source: strain 26695
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; J
Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A:Reference number: A71800; MUID:99120557; PMID:9923682
A:Accession: F71846
A:Molecule type: DNA
A:Residues: 1-141 <ARN>
A:Cross-references: GB:AE001540; GB:AE001439; NID:g4155717; PIDN:AAD06703.1; PID:g4155724
A:Experimental source: strain J99
C:Genetics:
A:Gene: rpiK; HPI202
C:Superfamily: Escherichia coli ribosomal protein L11

Query Match      4.2%; Score 6; DB 2; Length 141;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 110 KXKIAK 115
Db 94 KXKIAK 99

```

RESULT 65

C72430
hypothetical protein - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 28-Jul-2000
C:Accession: C72430
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.E.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.
C.M.

Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: C72430
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-142 <ARN>
A:Cross-references: GB:AE001689; GB:AE000512; NID:g4980483; PIDN:AAD35103.1; PID:g498049
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM0009
C:Superfamily: Thermotoga maritima hypothetical protein TM1526

Query Match 4.2%; Score 6; DB 2; Length 142;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 131 VRRRAIE 136
| | | | |
Db 96 VRRRAIE 101

RESULT 66

AF1517
hypothetical protein lin0678 [imported] - Listeria innocua (strain Clip11262)
C:Species: Listeria innocua
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C:Accession: AF1517
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kref, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A:Title: Comparative Genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669

A:Accession: AF1517
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-142 <GLA>
A:Cross-references: GB:AL592022; PIDN:CAC95910.1; PID:g164113130; GSPDB:GN00178
A:Experimental source: strain Clip11262
C:Genetics:
A:Gene: lin0678

Query Match 4.2%; Score 6; DB 2; Length 142;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 99 GEFLKL 104
| | | | |
Db 112 GEFLKL 117

RESULT 67

B56150
probable general secretion pathway protein g precursor - Escherichia coli (strain K-12)
N:Alternate names: hopG protein
C:Species: Escherichia coli
C>Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 01-Mar-2002
C:Accession: B56150; C65126
R:Stojiljkovic, I.; Schoenherr, R.; Kusters, J.G.
J. Bacteriol. 177, 1892-1895, 1995
A:Title: Identification of the hopG gene, a component of Escherichia coli K-12 type II e

A:Reference number: A56150; MUID:95204361; PMID:7896718

A:Accession: B56150
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-145 <STO>
A:Cross-references: GB:U20786; NID:g693704; PIDN:AAA69031.1; PID:g693706
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of Escherichia coli K-12.

A:Reference number: A64720; MUID:97426617; PMID:9278503

A:Accession: C65126
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-145 <BLAT>
A:Cross-references: GB:AE000409; GB:U00096; NID:g1789718; PIDN:AAC76353.1; PID:g1789725;
A:Experimental source: strain K-12, substrain MG1655
C:Genetics:
A:Gene: hofG
C:Superfamily: secretion protein xcpT

Query Match 4.2%; Score 6; DB 2; Length 145;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 APTLPP 8
| | | | |
Db 79 APTLPP 84

RESULT 68

AB1277
transcription regulator MarR family homolog lmo1618 [imported] - Listeria monocytogenes
C:Species: Listeria monocytogenes
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C:Accession: AB1277
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001

A:Authors: Kref, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A:Title: Comparative Genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669

A:Accession: AB1277
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-146 <GLA>
A:Cross-references: GB:NC_003210; PIDN:CAC99696.1; PID:g16411054; GSPDB:GN00177
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmo1618

Query Match 4.2%; Score 6; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 95 BLTLGE 100
| | | | |
Db 49 BLTLGE 54

RESULT 69

H71205
hypothetical protein PH1914 - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C>Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 21-Jul-2000
C:Accession: H71205
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekine
N.; Chikuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi,
DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A:Reference number: A71000; MUID:98344137; PMID:9679194

A:Accession: H71205
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-149 <KAW>
A:Cross-references: GB:AP000007; NID:G3236134; PIDN:BAA31039.1; PID:G3258356
A:Experimental source: strain OT3
A:Note: this accession replaces an interim accession for a sequence replaced by GenBank
C:Genetics:
A:Gene: PH1914
C:Superfamily: Escherichia coli ybQ protein

Query Match 4.2%; Score 6; DB 2; Length 149;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 122 KEFEET 127
|||||
DB 60 KEFEET 65

RESULT 70
AB1255
Hypothetical protein lmo1522 [imported] - Listeria monocytogenes (strain EGD-e)
C:Species: Listeria monocytogenes
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C:Accession: AB1265
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.N.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Krett, J.; Kuhn, M.; Kunst, F.; Kurapat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AB1265
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-150 <GLA>
A:Cross-references: GB:NC 003210; PIDN:CAC99600.1; PID:G16410951; GSPDB:GN00177
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmo1522
C:Superfamily: conserved hypothetical protein HI0670

Query Match 4.2%; Score 6; DB 2; Length 150;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 AEAGFI 44
|||||
DB 114 AEAGFI 119

RESULT 71
S43727
Hypothetical protein - thermophilic bacterium PS-3 (fragment)
C:Species: thermophilic bacterium PS-3
C:Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 18-Sep-1998
C:Accession: S43727
R:Fujiwara, Y.; Oka, M.; Hamamoto, T.; Sone, N.
Biochim. Biophys. Acta 1144, 213-219, 1993
A:Title: Cytochrome c-551 of the thermophilic bacterium PS3, DNA sequence and analysis
A:Reference number: S43726; MUID:93379042; PMID:7916623
A:Accession: S43727
A:Molecule type: DNA
A:Residues: 1-151 <FUJ>
A:Cross-references: EMBL:X63125
C:Superfamily: conserved hypothetical protein yltT

Query Match 4.2%; Score 6; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 KVRRAI 135
|||||
DB 80 KVRRAI 85

RESULT 72
AB7707
Conserved hypothetical protein CC3691 [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C:Accession: AB7707
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.I.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolonitskii, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: AB7249; MUID:21173698; PMID:11259647
A:Accession: AB7707
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-152 <STO>
A:Cross-references: GB:AE005673; NID:G13425453; PIDN:AAK25653.1; GSPDB:GN00148
C:Genetics:
A:Gene: CC3691

Query Match 4.2%; Score 6; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 ERMAEA 41
|||||
DB 94 ERMAEA 99

RESULT 73
R3TW7
Ribosomal protein S7 - Thermus aquaticus
C:Species: Thermus aquaticus
C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 12-Jun-2003
C:Accession: S10250
R:Yakhnin, A.V.; Vorozheykina, D.P.; Matvienko, N.I.
Nucleic Acids Res. 18, 3659, 1990
A:Title: Nucleotide sequence of the Thermus thermophilus HB8 rps12 and rps7 genes coding
A:Reference number: S10249; MUID:90301504; PMID:2362824
A:Accession: S10250
A:Molecule type: DNA
A:Residues: 1-156 <YAK>
A:Cross-references: EMBL:X52165; NID:G48273; PIDN:CAA36419.1; PID:G48275
A:Experimental source: strain HB8
A:Note: the source is designated as Thermus thermophilus
R:Tsibolli, P.; Herfurth, E.; Choi, T.
Eur. J. Biochem. 226, 169-177, 1994
A:Title: Purification and characterization of the 30S ribosomal proteins from the bacteri
A:Reference number: S51053; MUID:95045586; PMID:7957245
A:Accession: S51058
A:Molecule type: protein
A:Residues: 2-50 <TSI>
A:Note: the source is given as Thermus thermophilus
C:Superfamily: ribosomal protein S7
C:Keywords: protein biosynthesis; ribosome

Query Match 4.2%; Score 6; DB 1; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 ERMAEA 41
|||||
DB 142 ERMAEA 147

RESULT 74
D75536
ribosomal protein S7 - Deinococcus radiodurans (strain R1)

C;Species: Deinococcus radiodurans
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 12-Jun-2003
 C;Accession: D75536
 R;White, O.; Eisen, J.A.; Heideberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999

A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A;Reference number: A75250; MUID:20036896; PMID:10567266

A;Accession: D75536

A;Status: Preliminary

A;Molecule type: DNA

A;Residues: 1-156 <WHI>

A;Cross-references: GB:AE001891; GB:AE000513; NID:G6457973; PIDN:AAF09886.1; PID:G645797

A;Experimental source: strain R1

C;Genetics:

A;Gene: DR0306

A;Map position: 1

C;Superfamily: ribosomal protein S7

Query Match 4.2%; Score 6; DB 2; Length 156;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 ERVAA 41

Db 142 ERVAA 147

RESULT 75

D82044

RNA methylase, SpoU family VC2695 [imported] - Vibrio cholerae (strain N16961 serogroup
 C;Species: Vibrio cholerae

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001

C;Accession: D82044

R;Heideberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;

chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, E

l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A;Title: DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A;Reference number: A82035; MUID:20406833; PMID:10952301

A;Accession: D82044

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-158 <HEI>

A;Cross-references: GB:AE004335; GB:AE003852; NID:G9657289; PIDN:AAF95836.1; GSPDB:GN001

A;Experimental source: serogroup O1; strain N16961; biotype El Tor

C;Genetics:

A;Gene: VC2695

A;Map position: 1

C;Superfamily: Chlamydia pneumoniae rRNA methylase

Query Match 4.2%; Score 6; DB 2; Length 158;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 KVVRA 134

Db 42 KVVRA 47

Search completed: August 11, 2004, 14:25:32
 Job time : 18 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 11, 2004, 14:18:12 ; Search time 13 Seconds
(without alignments)

568.766 Million cell updates/sec

Title: US-09-690-825-34

Perfect score: 142

Sequence: 1 MGAPTLPPAQPFLLKDHRS.....EFEETAKKVRRAIEQLAAMD 142

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	142	100.0	142	1	BIR5_HUMAN
2	41	28.9	140	1	BIR5_MOUSE
3	39	27.5	142	1	BIR5_RAT
4	7	4.9	140	1	BM38_PIG
5	7	4.9	179	1	HSLV_LISIN
6	7	4.9	179	1	HSLV_LISMO
7	7	4.9	697	1	SENT_CAEEL
8	7	4.9	744	1	CUL3_YEAST
9	7	4.9	997	1	BIR1_SCHPO
10	7	4.9	2116	1	MY32_DICDI
11	6	4.2	78	1	ACP_TREHY
12	6	4.2	82	1	COM5_BPIKE
13	6	4.2	87	1	IMM1_PSEAE
14	6	4.2	87	1	IMM2_PSEAE
15	6	4.2	100	1	Y031_CHLTR
16	6	4.2	108	1	YGRB_BACPF
17	6	4.2	134	1	RS11_SPAW
18	6	4.2	134	1	RS11_STRCO
19	6	4.2	136	1	Y056_METJA
20	6	4.2	137	1	RL16_LEPIN
21	6	4.2	141	1	RL11_HELPY
22	6	4.2	145	1	GSPG_ECOLI
23	6	4.2	148	1	MSCL_PESM
24	6	4.2	150	1	DTD_LISMO
25	6	4.2	150	1	YCC1_BACP3
26	6	4.2	155	1	RS7_THETH
27	6	4.2	156	1	RS7_DEIRA
28	6	4.2	157	1	Y839_HELHP
29	6	4.2	168	1	UBC7_WHEAT
30	6	4.2	173	1	HSLV_SHEON
31	6	4.2	173	1	HSLV_YERPE
32	6	4.2	175	1	HSLV_PSEPK
33	6	4.2	175	1	HSLV_PSESM

34	6	4.2	175	1	IPYR_ECOL6	Q8fag0	escherichia
35	6	4.2	175	1	IPYR_ECOLI	P17288	escherichia
36	6	4.2	176	1	HSLV_PSEAE	Q9huc6	pseudomonas
37	6	4.2	178	1	YGV5_YEAST	P53071	saccharomyc
38	6	4.2	198	1	XJW7_YEAST	P40893	saccharomyc
39	6	4.2	201	1	RNH2_FORGI	O51832	porphyromon
40	6	4.2	201	1	TRI_FONLE	P05547	pentastacus
41	6	4.2	208	1	ZFP_IRV6	P47732	chilo iride
42	6	4.2	214	1	CYB6_EUGGR	P31480	mycoplasma gra
43	6	4.2	216	1	DEF_MYCGE	P47352	mycoplasma
44	6	4.2	217	1	YMG3_YEAST	P48238	saccharomyc
45	6	4.2	219	1	YMS1_ARCFU	O28013	archaeoglob
46	6	4.2	249	1	YGB1_FUSNN	O8rie0	fusobacteri
47	6	4.2	250	1	PUR7_SYNPK	Q7ub99	synthetococc
48	6	4.2	255	1	UPPS_METTH	O28881	archaeoglob
49	6	4.2	257	1	LIVG_ARCFU	P34714	caenorhabdi
50	6	4.2	264	1	SPRC_CABEL	P34714	caenorhabdi
51	6	4.2	273	1	TRY6_ANOGA	P35040	anopheles g
52	6	4.2	281	1	SPEE_PYRFU	Q8u4g1	pyrococcus
53	6	4.2	282	1	Y765_HAEIN	O57125	haemophilus
54	6	4.2	286	1	FPG_STRCO	Q9zba6	streptomyces
55	6	4.2	286	1	SGBU_HABIN	P44990	haemophilus
56	6	4.2	289	1	NOLT_RHIFR	P33209	rhizobium f
57	6	4.2	292	1	CHIA_CUCSA	P17541	cucumis sat
58	6	4.2	293	1	ENGC_BACAA	Q81wh7	bacillus an
59	6	4.2	294	1	Y237_MYCPN	P75455	mycoplasma
60	6	4.2	298	1	Y680_HAEIN	O57389	haemophilus
61	6	4.2	305	1	LXD2_PHOLE	Q57878	photobacter
62	6	4.2	312	1	OTCC_MYCCC	P59779	mycoplasma
63	6	4.2	312	1	PANE_LACLA	Q9cfy8	lactococcus
64	6	4.2	314	1	CPKA_PYRAB	Q9uwf8	pyrococcus
65	6	4.2	318	1	NIA_CHLVU	Q01170	chlorella v
66	6	4.2	319	1	K6PF_OCEIH	Q8epd6	oceanobacil
67	6	4.2	324	1	ODPE_BACST	P21874	bacillus st
68	6	4.2	326	1	K6PF_MYCPU	Q98pw8	mycoplasma
69	6	4.2	340	1	HUR_STRAU	Q00923	streptomyces
70	6	4.2	340	1	RECA_MYCGE	P47581	mycoplasma
71	6	4.2	342	1	VANB_ENTFA	Q06893	enterococcus
72	6	4.2	342	1	VU7_HSV6U	Q01353	human herpe
73	6	4.2	347	1	MURE_VIBCH	Q9k440	vibrio chol
74	6	4.2	348	1	SYFA_STRPN	Q97836	streptococc
75	6	4.2	350	1	EGSA_SULTO	P58460	sulfolobus
76	6	4.2	352	1	NDR4_HUMAN	Q9ulp0	homo sapien
77	6	4.2	355	1	Y198_RICPR	Q9zdw7	rickettsia
78	6	4.2	361	1	CB45_MOUSE	O61112	mus musculus
79	6	4.2	361	1	CB45_RAT	Q91283	rattus norv
80	6	4.2	362	1	CB45_HUMAN	Q9brk5	homo sapien
81	6	4.2	365	1	CXAR_HUMAN	P78310	homo sapien
82	6	4.2	366	1	LEU3_BACCO	P12010	bacillus co
83	6	4.2	366	1	YQCC_BACSU	P45938	bacillus su
84	6	4.2	368	1	TRMU_ECO57	Q8x735	escherichia
85	6	4.2	368	1	TRMU_ECOL6	Q8cx28	escherichia
86	6	4.2	368	1	TRMU_ECOLI	P25745	escherichia
87	6	4.2	372	1	B4G2_HUMAN	O60909	h beta-1.4-
88	6	4.2	386	1	ICEA_XENIA	P55865	xenopus lae
89	6	4.2	387	1	YF20_METJA	Q58915	methanococc
90	6	4.2	390	1	YL35_CABEL	P34426	caenorhabdi
91	6	4.2	392	1	PORA_THEMA	O05651	thermotoga
92	6	4.2	399	1	ACKA_WIGER	Q8d320	wiggleswort
93	6	4.2	400	1	PBP2_NEIFL	P16873	neisseria f
94	6	4.2	401	1	ASSV_EUCAP	Q8ka60	baccharomyc
95	6	4.2	405	1	IFS_YEAST	P38431	saccharomyc
96	6	4.2	421	1	FXJ1_MOUSE	Q61660	mus musculus
97	6	4.2	421	1	FXJ1_RAT	Q63247	rattus norv
98	6	4.2	424	1	Y963_PYRHO	O58701	pyrococcus
99	6	4.2	425	1	SYS_THETN	Q8rdj5	thermoanaer
100	6	4.2	430	1	SECV_BACHD	P38375	bacillus ha

ALIGNMENTS

RESULT 1

BIRS HUMAN
 ID BIRS HUMAN STANDARD; PRT: 142 AA.
 AC C15392; Q9P2W8;
 DT 16-MAY-2000 (Rel. 39, Created)
 DT 15-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Baculoviral IAP repeat-containing protein 5 (Apoptosis inhibitor
 DE survivin) (Apoptosis inhibitor 4).
 CN BIRC5 OR API4 OR IAP4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN SEQUENCE FROM N.A. (ISOFORM ALPHA).
 RP MEDLINE=97398388; PubMed=9256286;
 RA Ambrosini G.; Adida C.; Altieri D.C.;
 RT "A novel anti-apoptosis gene, survivin, expressed in cancer and
 RT lymphoma.";
 RL Nat. Med. 3:917-921(1997).
 RN (2)
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
 EC TISSUE=Pancratic carcinoma;
 RA Uren A.G.; Vaux D.L.;
 RT "Mammalian inhibitor of apoptosis (IAP) homolog.";
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 RN (3)
 RP SEQUENCE FROM N.A. (ISOFORM BETA).
 RA Kageyama H.; Islam A.; Takayasu H.; Nakagawara A.;
 RT "An isoform of survivin (survivin-beta) which has 23 amino acids
 RT insertion into the BIR domain.";
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 RN (4)
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
 RC TISSUE=Lung, and Muscle;
 RX MEDLINE=22389257; PubMed=12477932;
 RA Strausberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.,
 RA Klausner R.D.; Collins F.S.; Wagner L.; Shenmen C.M.; Schuler G.D.,
 RA Altshul S.F.; Jordan B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallaloon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN (5)
 RP FUNCTION
 RX MEDLINE=99075336; PubMed=98599993;
 RA Li F., Ambrosini G., Chu E.Y., Plescia J., Tognin S., Marchisio P.C.,
 RA Altieri D.C.;
 RT "Control of apoptosis and mitotic spindle checkpoint by survivin.";
 RL Nature 396:580-584(1998).
 RN (6)
 RP X-RAY CRYSTALLOGRAPHY (2.71 ANGSTROMS) OF ISOFORM ALPHA.
 RX MEDLINE=20403315; PubMed=10949039;
 RA Chantalat L., Skoufias D.A., Klemm J.P., Jung B., Dideberg O.,
 RA Margolis R.L.;
 RT "Crystal structure of human survivin reveals a bow tie-shaped dimer
 RT with two unusual alpha-helical extensions.";
 RL Mol. Cell 6:183-185(2000).
 RN (7)
 RP X-RAY CRYSTALLOGRAPHY (2.58 ANGSTROMS) OF ISOFORM ALPHA.
 RX MEDLINE=20336902; PubMed=10876248;
 RA Verdecia M.A., Huang H., Dutil E., Kaiser D.A., Hunter T., Noel J.P.;
 RT "Structure of the human anti-apoptotic protein survivin reveals a
 RT dimeric arrangement.";
 RL Nat. Struct. Biol. 7:602-608(2000).
 RN (8)
 RP PHOSPHORYLATION OF THR-34.
 RX MEDLINE=20542086; PubMed=11069302;
 RA O'Connor D.S., Grossman D., Plescia J., Li F., Zhang H., Villa A.,
 RA Tognin S., Marchisio P.C., Altieri D.C.;
 RT "Regulation of apoptosis at cell division by p34cdc2 phosphorylation
 RT of survivin.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:13103-13107(2000).
 CC -!- FUNCTION: May play a role in neoplasia. May counteract a default
 CC induction of apoptosis in G2/M phase. Interacts with tubulin.
 CC inhibitor of caspase-3 and caspase-7.
 CC -!- SUBUNIT: Homodimer.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=Alpha;
 CC IsoId=O15392-1; Sequence=Displayed;
 CC Name=Beta;
 CC IsoId=O15392-2; Sequence=VSP_002454;
 CC -!- TISSUE SPECIFICITY: Expressed only in fetal kidney and liver, and
 CC to lesser extent, lung and brain. Abundantly expressed in
 CC adenocarcinoma (lung, pancreas, colon, breast, and prostate) and
 CC in high-grade lymphomas.
 CC -!- SIMILARITY: Contains 1 BIR repeat.
 CC -!- SIMILARITY: Belongs to the IAP family.
 CC
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 CC
 CC EMBL; U75285; AAC51660.1; -;
 CC EMBL; AF077350; AAD34226.1; -;
 CC EMBL; AB028869; BA93676.1; -;
 CC EMBL; BC008718; AA080718.1; -;
 CC EMBL; BC034148; AA034148.1; -;
 CC FDB; IB31; 03-JAN-01.
 CC FDB; IF3H; 16-MAY-01.
 CC Genew; HGNC:593; BIRC5.
 CC MIM; 603352; -;
 CC GO; GO:0005876; C:spindle microtubule; TAS
 CC GO; GO:0008189; P:apoptosis inhibitor activity; TAS.
 CC GO; GO:0006916; P:anti-apoptosis; TAS.
 CC GO; GO:0000086; P:G2/M transition of mitotic cell cycle; TAS.
 CC InterPro; IPR001370; BIR.
 CC Pfam; PF00653; BIR; 1.
 CC SMART; SM00238; BIR; 1.
 CC PROSITE; PS01262; BIR_REPEAT_1; FALSE_NEG.
 CC PROSITE; PS0143; BIR_REPEAT_2; 1.
 CC Apoptosis; thiol protease inhibitor; Alternative splicing;
 CC Metal-binding; Zinc; Phosphorylation; 3D-structure.
 CC REPEAT 15 87
 CC METAL 57 57 ZINC.
 CC METAL 60 60 ZINC.
 CC METAL 77 77 ZINC.
 CC METAL 84 84 ZINC.
 CC MOD_RES 34 34
 CC VARSPLIC 74 74
 CC
 CC MUTAGEN 84 84
 CC HELIX 8 13
 CC HELIX 15 20
 CC TURN 21 21
 CC TURN 29 30

FT	HELIX	35	40
FT	TURN	41	42
FT	STRAND	43	45
FT	STRAND	55	57
FT	TURN	58	60
FT	STRAND	63	64
FT	TURN	69	70
FT	HELIX	73	80
FT	TURN	82	83
FT	HELIX	85	87
FT	TURN	88	88
FT	HELIX	93	95
FT	STRAND	97	97
FT	HELIX	98	139
SQ	SEQUENCE	142 AA;	16389 MW; 9E7CADCDF282286 CRC64;

Query Match 100.0%; Score 142; DB 1; Length 142;
Best Local Similarity 100.0%; Pred.No. 7.2e-140;
Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MGAPTLPANQPFLKDHRISTFKKNWPTEGCACPTPEWMAEAGFTHCPTENEPDLAQCFCC	60
DB	1	MGAPTLPANQPFLKDHRISTFKKNWPTEGCACPTPEWMAEAGFTHCPTENEPDLAQCFCC	60
QY	61	FKELEGWEPPDDPTEEHHKHSSGCAFLSVKKQFPBELTLGEFLKLDLRRAKNKIATETNNK	120
DB	61	FKELEGWEPPDDPTEEHHKHSSGCAFLSVKKQFPBELTLGEFLKLDLRRAKNKIATETNNK	120
QY	121	KKFEETAKVRRRAIEQLAAMD	142
DB	121	KKFEETAKVRRRAIEQLAAMD	142

RESULT 2

ID	BIRS_MOUSE	STANDARD;	PRT;	140 AA.
AC	OY0201; Q923F7; Q9WU53; Q9WU54;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			-
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Baculoviral IAP repeat-containing protein 5 (Apoptosis inhibitor			
DE	survivin) (Apoptosis inhibitor 4) (TIAP).			
GN	BIRC5 OR AP14 OR IAP4.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Roentia; Sciurognathi; Muridae; Murinae; Mus.			
NCBI_TaxID	10090;			
[1]	SEQUENCE FROM N.A. (ISOFORM 1).			
RP	Uren A.G., Vaux D.L.;			
RA	"Mammalian inhibitor of apoptosis (IAP) homolog.";			
RL	Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.			
[2]	SEQUENCE FROM N.A. (ISOFORM 1).			
RP	TISSUE=Embryo;			
RC	Kobayashi K., Otaki M., Ogasawara T., Tokuhisa T.;			
RA	Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.			
[3]	SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).			
RP	MEDLINE=20129603; PubMed=1066222;			
RX	Conway E.M., Pollefeyt S., Cornelissen J., DeBaere I.,			
RA	Steiner-Mosonyi M., Ong K., Baens M., Collen D., Schuh A.C.;			
RA	"three differentially expressed survivin cDNA variants encode			
RT	proteins with distinct antiapoptotic functions.";			
RL	Blood 95:1435-1442 (2000).			
RL	[4]			
RN	SEQUENCE FROM N.A. (ISOFORM 2).			
RP	MEDLINE=22388257; PubMed=12477932;			
RX	Stausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,			
RA	Altshul S.F., Zeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusana K., Farmer A.A., Rubin G.M., Hong L.,			

Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Murry D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra W.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences." Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

[5].

X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 7-11S, AND PHOSPHORYLATION OF THR-34.

MEDLINE=204093314; PubMed=10949038;

Muchmore S.W., Chen J., Jakob C., Zakula D., Matayoshi E.D., Wu W., Zhang H., Li F., Ng S.C., Altieri D.C.;

"Crystal structure and mutagenic analysis of the inhibitor-of-apoptosis protein survivin.";

Mol. Cell 6:173-182(2000).

-!- FUNCTION: May play a role in neoplasia. May counteract a default induction of apoptosis in G2/M phase. Interacts with tubulin. Inhibitor of caspase-3 and caspase-7 (By similarity).

-!- SUBUNIT: Homodimer; zinc-dependent.

-!- SUBCELLULAR LOCATION: Cytoplasmic.

-!- ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=3;

Name=1; Synonyms=Survivin 140;

Isoid=070201-1; Sequence=Displayed;

Name=2; Synonyms=Survivin 121;

Isoid=070201-2; Sequence=VSP_002457;

Name=3; Synonyms=Survivin 40;

Isoid=070201-3; Sequence=VSP_002455, VSP_002456;

-!- SIMILARITY: Contains 1 BIR repeat.

-!- SIMILARITY: Belongs to the IAP family.

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EMBL; AF077349; AAD34225.1; -

EMBL; AB013849; BAA28266.1; -

EMBL; AF115517; AAD26199.1; -

EMBL; AF115517; AAD26200.1; -

EMBL; AF115517; AAD26201.1; -

EMBL; BC040702; AAH04702.1; -

FDB; IM4M; 25-SEP-02.

DR MGD; MGI:1203517; Birc5.

DR GO; GO:0005737; C:cytoplasm; IDA.

DR GO; GO:0008189; F:apoptosis inhibitor activity; IMP.

DR GO; GO:0006916; P:anti-apoptosis; IMP.

DR InterPro; IPR001370; BIR.

DR Pfam; PF00553; BIR; 1

DR SMART; SM00238; BIR; 1

DR PROSITE; PS01282; BIR_REPEAT_1; FALSE_NEG.

DR PROSITE; PS0143; BIR_REPEAT_1;

KW Apoptosis; Thiol protease inhibitor; Alternative splicing;

KW Phosphorylation; Metal-binding; zinc; 3D-structure.

REPEAT 15 87 BIR.

FT MOD_RES 34 34 PHOSPHORYLATION (BY CDC2).

FT METAL 57 57 ZINC 1.

FT METAL 60 60 ZINC 1.

FT METAL 76 76 ZINC 2.

FT METAL 77 77 ZINC 1.

FT METAL 80 80 ZINC 2.

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FT METAL 84 84 ZINC 1.
FT VARSPLIC 38 40 MAE -> RGA (in isoform 3).
FT VARSPLIC 41 140 /FTid=VSP_002455.
FT VARSPLIC 114 140 Missing (in isoform 3).
FT VARSPLIC 114 140 /FTid=VSP_002456.
FT VARSPLIC 114 140 AKETNNKKEFEETAKTTTQRIQLAA -> VCMENKD
FT VARSPLIC 114 140 (in isoform 2).
FT VARSPLIC 114 140 /FTid=VSP_002457.
FT VARSPLIC 114 140 /FTid=VSP_002458.
SQ SEQUENCE 140 AA; 16297 MW; 28F5ABF501A6D83C CRC64;

Query Match 28.9%; Score 41; DB 1; Length 140;
Best Local Similarity 100.0%; Pred. No. 3.9e-35;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 CACTPERVAEAGFTHCPTENEPDLAQCFFCFKELEGWEPDD 71
Db 31 CACTPERVAEAGFTHCPTENEPDLAQCFFCFKELEGWEPDD 71

RESULT 3
BIR5 RAT
ID BIR5 RAT STANDARD; PRT; 142 AA.
AC Q9JH7.
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Baculoviral IAP repeat-containing protein 5 (Apoptosis inhibitor
DE survivin).
GN BIRC5.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Chen D., Cao G., Chen J.;
RT Molecular cloning and characterization of rat survivin."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May play a role in neoplasia. May counteract a default
CC induction of apoptosis in G2/M phase. Interacts with tubulin.
CC Inhibitor of caspase-3 and caspase-7 (By similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Contains 1 BIR repeat.
CC -!- SIMILARITY: Belongs to the IAP family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF276775; AAF82586.1; -
CC HSPSP; O15392; IEF31.
CC InterPro; IPR001370; BIR.
CC Pfam; PF00653; BIR; 1.
CC SMART; SM00238; BIR; 1.
CC PROSITE; PS01282; BIR_REPEAT_1; FALSE_NEG.
CC PROSITE; PS0143; BIR_REPEAT_2; 1.
CC Apoptosis; Thiol protease inhibitor; Metal-binding; Zinc;
CC Phosphorylation.
CC REPEAT 15 87 BIR.
CC METAL 57 57 ZINC (BY SIMILARITY).
CC METAL 60 60 ZINC (BY SIMILARITY).
CC METAL 77 77 ZINC (BY SIMILARITY).
CC METAL 84 84 ZINC (BY SIMILARITY).
CC MOD_RES 34 34 PHOSPHORYLATION (BY CDC2)
CC (BY SIMILARITY).
CC SEQUENCE 142 AA; 16692 MW; 99BCFAE1584D0CAC CRC64;

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Query Match 27.5%; Score 39; DB 1; Length 142;
Best Local Similarity 100.0%; Pred. No. 4.7e-33;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 CTPERVAEAGFTHCPTENEPDLAQCFFCFKELEGWEPDD 71
Db 33 CTPERVAEAGFTHCPTENEPDLAQCFFCFKELEGWEPDD 71

RESULT 4
BM88 PIG
ID BM88 PIG STANDARD; PRT; 140 AA.
AC Q29026;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE BM88 antigen.
GN BM88.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A., SEQUENCE OF 7-17, AND CHARACTERIZATION.
RC TISSUE=Brain;
RX MEDLINE=955294030; PubMed=7775480;
RA Mamalaki A., Boucou E., Hurel C., Patsavoudi E., Tzartos S.,
RA Matsas R.;
RT "The BM88 antigen, a novel neuron-specific molecule, enhances the
RT differentiation of mouse neuroblastoma cells.";
RL J. Biol. Chem. 270:14201-14208(1995).
CC -!- FUNCTION: Involved in neuroblastoma cell differentiation.
CC -!- SUBUNIT: Homodimer
CC -!- SUBCELLULAR LOCATION: Type IV membrane protein. Associated with
CC the plasma membrane and the membranes of intracellular organelles
CC (Potential).
CC -!- TISSUE SPECIFICITY: Found in the spinal cord, cerebellum and
CC cerebrum, where it is localized in neurons.
CC -!- DEVELOPMENTAL STAGE: Appears during early brain development where
CC it increases with age to give high levels in the mature animal.
CC -!- SIMILARITY: BELONGS TO THE BM88 FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X82027; CAA57549.1; -
CC PIR; A57544; A57544.
CC Antigen; Transmembrane.
CC DOMAIN 1 115
CC TRANSMEM 116 136 CYTOPLASMIC (POTENTIAL).
CC ANCHOR FOR TYPE IV MEMBRANE PROTEIN
CC (POTENTIAL).
CC FT DOMAIN 137 140 EXTRACELLULAR (POTENTIAL).
CC FT DOMAIN 123 128 POLY-ALA.
CC SQ SEQUENCE 140 AA; 13968 MW; 1F4F6C2D2FEC60FD CRC64;

Query Match 4.9%; Score 7; DB 1; Length 140;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 APTLPPA 9
Db 50 APTLPPA 56

RESULT 5
HSLV LISIN STANDARD; PRT; 179 AA.
ID HSLV LISIN
AC Q92C74;

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DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE ATP-dependent protease hslv (EC 3.4.25.-).
GN HSLV OR CLPQ OR L1N1317.
OS Listeria innocua
OX Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1642;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIP 11262 / Serovar 6a;
RX MEDLINE=21537279; PubMed=11679669;
RA Glaeser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
RA Domann E., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Entian K.-D., Fshih H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Krest J., Kuhn M., Kunst F., Kurapkat G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordsiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schluerer T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.,
RL "Comparative genomics of Listeria species.";
RT Science 294:849-852(2001).
CC -!- FUNCTION: Protease subunit of a proteasome-like degradation
CC complex (By similarity)
CC -!- SUBUNIT: A double ring-shaped homohexameric of hslv is capped on
CC each side by a ring-shaped hslu homohexameric (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to peptidase family T1B. Hslv subfamily.
CC -----
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CC -----
CC ENBL; A1596168; CAC96548.1; -.
DR PIR; A1597; A1597.
DR MEROPS; T01.007; -.
DR Listlist; L1N01317; -.
DR HAMAP; MF 00248; -.
DR InterPro; IPR001353; Peptidase_T1.
DR Pfam; PF00227; Proteasome; 1.
KW Hydrolase; Protease; Threonine protease; Complete proteome.
FT ACT SITE 6 BY SIMILARITY.
SQ SEQUENCE 179 AA; 19390 MW; D546A0476C5662B1 CRC64;

Query Match 4.9%; Score 7; DB 1; Length 179;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 TAKKVR 133
Db 36 TAKKVR 42

RESULT 6
HSLV LISMO STANDARD; PRT; 179 AA.
AC Q8Y7J9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE ATP-dependent protease hslv (EC 3.4.25.-).
GN HSLV OR CLPQ OR LMO1276.
OS Listeria monocytogenes.
OX Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1639;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=EGD-e / Serovar 1/2a;
RX MEDLINE=21537279; PubMed=11679669;
RA Glaeser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
RA Domann E., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Entian K.-D., Fshih H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Krest J., Kuhn M., Kunst F., Kurapkat G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordsiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schluerer T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.,
RL "Comparative genomics of Listeria species.";
RT Science 294:849-852(2001).
CC -!- FUNCTION: Protease subunit of a proteasome-like degradation
CC complex (By similarity)
CC -!- SUBUNIT: A double ring-shaped homohexameric of hslv is capped on
CC each side by a ring-shaped hslu homohexameric (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to peptidase family T1B. Hslv subfamily.
CC -----
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CC -----
CC ENBL; A1591978; CAC99356.1; -.
DR PIR; A1234; A1234.
DR MEROPS; T01.007; -.
DR Listlist; LMO01278; -.
DR HAMAP; MF 00248; -.
DR InterPro; IPR001353; Peptidase_T1.
DR Pfam; PF00227; Proteasome; 1.
KW Hydrolase; Protease; Threonine protease; Complete proteome.
FT ACT SITE 6 BY SIMILARITY.
SQ SEQUENCE 179 AA; 19406 MW; 443CB9B915B1FCC8 CRC64;

Query Match 4.9%; Score 7; DB 1; Length 179;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 TAKKVR 133
Db 36 TAKKVR 42

RESULT 7
SENT CABEL STANDARD; PRT; 697 AA.
ID AC Q09353; Q8IU18;
DT 01-NOV-1997 (Rel. 35, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Probable sentrin-specific protease (EC 3.4.22.-).
GN T10F2.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Tsubaki A., Incue H., Takahashi K.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
OX NCBI_TaxID=1639;
RN [1]

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RX MEDLINE=99398681; PubMed=10468581;
RA Uren A.G., Beilharz T., O'Connell M.J., Bugg S.J., van Driel R.,
RA Vaux D.L., Litrow T.,
RT "Role for yeast inhibitor of apoptosis (IAP)-like proteins in cell
RT division.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10170-10175(1999).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=21850422; PubMed=11861551;
RA Rajagopalan S., Balasubramanian M.K.;
RA "Schizosaccharomyces pombe Birp, a nuclear protein that localizes to
RT kinetochores and the spindle midzone, is essential for chromosome
RT condensation and spindle elongation during mitosis.";
RL Genetics 160:445-456(2002).
RN [5]
RP FUNCTION.
RX MEDLINE=20035862; PubMed=10571085;
RA Rajagopalan S., Balasubramanian M.K.;
RA "S. pombe Birp: an inhibitor of apoptosis domain containing protein
RT is essential for chromosome segregation.";
RL FEBS Lett. 460:187-190(1999).
RN CC
CC -!- FUNCTION: Seems to act in the pleiotropic control of cell
CC division. Has a role in chromosome segregation by recruiting
CC condensin and ark1 kinase to appropriate sites as the cell
CC progresses through mitosis.
CC -!- SUBCELLULAR LOCATION: Nuclear. Interacts with the outer
CC centromeric regions of the chromosomes during interphase. After
CC chromatid separation moves to the middle of the spindle.
CC -!- SIMILARITY: Contains 2 BIR repeats.
CC -----
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CC -----
DR EMBL; AB031034; EAA83415.1; -
DR EMBL; AL0311323; CAA20434.1; -
DR EMBL; AL121859; CAB58376.1; -
DR FIC; T43523; T43523.
DR HSP; Q13490; 1QBH.
DR GenDB_SPombe; SPCC962.02c; -
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 2.
DR SMART; SM00238; BIR; 2.
DR PROSITE; PS01282; BIR_REPEAT 1; FALSE_NEG.
DR PROSITE; PS01433; BIR_REPEAT 2; 2.
KW Cell division; Mitosis; Nuclear protein; Repeat.
FT REPEAT 25 39 BIR 1.
FT REPEAT 120 194 BIR 2.
FT DOMAIN 80 83 POLY-ASP.
FT DOMAIN 312 319 POLY-ASP.
FT DOMAIN 487 490 POLY-SER.
SQ SEQUENCE 997 AA; 112579 MW; 952A6AFA5C489F4 CRC64;

Query Match 4.9%; Score 7; DB 1; Length 997;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 WEPDDDP 73
Db 173 WEPDDDP 179
|||||
|||||

RESULT 10
MYS2 DICDI STANDARD; PRT; 2116 AA.
AC P08789;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)

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DE Myosin II heavy chain, non muscle.
GN MHCA.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87092266; PubMed=3540939;
RA Warrick H.M., de Lozanne A., Leinwand L.A., Spudich J.A.;
RT "Conserved protein domains in a myosin heavy chain gene from
RT Dictyostelium discoideum.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:9433-9437(1986).
RN [2]
RP PHOSPHORYLATION SITES, AND MUTAGENESIS.
RC STRAIN=AX2;
RX MEDLINE=90353583; PubMed=2387408;
RA Lueck-Vielmeier D., Schleicher M., Grabatin B., Wippler J.,
RA Gerisch G.;
RT "Replacement of threonine residues by serine and alanine in a
RT phosphorylatable heavy chain fragment of Dictyostelium myosin II.";
RL FEBS Lett. 269:239-243(1990).
RN [3]
RP PHOSPHORYLATION SITES.
RX MEDLINE=88112226; PubMed=2828113;
RA Wagle G., Noegel A., Scheel J., Gerisch G.;
RT "Phosphorylation of threonine residues on cloned fragments of the
RT Dictyostelium myosin heavy chain.";
RL FEBS Lett. 227:71-75(1988).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 1-762.
RX MEDLINE=95345066; PubMed=7619795;
RA Fisher A.J., Smith C.A., Thoden J.B., Smith R., Sutoh K., Holden H.M.,
RA Rayment I.;
RT "X-ray structures of the myosin motor domain of Dictyostelium
RT discoideum complexed with MgADP.Befx and MgADP.ALFA-.";
RL Biochemistry 34:8960-8972(1995).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 1-762.
RX MEDLINE=95345067; PubMed=7619796;
RA Smith C.A., Rayment I.;
RT "X-ray structure of the magnesium(II)-pyrophosphate complex of the
RT truncated head of Dictyostelium discoideum myosin to 2.7-A
RT resolution.";
RL Biochemistry 34:8973-8981(1995).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 1-762.
RX MEDLINE=96206189; PubMed=8611530;
RA Smith C.A., Rayment I.;
RT "X-ray structure of the magnesium(II) ADP.vanadate complex of the
RT Dictyostelium discoideum myosin motor domain to 1.9-A resolution.";
RL Biochemistry 35:5404-5417(1996).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 1-762.
RX MEDLINE=97452580; PubMed=9305951;
RA Gulick A.M., Bauer C.B., Thoden J.B., Rayment I.;
RT "X-ray structures of the MgADP, MgATPgammass, and MgATPPNP complexes
RT of the Dictyostelium discoideum myosin motor domain.";
RL Biochemistry 36:11619-11628(1997).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 1-762.
RX MEDLINE=98070605; PubMed=9405148;
RA Bauer C.B., Kuhlman P.A., Bagshaw C.R., Rayment I.;
RT "X-ray crystal structure and solution fluorescence characterization
RT of Mg.2'(3')-O-(N-methylanthraniloyl) nucleotides bound to the
RT Dictyostelium discoideum myosin motor domain.";
RL J. Mol. Biol. 274:394-407(1997).
RN CC
CC -!- FUNCTION: Myosin is a protein that binds to actin and has ATPase
CC activity that is activated by actin.
CC -!- SUBUNIT: Myosin II heavy chain is two-headed. It self-assembles
CC into filaments. Hexamer of 2 heavy chain subunits (MHC), 2 alkali
CC light chain subunits (MLC) and 2 regulatory light chain subunits
CC (MLC-2).
CC -!- SUBCELLULAR LOCATION: HIGHEST CONCENTRATION IN THE POSTERIOR CELL

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RC STRAIN=B204;
RX MEDLINE=21101013; PubMed=11159958;
RA Hsu T., Hutto D.L., Minion F.C., Wannemuehler M.J.;
RT "Cloning of a beta-hemolysin gene of Brachyspira (Serpulina)
RL hyodysenteriae and its expression in Escherichia coli.";
RL Infect. Immun. 69:706-711(2001).
CC -!- FUNCTION: Carrier of the growing fatty acid chain in fatty acid
CC biosynthesis (By similarity). Has hemolytic activity forming pores
CC approximately 1 nm in diameter into erythrocytes. Is able to
CC induce murine colonic lesions and to disrupt the integrity of
CC epithelial cell monolayers.
CC -!- PATHWAY: De novo fatty acid biosynthesis.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: 4'-phosphopantetheine is transferred from CoA to a specific
CC serine of apo-ACP by acps. This modification is essential for
CC activity because fatty acids are bound in thioester linkage to the
CC sulphydryl of the prosthetic group (By similarity).
CC -!- SIMILARITY: Contains 1 acyl carrier domain.
CC
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CC
CC EMBL; U94866; AA868774.1; -.
CC HSSP; P02901; IACP.
CC HAMAP; MF_01217; -.
CC InterPro; IPR003231; Acyl_carrier.
CC InterPro; IPR006163; Pp_bind.
CC InterPro; IPR006162; Pantne_S.
CC Pfam; PF00550; pp-binding; 1.
CC ProDom; PD00887; Acyl_carrier; 1.
CC TIGRFAMs; TIGR00517; acyl_carrier; 1.
CC PROSITE; PS00075; ACP_DOMAIN; 1.
CC PROSITE; PS00012; PHOSPHOPANTHEINE; 1.
CC KW Lipid synthesis; Fatty acid biosynthesis; Phosphopantetheine;
CC Virulence; Hemolysis; Toxin.
CC FT PROPEP 1 7
CC CHAIN 8 78 BETA-HEMOLYSIN.
CC BINDING 37 37 PHOSPHOPANTHEINE (BY SIMILARITY).
CC SEQUENCE 78 AA; 8934 MW; 5F21E7ED0102C715 CRC64;

Query Match 4.2%; Score 6; DB 1; Length 78;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 IEHKK 79
Db |||||
73 IEHKK 78

RESULT 12
COAB.BPIKE STANDARD; PRT; 82 AA.
AC P03620;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Coat protein B precursor (Major coat protein).
GN Vill.
OS Bacteriophage IKe.
OC Viruses; ssDNA viruses; Inoviridae; Inovirus.
OX NCBI_TaxID=10867;
RN [1]
CC SEQUENCE FROM N.A.
RX MEDLINE=85160831; PubMed=3981635;
RA Peeters B.P.H., Peters R.M., Schoenmakers J.G.G., Konings R.N.H.;
RT "Nucleotide sequence and genetic organization of the genome of the N-
RT specific filamentous bacteriophage IKe. Comparison with the genome of
RT the F-specific filamentous phages M13, fd and f1.";
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RL J. Mol. Biol. 181:27-39(1985).
RN [2]
RP SEQUENCE OF 30-82.
RX MEDLINE=81215498; PubMed=7240173;
RA Nakashima Y., Frangione B., Wiseman R.L., Konigsberg W.H.;
RT "Primary structure of the major coat protein of the filamentous
RT bacterial viruses, Ifi and Ike.";
RL J. Biol. Chem. 256:5792-5797(1981).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (5.0 ANGSTROMS).
RX MEDLINE=94118269; PubMed=8289247;
RA Marvin D.A., Hale R.D., Nave C., Citterich M.H.;
RT "Molecular models and structural comparisons of native and mutant
RT class I filamentous bacteriophages Ff (fd, f1, M13), Ifi and Ike.";
RL J. Mol. Biol. 235:260-285(1994).
CC -!- FUNCTION: Coat protein B is the major coat protein of the virion.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC
CC EMBL; X02139; CAA36072.1; -.
CC PIR; A92912; VCBPTK.
CC PDB; 1IEF; 31-JUL-94.
CC InterPro; IPR008033; Phage_coat_Gp8.
CC Pfam; PF05371; Phage_Coat_Gp8; 1.
CC Coat protein; Signal; 3D-structure.
CC SIGNAL 1 29
CC CHAIN 30 82 COAT PROTEIN B.
CC HELIX 31 82
CC SEQUENCE 82 AA; 8570 MW; C8F24F55A053799A CRC64;

Query Match 4.2%; Score 6; DB 1; Length 82;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 AKNKIA 114
Db |||||
10 AKNKIA 15

RESULT 13
IMM1.PSEAE STANDARD; PRT; 87 AA.
AC Q06578;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Immunity protein for pyocin S1.
GN IMM1.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
CC SEQUENCE FROM N.A., AND SEQUENCE OF 1-20.
RP STRAIN=NTH-H;
RX MEDLINE=9259934; PubMed=8491711;
RA Sano Y., Matsui H., Kobayashi M., Kageyama M.;
RT "Molecular structures and functions of pyocins S1 and S2 in
RT Pseudomonas aeruginosa.";
RL J. Bacteriol. 175:2907-2916(1993).
CC -!- SIMILARITY: BELONGS TO THE COLICINS COLE2/COLE8/COLE9 AND PYOCINS
CC S1/S2 FAMILY.
CC
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DR EMBL; D12707; BAA02202.1; --
 DR PIR; B36907; B36907.
 DR HSSP; Q03708; 1CEI.
 DR InterPro; IPR000290; Colicin_pyocin.
 DR Pfam; PF01320; Colicin_Pyocin; 1.
 DR PRINTS; PR01299; PYOCIN.
 DR ProDom; PD007225; Colicin_pyocin; 1.
 DR KW Bacteriocin immunity.
 SQ SEQUENCE 87 AA; 10040 MW; D332D0FD48556A6C CRC64;

Query Match 4.2%; Score 6; DB 1; Length 87;
 Best Local Similarity 100.0%; Pred. No. 50;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 117 TNNKKK 122
 |||||
 DB 22 TNNKKK 27

RESULT 14

IMM2_PSEAE STANDARD; PRT; 87 AA.
 AC Q06579;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Immunity protein for pyocin S2.
 GN IMM2 OR PA1151.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=287;
 [1]
 SEQUENCE FROM N.A., AND SEQUENCE OF 1-20.
 RN RP STRAIN=PAO;
 RC MEDLINE=93259934; PubMed=8491711;
 RA Sano Y., Matsui H., Kobayashi M., Kageyama M.;
 RT "Molecular structures and functions of pyocins S1 and S2 in Pseudomonas aeruginosa."
 RL J. Bacteriol. 175:2907-2916(1993).
 [2]
 SEQUENCE FROM N.A.
 RN RP STRAIN=ATCC 15692 / PAO1;
 RC MEDLINE=20437337; PubMed=10984043;
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P., Hickey M.J., Brinkman F.S.L., Ruffnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y., Brady L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Raizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RT "Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen."
 RL Nature 406:959-964(2000).
 CC -!- SIMILARITY: BELONGS TO THE COLICINS COLE2/COLE9 AND PYOCINS S1/S2 FAMILY.
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EMBL; D12708; BAA02204.1; --
 DR EMBL; AE004545; AAG04540.1; --
 DR PIR; D36907; D36907.
 DR HSSP; Q03708; 1CEI.
 DR InterPro; IPR000290; Colicin_pyocin.

DR Pfam; PF01320; Colicin_Pyocin; 1.
 DR PRINTS; PR01299; PYOCIN.
 DR ProDom; PD007225; Colicin_pyocin; 1.
 DR KW Bacteriocin immunity; Complete proteome.
 SQ SEQUENCE 87 AA; 10039 MW; DE9965FD485D424C CRC64;

Query Match 4.2%; Score 6; DB 1; Length 87;
 Best Local Similarity 100.0%; Pred. No. 50;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 117 TNNKKK 122
 |||||
 DB 22 TNNKKK 27

RESULT 15

Y031_CHLTR STANDARD; PRT; 100 AA.
 AC Q84034;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein CT031.
 GN CT031.
 OS Chlamydia trachomatis.
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_TaxID=813;
 [1]
 SEQUENCE FROM N.A.
 RN RP STRAIN=D/UW-3/Cx;
 RC MEDLINE=99000809; PubMed=9784136;
 RA Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L., Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V., Davis R.W.;
 RA "Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis."
 RT Science 282:754-759(1998).
 RL -!- SIMILARITY: BELONGS TO THE CHLAMYDIAL CPN0121/CT031/TC0300 FAMILY.
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EMBL; AE001277; AAC67621.1; --
 DR PIR; B71567; B71567.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 100 AA; 11680 MW; 2A12B8A53EAA4F3C CRC64;

Query Match 4.2%; Score 6; DB 1; Length 100;
 Best Local Similarity 100.0%; Pred. No. 57;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 AKNKIA 114
 |||||
 DB 30 AKNKIA 35

RESULT 16

YGRB_BACPF STANDARD; PRT; 108 AA.
 ID YGRB_BACPF
 AC Q45130;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Hypothetical 12.6 kDa protein in grpa 5'-region (ORF).
 OS Bacillus pseudofirmus.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=79885;

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CC -1- SIMILARITY: Belongs to the SLP family of ribosomal proteins.
CC -----
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CC -----
DR EMEL; AF005041; BAC72664.1; -.
DR HAMAP; MF 01310; -.
DR InterPro; IPR001971; Ribosomal_S11.
DR Pfam; PF00411; Ribosomal_S11; 1.
DR ProDom; PD001010; Ribosomal_S11; 1.
DR PROSITE; PS00054; RIBOSOMAL_S11; 1.
KW Ribosomal protein; RNA-binding; rRNA-binding; Complete proteome.
SQ SEQUENCE 134 AA; 14384 MW; 82DE7DB9D0D48982 CRC64;
-----
Query Match 4.2%; Score 6; DB 1; Length 134;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
-----
QY 128 AKKVR 133
DB 10 AKKVR 15
-----
RESULT 18
RS11_STRCO STANDARD; PRT; 134 AA.
AC P72403;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 30S ribosomal protein S11.
GN RPSK OR SCO4728 OR SC6G4.06.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitz B., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Taylor K.,
RA Warren T., Wietzorek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147 (2002).
[2]
RP SEQUENCE OF 105-134 FROM N.A.
RP STRAIN=A3(2) / M145;
RX MEDLINE=37105902; PubMed=8948650;
RA Cho E.-J., Bae J.-B., Kang J.-G., Roe J.-H.;
RT "Molecular analysis of RNA polymerase alpha subunit gene from
RT Streptomyces coelicolor A3(2).";
RL Nucleic Acids Res. 24:4565-4571 (1996).
CC -1- FUNCTION: Located on the platform of the 30S subunit, it bridges
CC several disparate RNA helices of the 16S rRNA. Forms part of the
CC Shine-Dalgarno cleft in the 70S ribosome (By similarity).
CC SUBUNIT: Part of the 30S ribosomal subunit. Interacts with
CC proteins S7 and S18. Binds to IF-3 (By similarity).
CC -1- SIMILARITY: Belongs to the SLP family of ribosomal proteins.
CC -----
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-----
DR EMBL; AL939121; CAA20384.1; -
DR EMBL; X92107; CAA63079.1; -
DR PIR; T35557; T35557.
DR HAWAP; MF_01310; -; 1.
DR InterPro; IPR001971; Ribosomal S11.
DR Pfam; PF00411; Ribosomal_S11; 1.
DR ProDom; PD001010; Ribosomal_S11; 1.
DR PROSITE; PS00054; RIBOSOMAL_S11; 1.
KW Ribosomal protein; RNA-binding; Complete proteome.
SQ SEQUENCE 134 AA; 14398 MW; 858B6DBEA7D3F9F5 CRC64;

Query Match 4.2%; Score 6; DB 1; Length 134;
Best Local Similarity 100.0%; Pred.No.74;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 128 AKVRR 133
DB 10 AKVRR 15
|||||

RESULT 19
Y056 METJA STANDARD; PRT; 136 AA.
AC Q60365.
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MJ0056.
GN MJ0056.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Uitterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii."
RL Science 273:1058-1073(1996).
-----
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-----
DR EMBL; U67463; AAB98036.1; -
DR PIR; H64306; H64306.
DR TIGR; MJ0056; -
DR InterPro; IPR002834; DUF120.
DR Pfam; PF01982; DUF120; 1.
DR ProDom; PD015839; DUF120; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 136 AA; 15685 MW; 9F58C831BB21418C CRC64;

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Query Match 4.2%; Score 6; DB 1; Length 136;
Best Local Similarity 100.0%; Pred.No.75;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 LKLDRE 107
DB 46 LKLDRE 51
|||||

RESULT 20
RL16 LEPIN STANDARD; PRT; 137 AA.
ID RL16 LEPIN
AC Q9XD29;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 50S ribosomal protein L16.
GN RPL16 OR RPLP OR LA0746.
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=173;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Lai / Serogroup Icterohaemorrhagiae / Serovar lai;
RX MEDLINE=2008835; PubMed=10620683;
RA Zuerner R.L., Hartskeerl R.A., van de Kemp H., Bal A.E.;
RT "Characterization of the Leptospira interrogans S10-spc-alpha
RT operon."
RL FEMS Microbiol. Lett. 182:303-308(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
RX MEDLINE=22598143; PubMed=12712204;
RA Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
RA Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,
RA Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
RA Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
RA Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,
RA Sait Gironi I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,
RA Xu J.-G., Zhao G.-P.;
RT "Unique physiological and pathogenic features of Leptospira
RT interrogans revealed by whole-genome sequencing."
RL Nature 422:888-893(2003).
CC -!- FUNCTION: This protein binds directly to 23S ribosomal RNA and is
CC located at the a site of the peptidyltransferase center (By
CC similarity).
CC -!- SIMILARITY: Belongs to the L16P family of ribosomal proteins.
-----
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-----
DR EMBL; AF115283; AAN40590.1; -
DR EMBL; AF011262; AAD47945.1; -
DR InterPro; IPR00114; Ribosomal L16.
DR Pfam; PF00252; Ribosomal_L16; 1.
DR PRINTS; PR00060; RIBOSOMALL16.
DR TIGRfams; TIGR01164; rplP_bact; 1.
DR PROSITE; PS00566; RIBOSOMAL_L16_1; 1.
DR PROSITE; PS00701; RIBOSOMAL_L16_2; 1.
KW Ribosomal protein; rRNA-binding; Complete proteome.
SQ SEQUENCE 137 AA; 15505 MW; 24F371E7450FE257 CRC64;

Query Match 4.2%; Score 6; DB 1; Length 137;
Best Local Similarity 100.0%; Pred.No.75;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EETAKK 130
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DB 111 BETAKK 116

RESULT 21

RL11 HELP

ID RL11 HELP STANDARD; PRT; 141 AA.

AC P56037;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE SOS ribosomal protein L11.

GN RPLK OR HP1202 OR JHP1125.

OS Helicobacter pylori (Campylobacter pylori), and

OS Helicobacter pylori J99 (Campylobacter pylori J99).

OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;

OC Helicobacteriaceae; Helicobacter.

OX NCBI_TaxID=216, 85963;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=26695 / ATCC 700392;

RX MEDLINE=97394467; PubMed=9252185;

RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,

RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,

RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,

RA Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,

RA McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,

RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,

RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,

RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,

RA Venter J.C.;

RT "The complete genome sequence of the gastric pathogen Helicobacter pylori.";

RL Nature 388:539-547(1997).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=J99;

RX MEDLINE=99120557; PubMed=9923662;

RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,

RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,

RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,

RA Gibson T., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,

RA Trust T.J.;

RT "Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori.";

RL Nature 397:176-180(1999).

CC -!- FUNCTION: This protein binds directly to 23S ribosomal RNA (By similarity).

CC -!- PTM: One or more lysine residues are methylated (By similarity).

CC -!- SIMILARITY: Belongs to the L11p family of ribosomal proteins.

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CC -----

CC EMBL; A8000626; AAD08248.1; -.

CC EMBL; A8001540; AAD06703.1; -.

CC PIR; B64670; B64670.

CC HGSP; P29395; 1MMS.

CC TIGR; HP1202; -.

CC HAMAP; MF_00736; -; 1.

CC InterPro; IPR000911; Ribosomal_L11.

CC InterPro; IPR006519; Ribosomal_L11bac.

CC Pfam; PF00238; Ribosomal_L11; 1.

CC Pfam; PF03946; Ribosomal_L11_N; 1.

CC ProDom; PD001367; Ribosomal_L11; 1.

CC SMART; SM00649; RL11; 1.

CC TIGRfam; TIGR01632; RL1_bact; 1.

CC ProSITE; PS00359; RIBOSOMAL_L11; 1.

CC Ribosomal protein; rRNA-binding; Methylation; Complete proteome.

SQ SEQUENCE 141 AA; 15329 MW; D1BE047F62F5FAAB CRC64;

Query Match 4.2%; Score 6; DB 1; Length 141;

Best Local Similarity 100.0%; Pred.No.77; 0; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 0;

Qy 110 KNKIAK 115

Db 94 KNKIAK 99

RESULT 22

GSFG ECOLI

ID GSFG ECOLI STANDARD; PRT; 145 AA.

AC P41442;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Putative general secretion pathway protein G precursor (Protein transport protein hofG).

DE HOFG OR HOPG OR B3328.

OS Escherichia coli.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Escherichia.

OX NCBI_TaxID=562;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=K12;

RX MEDLINE=95204361; PubMed=7896718;

RA Stojiljkovic I., Schoenher R., Kusters J.G.;

RT "Identification of the hopG gene, a component of Escherichia coli K-12 type II export system, and its conservation among different pathogenic Escherichia coli and Shigella isolates.";

RL J. Bacteriol. 177:1892-1895(1995).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=K12 / MG1655;

RX MEDLINE=97426617; PubMed=9278503;

RA Blatter F.R., Blunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;

RT "The complete genome sequence of Escherichia coli K-12.";

RL Science 277:1453-1474(1997).

CC -!- FUNCTION: Involved in a general secretion pathway (GSP) for the export of proteins (By similarity).

CC -!- SIMILARITY: BELONGS TO THE PULG/OUTG/XPSG/EXEG/XCPT FAMILY.

CC -----

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CC -----

CC EMBL; U20786; AAA69031.1; -.

CC EMBL; U18397; AAA58125.1; -.

CC EMBL; AB000409; AAC76353.1; -.

CC PIR; B56150; B56150.

CC EcoGene; EG12886; hofG.

CC InterPro; IPR000983; Bac_GSPH.

CC InterPro; IPR002416; Bac_GSPH.

CC InterPro; IPR001120; Prok_N_methyl_S.

CC PRINTS; PR00813; BCTERIALGSPH.

CC PRINTS; PR00885; BCTERIALGSPH.

CC PROSITE; PS00409; PROKAR_NTER_METHYL; 1.

CC Transport; Methylation; Complete proteome.

FT PROPEP 1 9

FT CHAIN 10 145

FT PUTATIVE GENERAL SECRETION PATHWAY

FT PROTEIN G.

FT MOD RES 10 10 METHYLATION (By similarity).

FT SEQUENCE 145 AA; 15905 MW; C8CD67D743810072 CRC64;

Query Match 4.2%; Score 6; DB 1; Length 145;
 Best Local Similarity 100.0%; Pred. No. 79;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 APTLPP 8
 DTD LISMO STANDARD; PRT; 148 AA.
 AC Q87WB2;
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DE Large-conductance mechanosensitive channel.
 GN MSCL OR PSPT04641.
 OS Pseudomonas syringae (pv. tomato).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=323;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DC3000;
 RX MEDLINE=22834015; PubMed=12928499;
 RA Buell C.R., Joardar V., Lindeberg M., Selengut J., Paulsen I.T.,
 RA Gwinn M.L., Dodson R.J., Deboy R.T., Durkin A.S., Kolonay J.F.,
 RA Madupu R., Daugherty S., Brinkac L., Beanan M.J., Haft D.H.,
 RA Nelson W.C., Davidson T., Zafar N., Zhou L., Liu J., Yuan Q.,
 RA Khouri H., Fedorova N., Tran B., Russell D., Berry K., Utterback T.,
 RA Van Aken J.E., Feldblyum T.V., D'Ascenzo M., Deng W.-L., Ramos A.R.,
 RA Lazarowitz S.G., Martin G.B., Chatterjee A.K., Delaney T.P.,
 RA White O., Fraser C.M., Collier A.;
 RT "The complete genome sequence of the Arabidopsis and tomato pathogen
 Pseudomonas syringae pv. tomato DC3000.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186(2003).
 CC -!- FUNCTION: Channel that opens in response to stretch forces in the
 membrane lipid bilayer. May participate in the regulation of
 osmotic pressure changes within the cell (By similarity).
 CC -!- SUBUNIT: Homopentamer (By similarity).
 CC -!- SIMILARITY: Belongs to the mscl family.
 CC
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 CC
 CC EMBL; AB016872; A058087.1; -;
 DR TIGR; PSPT04641; -;
 DR HAMAP; MF_00115; 1.
 DR InterPro; IPR001185; MS channel.
 DR Pfam; PF01741; Mscl; 1.
 DR PRINTS; PR01264; MECHCHANNEL.
 DR PROSITE; PS01327; MSCL; 1.
 KW Ionic channel; transmembrane; Inner membrane; Complete proteome.
 FT DOMAIN 1 15 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 16 42 BY SIMILARITY.
 FT DOMAIN 43 73 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 74 95 BY SIMILARITY.
 FT DOMAIN 96 148 CYTOPLASMIC (POTENTIAL).
 SQ SEQUENCE 148 AA; 15617 MW; 3DE4BDA862605A2A CRC64;
 Query Match 4.2%; Score 6; DB 1; Length 148;
 Best Local Similarity 100.0%; Pred. No. 81;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 APTLPP 8
 DTD LISMO STANDARD; PRT; 150 AA.
 AC Q93RD9;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE D-tyrosyl-tRNA(Tyr) deacylase (EC 3.1.1.-).
 DTD OR LMO1522.
 OS Listeria monocytogenes.
 OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
 OX NCBI_TaxID=1639;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EGD / Serovar 1/2a;
 RA Okada Y.;
 RT "Listeria monocytogenes rel and flanking regions.";
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EGD-e / Serovar 1/2a;
 RX MEDLINE=21537279; PubMed=11679669;
 RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
 RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
 RA Chatbit B., Chetoui F., Couve E., de Daruvar A., Dehoux P.,
 RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
 RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
 RA Gaudier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
 RA Jones L.-M., Kaeber U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
 RA Madsen E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
 RA Nordstieck G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
 RA Remmel B., Rose M., Schluter T., Simoes N., Tierrez A.,
 RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
 RT "Comparative genomics of Listeria species.";
 RL Science 294:849-852(2001).
 CC -!- FUNCTION: Hydrolyzes D-tyrosyl-tRNA(Tyr) into D-tyrosine and free
 tRNA(Tyr). Could be a defense mechanism against a harmful effect
 of D-tyrosine (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
 CC -!- SIMILARITY: Belongs to the DTD family.
 CC
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 CC
 CC EMBL; AB051847; BAB50671.1; -;
 DR EMBL; AL581979; CAC99600.1; -;
 DR PIR; AB1265; AB1265.
 DR HSSP; P32147; 1JKE.
 DR ListList; LMO01522; -;
 DR HAMAP; MF_00518; 1.
 DR InterPro; IPR003732; DTYrRNA_deacylase.
 DR Pfam; PF02580; Tyr_deacylase; 1.
 DR ProDom; PD005653; DTYrRNA_deacylase; 1.
 DR TIGSFams; TIGR00256; TIGR00256; 1.
 KW Hydrolyase; Complete proteome.
 SQ SEQUENCE 150 AA; 16533 MW; 50FDD83497B7017D CRC64;
 Query Match 4.2%; Score 6; DB 1; Length 150;
 Best Local Similarity 100.0%; Pred. No. 82;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 AEAGFI 44
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Db      114 ABAGFI 119
RESULT 25
YCCA_BACP3
ID      YCCA_BACP3      STANDARD;      PRT;      150 AA.
AC      P55815;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Hypothetical protein in ccca 5' region (Fragment).
OS      Bacillus PS3 (Thermophilic bacterium PS-3).
OC      Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX      NCBI_TaxID=2334;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=93379042; PubMed=7916623;
RA      Fujiwara Y., Oka M., Hamamoto T., Sone N.;
RT      "Chromosome c-551 of the thermophilic bacterium PS3, DNA sequence and
RT      analysis of the mature cytochrome.";
RL      Biochim. Biophys. Acta 1144:213-219(1993).
CC      -!- SIMILARITY: TO B.SUBTILIS YPJC, YQFU AND YIT.
CC      -----
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CC      -----
DR      EMBL; X63125; -; NOT ANNOTATED_CDS.
DR      InterPro; IPR003740; DUF161.
DR      Pfam; PF02588; DUF161; 1.
KW      Hypothetical protein; Transmembrane.
FT      NON_TER
FT      TRANSMEM 19 39
FT      SEQUENCE 150 AA; 16394 MW; AEF892DB2CF7447 CRC64;
SQ      QUERY MATCH 4.2%; Score 6; DB 1; Length 150;
      Best Local Similarity 100.0%; Pred. No. 82;
      Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      130 KVRRAI 135
Db      80 KVRRAI 85
RESULT 26
RS7_THETH
ID      RS7_THETH      STANDARD;      PRT;      155 AA.
AC      P17591;
DT      01-AUG-1990 (Rel. 15, Created)
DT      01-FEB-1995 (Rel. 31, Last sequence update)
DT      10-OCT-2003 (Rel. 42, Last annotation update)
DE      30S ribosomal protein S7.
GN      rPSG OR RPS7.
OS      Thermus thermophilus.
OC      Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC      Thermus.
OX      NCBI_TaxID=274;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      STRAIN=HB8 / ATCC 27634;
RX      MEDLINE=90301504; PubMed=2362824;
RA      Yaknin A.V., Vorozheykina D.P., Matvienko N.I.;
RT      "Nucleotide sequence of the Thermus thermophilus HB8 rps12 and rps7
RT      genes coding for the ribosomal proteins S12 and S7.";
RL      Nucleic Acids Res. 18:3659-3659(1990).
RN      [2]
RP      SEQUENCE OF 1-49.
RX      STRAIN=HB8 / ATCC 27634;

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RX      MEDLINE=95045586; PubMed=7957245;
RA      Tsiboli P., Hefurth B., Choli T.;
RT      "Purification and characterization of the 30S ribosomal proteins from
RT      the bacterium Thermus thermophilus.";
RL      Eur. J. Biochem. 226:169-177(1994).
RN      [3]
RP      X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX      MEDLINE=97473002; PubMed=9331418;
RA      Wimberly B.T., White S.W., Ramakrishnan V.;
RT      "The structure of ribosomal protein S7 at 1.9-A resolution reveals a
RT      beta-hairpin motif that binds double-stranded nucleic acids.";
RL      Structure 5:1187-1198(1997).
RN      [4]
RP      X-RAY CRYSTALLOGRAPHY (5.5 ANGSTROMS) OF THE 30S SUBUNIT.
RX      MEDLINE=39404610; PubMed=10476960;
RA      Clemens W.M. Jr., May J.L.C., Wimberly B.T., McCutcheon J.P.;
RA      Capel M.S., Ramakrishnan V.;
RT      "Structure of a bacterial 30S ribosomal subunit at 5.5 A resolution.";
RL      Nature 400:833-840(1999).
RN      [5]
RP      X-RAY CRYSTALLOGRAPHY (4.5 ANGSTROMS).
RX      MEDLINE=20056231; PubMed=10588692;
RA      Tocilj A., Schluenzen F., Janeli D., Gluehmann M., Hansen H.A.,
RA      Harms J., Bashan A., Bartels H., Agmon I., Franceschi F., Yonath A.;
RT      "The small ribosomal subunit from Thermus thermophilus at 4.5 A
RT      resolution: pattern fittings and the identification of a functional
RT      site.";
RL      Proc. Natl. Acad. Sci. U.S.A. 96:14252-14257(1999).
RN      [6]
RP      X-RAY CRYSTALLOGRAPHY (3.05 ANGSTROMS) OF THE 30S SUBUNIT.
RX      MEDLINE=20466110; PubMed=11014182;
RA      Wimberly B.T., Brodersen D.E., Clemens W.M. Jr., Morgan-Warren R.J.,
RA      Carter A.P., Vornheim C., Hartsch T., Ramakrishnan V.;
RT      "Structure of the 30S ribosomal subunit.";
RL      Nature 407:327-339(2000).
RN      [7]
RP      X-RAY CRYSTALLOGRAPHY (3.3 ANGSTROMS) OF THE 30S SUBUNIT.
RX      MEDLINE=20460546; PubMed=11007480;
RA      Schluenzen F., Tocilj A., Zarivach R., Harms J., Gluehmann M.,
RA      Janeli D., Bashan A., Bartels H., Agmon I., Franceschi F., Yonath A.;
RT      "Structure of functionally activated small ribosomal subunit at 3.3
RT      A resolution.";
RL      Cell 102:615-623(2000).
RN      [8]
RP      X-RAY CRYSTALLOGRAPHY (3.3 ANGSTROMS) OF THE 30S SUBUNIT.
RX      MEDLINE=21097713; PubMed=1163189;
RA      Brodersen D.E., Clemens W.M. Jr., Carter A.P., Morgan-Warren R.J.,
RA      Wimberly B.T., Ramakrishnan V.;
RT      "The structural basis for the action of the antibiotics tetracycline,
RT      pactamycin, and hygromycin B on the 30S ribosomal subunit.";
RL      Cell 103:1143-1154(2000).
RN      [9]
RP      X-RAY CRYSTALLOGRAPHY (3.00 ANGSTROMS) OF THE 30S SUBUNIT.
RX      MEDLINE=20466111; PubMed=11014183;
RA      Carter A.P., Clemens W.M. Jr., Brodersen D.E., Morgan-Warren R.J.,
RA      Wimberly B.T., Ramakrishnan V.;
RT      "Functional insights from the structure of the 30S ribosomal subunit
RT      and its interactions with antibiotics.";
RL      Nature 407:340-348(2000).
RN      [10]
RP      X-RAY CRYSTALLOGRAPHY (5.00 ANGSTROMS) OF THE RIBOSOME.
RX      MEDLINE=21402420; PubMed=11511350;
RA      Yusupova G.Z., Yusupov M.M., Cate J.H.D., Noller H.F.;
RT      "The path of messenger RNA through the ribosome.";
RL      Cell 106:233-241(2001).
RN      [11]
RP      X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS) OF THE 30S SUBUNIT.
RX      STRAIN=HB27;
RA      MEDLINE=211192023; PubMed=11296217;
RA      Pioletti M., Schluenzen F., Harms J., Zarivach R., Gluehmann M.,
RA      Avila H., Bashan A., Bartels H., Auerbach T., Jacobi C., Hartsch T.,
RA      Yonath A., Franceschi F.;
RT      "Crystals structures of complexes of the small ribosomal subunit with

```

RT tetracycline, edeine and IF3.";
 RL ENBO J. 20:1829-1839(2001).
 RP [12]
 RP X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS) OF THE 30S SUBUNIT.
 RX MEDLINE=21119514; PubMed=1228145;
 RA Carter A.P., Clemons W.M. Jr., Brodersen D.E., Morgan-Warren R.J.,
 RA Hartsh T., Wimberly B.T., Ramakrishnan V.;
 RA "Crystal structure of an initiation factor bound to the 30S ribosomal
 RT subunit.";
 RT Science 291:498-501(2001).
 RL [13]
 RL X-RAY CRYSTALLOGRAPHY (5.5 ANGSTROMS) OF THE RIBOSOME.
 RP MEDLINE=21238793; PubMed=11283358;
 RX Yusupov M.M., Yusupova G.Z., Baucom A., Lieberman K., Earnest T.N.,
 RA Cate J.H.D., Noller H.F.;
 RA "Crystal structure of the ribosome at 5.5 A resolution.";
 RT Science 292:883-896(2001).
 RL [14]
 RL X-RAY CRYSTALLOGRAPHY (3.11 ANGSTROMS) OF THE 30S SUBUNIT.
 RP MEDLINE=21238794; PubMed=11340196;
 RX Ogle J.M., Brodersen D.E., Clemons W.M. Jr., Tarry M.J., Carter A.P.,
 RA Ramakrishnan V.;
 RA "Recognition of cognate transfer RNA by the 30S ribosomal subunit.";
 RT Science 292:897-902(2001).
 RL [15]
 RL X-RAY CRYSTALLOGRAPHY (3.05 ANGSTROMS) OF THE 30S SUBUNIT.
 RP MEDLINE=21856772; PubMed=11866529;
 RX Brodersen D.E., Clemons W.M. Jr., Carter A.P., Wimberly B.T.,
 RA Ramakrishnan V.;
 RA "Crystal structure of the 30S ribosomal subunit from Thermus
 RT thermophilus: structure of the proteins and their interactions with
 RT 16S RNA.";
 RT J. Mol. Biol. 316:725-768(2002).
 RL CC -!- FUNCTION: One of the primary rRNA binding proteins, it binds
 CC directly to 3' end of the 16S rRNA where it nucleates assembly of
 CC the head domain of the 30S subunit. Is located at the subunit
 CC interface close to the decoding center. Binds mRNA and the E-site
 CC tRNA blocking its exit path in the ribosome.
 CC -!- SUBUNIT: Part of the 30S ribosomal subunit. Contacts proteins S9
 CC and S11. Binds to the C-terminus of IF3.
 CC -!- SIMILARITY: Belongs to the S7P family of ribosomal proteins.
 CC -!- DATABASE: NAME=thermophilus 30S ribosomal subunit structure;
 CC WWW="http://alfi.mrc-lmb.cam.ac.uk/-ribo/30S/".
 CC -----
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 CC -----
 CC EMBL; X52165; CAA36419.1; -.
 DR PDB; 1RSS; 11-FEB-98.
 DR PDB; 1DV4; 24-APR-00.
 DR PDB; 1FKA; 04-SEP-00.
 DR PDB; 1FJG; 25-SEP-00.
 DR PDB; 1QD7; 17-JAN-01.
 DR PDB; 1HR0; 24-JAN-01.
 DR PDB; 1HNW; 21-FEB-01.
 DR PDB; 1HNX; 21-FEB-01.
 DR PDB; 1HNZ; 21-FEB-01.
 DR PDB; 1I94; 12-APR-01.
 DR PDB; 1I95; 12-APR-01.
 DR PDB; 1I96; 12-APR-01.
 DR PDB; 1I97; 12-APR-01.
 DR PDB; 1GIX; 01-JUN-01.
 DR PDB; 1IBK; 04-MAY-01.
 DR PDB; 1IBL; 04-MAY-01.
 DR PDB; 1IBM; 04-MAY-01.
 DR PDB; 1JGO; 14-SEP-01.
 DR PDB; 1JGP; 14-SEP-01.
 DR PDB; 1JGQ; 14-SEP-01.

DR PDB; 1LIU; 22-MAR-02.
 DR PDB; 1JSE; 12-APR-02.
 DR PDB; 1N32; 29-NOV-02.
 DR HAMAP; MF_00480; -; 1.
 DR InterPro; IPR000235; Ribosomal_S7.
 DR InterPro; IPR005717; Ribosomal_S7_b/o.
 DR Pfam; PF00177; Ribosomal_S7; 1.
 DR ProDom; PD000817; Ribosomal_S7; 1.
 DR TIGRFAMs; TIGR01029; rpsG_bact; 1.
 DR PROSITE; PS00052; RIBOSOMAL_S7; 1.
 DR Ribosomal protein; RNA-binding; rRNA-binding; tRNA-binding;
 KW 3D-structure.
 FT INIT MET 0
 FT TURN 15 17
 FT HELIX 20 29
 FT TURN 32 33
 FT HELIX 35 53
 FT HELIX 57 68
 FT STRAND 72 79
 FT TURN 80 81
 FT STRAND 82 89
 FT HELIX 92 107
 FT TURN 108 109
 FT HELIX 115 127
 FT TURN 128 129
 FT HELIX 132 144
 SQ SEQUENCE 155 AA; 17885 MW; BC405D68CBFE9474 CRC64;
 Query Match 4.2%; Score 6; DB 1; Length 155;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 36 ERMAEA 41
 DB 141 ERMAEA 146
 RESULT 27
 RS7_DEIRA STANDARD; PRT; 156 AA.
 ID RS7 DEIRA
 AC Q9RXK6;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 30S ribosomal protein S7.
 GN RPSG OR DR0306.
 OS Deinococcus radiodurans.
 OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
 OC Deinococcaceae; Deinococcus.
 OX NCBI_TaxID=1299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=81 / ATCC 13939 / DSM 20539 / NCIB 9279;
 RX MEDLINE=20036896; PubMed=10567266;
 RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
 RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
 RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
 RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zaleski C.,
 RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
 RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
 RA Fraser C.M.;
 RT "Genome sequence of the radioresistant bacterium Deinococcus
 RT radiodurans R1.";
 RL Science 286:1571-1577(1999).
 CC -!- FUNCTION: One of the primary rRNA binding proteins, it binds
 CC directly to 16S rRNA where it nucleates assembly of the head
 CC domain of the 30S subunit. Is located at the subunit interface
 CC close to the decoding center, probably blocks exit of the E-site
 CC tRNA (By similarity).
 CC -!- SUBUNIT: Part of the 30S ribosomal subunit. Contacts proteins S9
 CC and S11 (By similarity).
 CC -!- SIMILARITY: Belongs to the S7P family of ribosomal proteins.
 CC -----

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CC -----

CC EMBL; AE001891; AAF09886.1; -
CC PIR; D75536; D75536.
CC HSP; P17291; 1RSS.
CC TIGR; DR0305; -
CC HAMAP; MF_00480; -; 1.
CC InterPro; IPR000235; Ribosomal_S7.
CC InterPro; IPR005717; Ribosomal_S7_b/o.
CC Pfam; PF00177; Ribosomal_S7; 1.
CC ProDom; PD000817; Ribosomal_S7; 1.
CC TIGRFAMs; TIGR01029; rpsG_bact; 1.
CC PROSITE; PS00052; RIBOSOMAL_S7; 1.
CC Ribosomal protein; RNA-binding; rRNA-binding; tRNA-binding;
CC Complete proteome.
CC KW
CC SEQUENCE 156 AA; 17942 MW; C82E39470D6C4542 CRC64;

Query Match 4.2%; Score 6; DB 1; Length 156;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 ERNVEA 41
DB 142 ERNVEA 147
|||||

RESULT 28
Y839_HELHP
ID Y839_HELHP STANDARD; PRT; 157 AA.
AC PS9821;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Hypothetical UPF0090 protein H80839.
GN H80839.

OS Helicobacter hepaticus.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=32025;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 51449 / 3B1;
RX MEDLINE=22709201; PubMed=12810954;
RA Suerbaum S., Josenhans C., Sterzenbach T., Drescher B., Brandt P.,
RA Bell M., Droege M., Partmann B., Fischer H.-P., Ge Z., Hoerster A.,
RA Holland R., Klein K., Koenig J., Macko L., Mendz G.L., Nyakatura G.,
RA Schauer D.B., Shen Z., Weber J., Frosch M., Fox J.G.;
RT "The complete genome sequence of the carcinogenic bacterium
RT Helicobacter hepaticus."
RL Proc. Natl. Acad. Sci. U.S.A. 100:7901-7906(2003).
CC -!- SIMILARITY: Belongs to the UPF0090 family.
CC -----

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CC -----

CC EMBL; AS017146; AAP7436.1; -
CC HAMAP; MF_01077; -; 1.
CC InterPro; IPR003728; DUF150.
CC Pfam; PF02576; DUF150; 1.
CC KW Hypothetical protein; Complete proteome.
CC SEQUENCE 157 AA; 17843 MW; 574FE08D88473BCD CRC64;

Query Match 4.2%; Score 6; DB 1; Length 157;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 135 IEQLAA 140
DB 10 IEQLAA 15
|||||

RESULT 29
UBC7_WHEAT
ID UBC7_WHEAT STANDARD; PRT; 168 AA.
AC P25868;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ubiquitin-conjugating enzyme E2 7 (EC 6.3.2.19) (Ubiquitin-protein
DE ligase 7) (Ubiquitin carrier protein 7).
GN UBC7.
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A., AND FUNCTION.
RC STRAIN=cv. Augusta;
RX MEDLINE=92052257; PubMed=1658801;
RA van Nocker S., Vierstra R.D.;
RT "Cloning and characterization of a 20-kDa ubiquitin carrier protein
RT from wheat that catalyzes multiubiquitin chain formation in vitro.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:10297-10301(1991).
CC -!- FUNCTION: Catalyzes the covalent attachment of ubiquitin to other
CC proteins so as to signal them for selective protein degradation.
CC Involved in the formation of multiubiquitin chains.
CC -!- CATALYTIC ACTIVITY: ATP + ubiquitin + protein lysine = AMP +
CC diphosphate + protein N-ubiquityllysine.
CC -!- PATHWAY: Ubiquitin conjugation; second step.
CC -!- MISCELLANEOUS: A cysteine residue is required for ubiquitin-
CC thiolester formation (By similarity).
CC -!- SIMILARITY: Belongs to the ubiquitin-conjugating enzyme family.
CC -----

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CC -----

CC EMBL; M74077; -; NOT_ANNOTATED_CDS.
CC PIR; A41547; A41547.
CC HSP; Q02159; 2UCZ.
CC InterPro; IPR000608; UBQ_conjugat.
CC Pfam; PF00179; UBQ_con; 1.
CC ProDom; PD000461; UBQ_conjugat; 1.
CC SMART; SM00212; UBQC; 1.
CC PROSITE; PS00183; UBIQUITIN_CONJUGAT_1; 1.
CC PROSITE; PS00127; UBIQUITIN_CONJUGAT_2; 1.
CC KW Ubiquitin-conjugation pathway; Ligase; Multigene family.
FT BINDING 92 92 UBIQUITIN (BY SIMILARITY).
SQ SEQUENCE 168 AA; 18897 MW; 6ED5127DCAB415E2 CRC64;

Query Match 4.2%; Score 6; DB 1; Length 168;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 KKVRRR 134
DB 155 KKVRRR 160
|||||

RESULT 30

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HSLV SHEON
ID HSLV SHEON STANDARD; PRT; 173 AA.
AC Q859V0;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DE ATP-dependent protease hslv (EC 3.4.25.-)
GN HSLV OR S04162
OS Shewanella oneidensis
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Alteromonadaceae; Shewanella.
NCBI_TaxID=70863;
RX STRAIN=MR-1;
RC SEQUENCE FROM N.A.
RX MEDLINE=22297686; PubMed=12368813;
RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
RA Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A.,
RA Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,
RA Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M.,
RA Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,
RA Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A.,
RA Feldblyum T.V., Smith H.O., Venter J.C., Neilsen K.H., Fraser C.M.;
RT "Genome sequence of the dissimilatory metal ion-reducing bacterium
RT Shewanella oneidensis."
RL Nat. Biotechnol. 20:1118-1123(2002).
CC -!- FUNCTION: Protease subunit of a proteasome-like degradation
CC complex (By similarity).
CC -!- SUBUNIT: A double ring-shaped homohexamer of hslv is capped on
CC each side by a ring-shaped hslu homohexamer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to peptidase family T1B. Hslv subfamily.
CC
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CC
CC EMBL; AF015849; AAN57135.1; -
CC TIGR; S04162; -
CC DR HAMAP; MF_00248; -; 1.
CC DR InterPro; IPR001353; Peptidase T1.
CC DR Pfam; PF00227; Proteasome; 1.
CC DR Hydrolase; Protease; Threonine protease; Complete proteome.
CC KW Hydrolyase; Protease; Threonine protease; Complete proteome.
CC FT INIT MET 0 0 BY SIMILARITY.
CC FT ACT_SITE 1 1 BY SIMILARITY.
CC SQ SEQUENCE 173 AA; 18786 MW; D33F5899C04783F2 CRC64;

Query Match 4.2%; Score 6; DB 1; Length 173;
Best Local Similarity 100.0%; Pred.No. 93;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 128 AKKVR 133
DB 31 AKKVR 36

RESULT 31
HSLV YERPE
ID HSLV YERPE STANDARD; PRT; 173 AA.
AC Q82J04;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE ATP-dependent protease hslv (EC 3.4.25.-)
GN HSLV OR YP00106 OR Y0295.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.

HSLV SHEON
ID HSLV SHEON STANDARD; PRT; 173 AA.
AC Q859V0;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DE ATP-dependent protease hslv (EC 3.4.25.-)
GN HSLV OR S04162
OS Shewanella oneidensis
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Alteromonadaceae; Shewanella.
NCBI_TaxID=70863;
RX STRAIN=MR-1;
RC SEQUENCE FROM N.A.
RX MEDLINE=22297686; PubMed=12368813;
RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
RA Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A.,
RA Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,
RA Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M.,
RA Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,
RA Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A.,
RA Feldblyum T.V., Smith H.O., Venter J.C., Neilsen K.H., Fraser C.M.;
RT "Genome sequence of the dissimilatory metal ion-reducing bacterium
RT Shewanella oneidensis."
RL Nat. Biotechnol. 20:1118-1123(2002).
CC -!- FUNCTION: Protease subunit of a proteasome-like degradation
CC complex (By similarity).
CC -!- SUBUNIT: A double ring-shaped homohexamer of hslv is capped on
CC each side by a ring-shaped hslu homohexamer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to peptidase family T1B. Hslv subfamily.
CC
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CC
CC EMBL; AF015849; AAN57135.1; -
CC TIGR; S04162; -
CC DR HAMAP; MF_00248; -; 1.
CC DR InterPro; IPR001353; Peptidase T1.
CC DR Pfam; PF00227; Proteasome; 1.
CC DR Hydrolase; Protease; Threonine protease; Complete proteome.
CC KW Hydrolyase; Protease; Threonine protease; Complete proteome.
CC FT INIT MET 0 0 BY SIMILARITY.
CC FT ACT_SITE 1 1 BY SIMILARITY.
CC SQ SEQUENCE 173 AA; 18786 MW; D33F5899C04783F2 CRC64;

Query Match 4.2%; Score 6; DB 1; Length 173;
Best Local Similarity 100.0%; Pred.No. 93;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 128 AKKVR 133
DB 31 AKKVR 36

RESULT 32
HSLV PSEPK
ID HSLV PSEPK STANDARD; PRT; 175 AA.
AC Q88D28;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DE ATP-dependent protease hslv (EC 3.4.25.-)
GN HSLV OR PP5000.
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.

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OX NCBI_TaxID=160488;
RN SEQUENCE FROM N.A.
RX MEDLINE=22423060; PubMed=12534463;
RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,
RA Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,
RA Chris Lee P., Holzapple E., Scanlan D., Tran K., Moazzes A.,
RA Uterback T., Rizzo M., Lee K., Koback D., Moesti D., Wedler H.,
RA Lauber J., Stjepandic D., Hohesael J., Straetz M., Heim S.,
RA Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuermler B.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative analysis of the
RT metabolically versatile Pseudomonas putida KT2440."
RL Environ. Microbiol. 4:799-808(2002).
CC -!- FUNCTION: Protease subunit of a proteasome-like degradation
CC complex (By similarity).
CC -!- SUBUNIT: A double ring-shaped homohexamer of hslv is capped on
CC each side by a ring-shaped hslU homohexamer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to peptidase family T1B. Hslv subfamily.
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CC
DR EMBL; AF016792; AAN70566.1; -
DR TIGR; PF5000; -
DR HAMAP; MF_00248; -; 1
DR InterPro; IPR001353; Peptidase_T1.
DR Pfam; PF00227; Proteasome; 1
KW Hydrolase; Protease; Threonine protease; Complete proteome.
FT INIT MET 0 0 BY SIMILARITY.
FT ACT SITE 1 1 BY SIMILARITY.
SQ SEQUENCE 175 AA; 18635 MW; 7789B55A54152B8B CRC64;

Query Match 4.2%; Score 6; DB 1; Length 175;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 128 AKKVR 133
Db |||||
31 AKKVR 36

RESULT 33
HSLV_PSESM STANDARD; PRT; 175 AA.
AC Q87V01;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE ATP-dependent protease hslv (EC 3.4.25.-).
GN HSLV OR PSPT05140.
OS Pseudomonas syringae (pv. tomato).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=323;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DC3000;
RX MEDLINE=22834015; PubMed=12928499;
RA Buell C.R., Joardar V., Lindeberg M., Selengut J., Paulsen I.T.,
RA Gwinn M.L., Dodson R.J., DeBoy R.T., Durkin A.S., Kolonay J.F.,
RA Madupu R., Daugherty S., Brinkac L., Reanan M.J., Haft D.H.,
RA Nelson W.C., Davidson T., Zafar N., Zhou L., Liu J., Yuan Q.,
RA Khouri H., Fedorova N., Tran B., Russell D., Berry K., Uterback T.,
RA Van Aken S.E., Feldblyum T.V., D'Ascenzo M., Deng W.-L., Ramos A.R.,

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RA Alfano J.R., Cartinhour S., Chatterjee A.K., Delaney T.P.,
RA Lazarewitz S.G., Martin G.B., Schneider D.J., Tang X., Bender C.L.,
RA White O., Fraser C.M., Collmer A.;
RT "The complete genome sequence of the Arabidopsis and tomato pathogen
RT Pseudomonas syringae pv. tomato DC3000."
RL Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186(2003).
CC -!- FUNCTION: Protease subunit of a proteasome-like degradation
CC complex (By similarity).
CC -!- SUBUNIT: A double ring-shaped homohexamer of hslv is capped on
CC each side by a ring-shaped hslU homohexamer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to peptidase family T1B. Hslv subfamily.
CC
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CC
DR EMBL; AF016874; AAC58567.1; -
DR TIGR; PSPT05140; -; 1
DR HAMAP; MF_00248; -; 1
DR InterPro; IPR001353; Proteasome; 1
DR Pfam; PF00227; Proteasome; 1
KW Hydrolase; Protease; Threonine protease; Complete proteome.
FT INIT MET 0 0 BY SIMILARITY.
FT ACT SITE 1 1 BY SIMILARITY.
SQ SEQUENCE 175 AA; 18695 MW; 8DBF852C017E80C2 CRC64;

Query Match 4.2%; Score 6; DB 1; Length 175;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 128 AKKVR 133
Db |||||
31 AKKVR 36

RESULT 34
IPYR_ECOL6 STANDARD; PRT; 175 AA.
AC Q8FAG0;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phospho-
DE hydrolase) (Pase).
GN PPA OR CS323.
OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=217992;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O6.H1 / CFT073 / ATCC 700928;
RX MEDLINE=22382334; PubMed=12471157;
RA Welch R.A., Surland V., Plunkett G. III, Redford P., Roesch P.,
RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Ferna N.T.,
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
RT of uropathogenic Escherichia coli."
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
CC -!- CATALYTIC ACTIVITY: Diphosphate + H(2)O = 2 phosphate.
CC -!- COFACTOR: Binds 4 magnesium ions per subunit. Other metal ions can
CC support activity, but at a lower rate. Two magnesium ions are
CC required for the activation of the enzyme and are present before
CC substrate binds. Two additional magnesium ions form complexes with
CC substrate and product (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the Ppase family.

```

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CC EMBL: AE016771; AAN83744.1; --
 DR HANAP, MF 00209; 1; Inorg_pphsph.
 DR InterPro: IPR008163; Inorg_pphsph.
 DR InterPro: IPR008163; Pyrophosphatase.
 DR Pfam: PF00719; Pyrophosphatase; 1.
 DR ProDom: PD002014; Inorg_pphsph; 1.
 DR PROSITE: PS00387; PPASE; 1.
 KW Hydrolase; Metal-binding; Magnesium; Complete proteome.
 FT INIT MET 0 0 BY SIMILARITY.
 FT METAL 65 65 MAGNESIUM 1 (BY SIMILARITY).
 FT METAL 70 70 MAGNESIUM 1 AND 2 (BY SIMILARITY).
 FT METAL 102 102 MAGNESIUM 1 (BY SIMILARITY).
 SQ SEQUENCE 175 AA; 19600 MW; 7DBAE4D08DAD8FDB CRC64;

Query Match 4.2%; Score 6; DB 1; Length 175;

Best Local Similarity 100.0%; Pred. No. 94; Gaps 0;

Matches 6; Conservative 0; Mismatches 0; Indels 0;

Qy 107 ERAKKNK 112

Db 170 ERAKKNK 175

RESULT 35

ID IPYR_ECOLI STANDARD; PRT; 175 AA.
 AC P17288;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phospho-
 DE hydrolase) (Ppase).
 GN PPA OR B4226 OR Z5837 OR RCS5204.
 OS Escherichia coli, and
 OS Escherichia coli O157:H7.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562, 83334;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=89053923; PubMed=2848015;
 RA Lahti R., Pitkaranta T., Valve E., Ilta I., Kukko-Kalske E.,
 RA Heinonen J.;
 RT "Cloning and characterization of the gene encoding inorganic
 RT pyrophosphatase of Escherichia coli K-12.";
 RL J. Bacteriol. 170:5901-5907(1988).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=95334362; PubMed=7610040;
 RA Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
 RA Blattner F.R.;
 RT "Analysis of the Escherichia coli genome VI: DNA sequence of the
 RT region from 92.8 through 100 minutes.";
 RL Nucleic Acids Res. 23:2105-2119(1995).
 [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
 RX MEDLINE=21074935; PubMed=11206551;
 RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
 RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
 RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamouis K.,

RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
 RA Welch R.A., Blattner F.R.;
 RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
 RL Nature 409:529-533(2001).
 [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=O157:H7 / RIMD 0509952;
 RX MEDLINE=21156231; PubMed=11258796;
 RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
 RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
 RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
 RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
 RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
 RT O157:H7 and genomic comparison with a laboratory strain K-12.";
 RL DNA Res. 8:11-22(2001).
 [5]
 RP SEQUENCE OF 1-20 AND 94-105.
 RC STRAIN=K12 / EMG2; PubMed=9298646;
 RX MEDLINE=97443975; PubMed=9298646;
 RA Link A.J., Robison K., Church G.M.;
 RT "Comparing the predicted and observed properties of proteins encoded
 RT in the genome of Escherichia coli K-12.";
 RL Electrophoresis 18:1259-1313(1997).
 [6]
 RP SIMILARITY TO YEAST AND K.LACTIS PPASES.
 RX MEDLINE=90254161; PubMed=2160278;
 RA Lahti R., Kolakowski L.P. Jr., Heinonen J., Vihinen M., Pohjanoksa K.,
 RA Cooperman B.S.;
 RT "Conservation of functional residues between yeast and E. coli
 RT inorganic pyrophosphatases.";
 RL Biochim. Biophys. Acta 1038:338-345(1990).
 [7]
 RP MUTAGENESIS.
 RX MEDLINE=90344799; PubMed=1974462;
 RA Lahti R., Pohjanoksa K., Pitkaranta T., Heikinheimo P., Salminen T.,
 RA Meyer P., Heinonen J.;
 RT "A site-directed mutagenesis study on Escherichia coli inorganic
 RT pyrophosphatase. Glutamic acid-98 and lysine-104 are important for
 RT structural integrity, whereas aspartic acids-97 and -102 are
 RT essential for catalytic activity.";
 RL Biochemistry 29:5761-5766(1990).
 [8]
 RP MUTAGENESIS OF TYROSINE RESIDUES.
 RX MEDLINE=91249822; PubMed=1645654;
 RA Lahti R., Salminen T., Latonen S., Heikinheimo P., Pohjanoksa K.,
 RA Heinonen J.;
 RT "Genetic engineering of Escherichia coli inorganic pyrophosphatase.
 RT Tyr55 and Tyr141 are important for the structural integrity.";
 RL Eur. J. Biochem. 198:293-297(1991).
 [9]
 RP MODIFICATION OF TYR-149.
 RX MEDLINE=93185983; PubMed=8383066;
 RA Kaneko S., Ichiba T., Hirano N., Hachimori A.;
 RT "Modification of tryptophan 149 of inorganic pyrophosphatase from
 RT Escherichia coli.";
 RL Int. J. Biochem. 25:233-238(1993).
 [10]
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
 RX MEDLINE=95062129; PubMed=7971944;
 RA Kankare J., Neal G.S., Salminen T., Glumhoffer T., Cooperman B.S.,
 RA Lahti R., Goldman A.;
 RT "The structure of E.coli soluble inorganic pyrophosphatase at 2.7-A
 RT resolution.";
 RL Protein Eng. 7:823-830(1994).
 [11]
 RP ERRATUM.
 RA Kankare J., Neal G.S., Salminen T., Glumhoffer T., Cooperman B.S.,
 RA Lahti R., Goldman A.;
 RL Protein Eng. 7:1173-1173(1994).
 [12]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RX MEDLINE=96267057; PubMed=8664256;
 RA Kankare J., Salminen T., Lahti R., Cooperman B.S., Baykov A.A.,

RA Goldman A.;
RT "Crystallographic identification of metal-binding sites in
RL Escherichia coli inorganic pyrophosphatase.";
RN Biochemistry 35:4670-4677(1996).
[13]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RA Kankare J., Salminen T., Lahti R., Cooperman B.S., Baykov A.A.,
RA Goldman A.;
RT "Structure of Escherichia coli inorganic pyrophosphatase at 2.2-A
RT resolution.";
RL Acta Crystallogr. D 52:551-563(1996).
RN [14]
RP X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS).
RX MEDLINE=97379370; PubMed=9237692;
RA Aavaeva S., Kurilova S., Nazarova T., Rodina E., Vorobyeva N.,
RA Sklyankina V., Grigorjeva O., Hartunyan E., Oganessyan V.,
RA Wilson K., Dauter Z., Huber R., Mather T.;
RT "Crystal structure of Escherichia coli inorganic pyrophosphatase
RT complexed with SO4(2-). Ligand-induced molecular asymmetry.";
RL FEBS Lett. 410:502-508(1997).
RN [15]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=97352630; PubMed=9201917;
RA Hartunyan E.H., Oganessyan V.Y., Oganessyan N.N., Aavaeva S.M.,
RA Nazarova T.I., Vorobyeva N.N., Kurilova S.A., Huber R., Mather T.;
RT "Crystal structure of holo inorganic pyrophosphatase from Escherichia
RT coli at 1.9 A resolution. Mechanism of hydrolysis.";
RL Biochemistry 36:7754-7760(1997).
CC -!- CATALYTIC ACTIVITY: Diphosphate + H(2)O = 2 phosphate.
CC -!- COFACTOR: Binds 4 magnesium ions per subunit. Other metal ions can
CC support activity, but at a lower rate. Two magnesium ions are
CC required for the activation of the enzyme and are present before
CC substrate binds, two additional magnesium ions form complexes with
CC substrate and product.
CC -!- SUBUNIT: Homohexamer.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the PPase family.

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DR EMBL; M23550; AAB88583.1; -;
DR EMBL; U14003; AAA97123.1; -;
DR EMBL; AB000494; AAC77183.1; -;
DR EMBL; AB000565; AAG59424.1; -;
DR EMBL; AF002568; BAB38627.1; -;
DR PIR; A27648; PWEC.
DR PIR; D86120;
DR PIR; D91279; D91279.
DR PDB; 1FAJ; 08-NOV-96.
DR PDB; 1IGF; 20-DEC-94.
DR PDB; 1INO; 03-APR-96.
DR PDB; 1IPW; 20-AUG-97.
DR PDB; 1JFD; 03-DEC-97.
DR PDB; 1MWJ; 03-DEC-97.
DR PDB; 1MXJ; 03-DEC-97.
DR PDB; 1MYJ; 03-DEC-97.
DR PDB; 1MUZ; 03-DEC-97.
DR PDB; 1OBW; 04-SEP-97.
DR PDB; 2EIP; 08-NOV-96.
DR SWISS-2DPAGE; P17288; COLI.
DR EcoGene; EG10755; ppa.
DR HAMAP; MF 00209; -; 1.
DR InterPro; IPR008163; Inorg_pphsh.
DR InterPro; IPR008162; Pyrophosphatase.
DR Pfam; PF00719; Pyrophosphatase; 1.
DR ProDom; PD002014; Inorg_pphsh; 1.
DR PROSITE; PS00387; PPASE; 1.

KW Hydrolase; Metal-binding; Magnesium; 3D-structure; Complete proteome.
FT INIT_MET 0
FT METAL 65 65 MAGNESIUM 1.
FT METAL 70 70 MAGNESIUM 1 AND 2.
FT METAL 102 102 MAGNESIUM 1.
FT MUTAGEN 20 20 E->D: 16% ACTIVITY.
FT MUTAGEN 29 29 K->R: 2% ACTIVITY.
FT MUTAGEN 31 31 E->D: 6% ACTIVITY.
FT MUTAGEN 43 43 R->K: 10% ACTIVITY.
FT MUTAGEN 51 51 Y->F: 64% ACTIVITY.
FT MUTAGEN 55 55 Y->F: 7% ACTIVITY.
FT MUTAGEN 65 65 D->E: 6% ACTIVITY.
FT MUTAGEN 67 67 D->E: 1% ACTIVITY.
FT MUTAGEN 70 70 D->E: NO ACTIVITY.
FT MUTAGEN 97 97 D->E: 22% ACTIVITY.

Query Match 4.2%; Score 6; DB 1; Length 175;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 ERAKNK 112
| | | | |
DB 170 ERAKNK 175

RESULT 36
HSLV PSEAE STANDARD; PRT; 176 AA.
ID HSLV PSEAE
AC QSHUC6; 2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE ATP-dependent protease hslv (EC 3.4.25.-).
GN HSLV OR PA5053.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Brody L.L., Coulter S.N., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Smith K.A., Spencer D.H., Hancock R.E.W., Lory S., Olson M.V.;
RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
CC -!- FUNCTION: Protease subunit of a proteasome-like degradation
CC complex (By similarity).
CC -!- SUBUNIT: A double ring-shaped homohexamer of hslv is capped on
CC each side by a ring-shaped helu homohexamer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to peptidase family T1B. Hslv subfamily.

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DR EMBL; AE004918; AAG08438.1; -;
DR PIR; D83015; D83015.
DR HSSP; P31059; 1B94.
DR MEROPS; T01.006; -;
DR HAMAP; MF_00248; -; 1.
DR InterPro; IPR001353; Peptidase_T1.
DR Pfam; PF00227; proteasome; 1.

KW Hydrolase; Protease; Threonine protease; Complete proteome.

FT INIT MET 0 BY SIMILARITY.

FT ACT SITE 1 BY SIMILARITY.

SQ SEQUENCE 176 AA; 18654 MW; 291076FF451B5B09 CRC64;

Query Match 4.2%; Score 6; DB 1; Length 176;

Best Local Similarity 100.0%; Pred. No. 94; 0; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 0;

YQ 128 AKVRR 133

Db 31 AKVRR 36

RESULT 37

YGV5 YEAST

ID YGV5 YEAST

AC P53071;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 01-OCT-1996 (Rel. 34, Last annotation update)

DE Hypothetical 19.3 kDa protein in HAP2-ADE5,6 intergenic region.

GN YGL235W.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.

OX NCBI_TaxID=4932;

RN [1]

RP SEQUENCE FROM N.A.

RA Farman B., Kramer B., Kramer W.;

RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.

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CC -----

DR EMBL; 272758; CAA96954.1; --

DR PIR; S64257; S64257.

DR Germonline; 141284; --

DR SGD; S0003204; YGL235W.

KW Hypothetical protein.

SQ SEQUENCE 178 AA; 19334 MW; 2972A987E576A6E9 CRC64;

Query Match 4.2%; Score 6; DB 1; Length 178;

Best Local Similarity 100.0%; Pred. No. 95;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

YQ 83 GCAPLS 88

Db 25 GCAPLS 30

RESULT 38

YJV7 YEAST

ID YJV7 YEAST

AC P40853;

DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 01-OCT-1996 (Rel. 34, Last annotation update)

DE Hypothetical 22.0 kDa protein in HX11-HX18 intergenic region.

GN YJL217W OR J0226 OR HRC198.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.

OX NCBI_TaxID=4932;

RN [1]

RP SEQUENCE FROM N.A.

RA STRAIN=S288c;

RX MEDLINE=95242842; PubMed=7725802;

RA Vandebol M., Durand P., Bolle P.-A., Dion C., Portetelle D.,

RA Hilger F.;

RT "Sequence analysis of a 40.2 kb DNA fragment located near the left

RT telomere of yeast chromosome X.;"

RL Yeast 10:1657-1662(1994).

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CC -----

DR EMBL; 234098; CAA83993.1; --

DR EMBL; 249492; CAA89514.1; --

DR PIR; S50710; S50710.

DR Germonline; 141829; --

DR SGD; S0003753; YJL217W.

KW Hypothetical protein.

SQ SEQUENCE 198 AA; 21967 MW; 52F6BE7CEA722D37 CRC64;

Query Match 4.2%; Score 6; DB 1; Length 198;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

YQ 32 ACTPER 37

Db 169 ACTPER 174

RESULT 39

RNH2 FORGI

ID RNH2 FORGI

AC Q51832;

DT 30-MAY-2000 (Rel. 39, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Ribonuclease HII (EC 3.1.26.4) (RNase HII).

GN RNHB OR PG0736.

OS Porphyromonas gingivalis (Bacteroides gingivalis).

OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;

OC Porphyromonadaceae; Porphyromonas.

OX NCBI_TaxID=837;

RN [1]

RP SEQUENCE FROM N.A.

RA STRAIN=W83;

RX MEDLINE=22629867; PubMed=12949112;

RA Nelson K.E., Fleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts D.E.,

RA Eisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwin M.,

RA Haft D.H., Kolonay J.F., Nelson W.C., Mason T., Tallon L., Gray J.,

RA Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J.,

RA Dewhirst F.E., Fraser C.M.;

RT "Complete genome sequence of the oral pathogenic bacterium

RT Porphyromonas gingivalis strain W83.;"

RL J. Bacteriol. 185:5591-5601(2003).

RN [2]

RP SEQUENCE OF 34-201 FROM N.A.

RC STRAIN=W83;

RA Rigg G.P., Roberts I.S.;

RT "Molecular analysis of PgaA an antigen from periodontopathogen

RT Porphyromonas gingivalis.;"

RT Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: This enzyme is an endonuclease that degrades the RNA of

CC RNA-DNA hybrids specifically (By similarity).

CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-

CC phosphomonoester.

CC -!- COFACTOR: Manganese (By similarity).

CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).

CC -!- SIMILARITY: Belongs to the RNase HII family.

CC -----

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DR EMBL; A5017174; RAQ65905.1; --
 DR EMBL; X59338; CAAG5177.1; --
 DR TIGR; PG0736; --
 DR HAMAP; MF_00052; -- 1.
 DR InterPro; IPR001352; RNase_HII/HIII.
 DR Pfam; PF01351; RNase_HII; 1.
 KW Hydrolase; Nuclease; Endonuclease; Manganese; Complete proteome.
 FT ACT_SITE 17 17 BY SIMILARITY.
 FT ACT_SITE 109 109 BY SIMILARITY.
 FT ACT_SITE 128 128 BY SIMILARITY.
 SQ SEQUENCE 201 AA; 22733 MW; 812CF1455A59B20C CRC64;

Query Match 4.2%; Score 6; DB 1; Length 201;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 133 RATEQL 138
 DB 94 RATEQL 99

RESULT 40

TRI_PONLE STANDARD; PRT; 201 AA.
 AC P05547;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Troponin I.
 OS leptoactylus (Narrow-fingered crayfish) (Astacus
 leptoactylus).
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
 CC Astacoidea; Astacidae; Pontastacus.
 OX NCBI_TaxID=6717;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=89109165; PubMed=2912973;
 RA Kobayashi T., Takagi T., Konishi K., Cox J.A.;
 RT "Amino acid sequence of crayfish troponin I.";
 RL J. Biol. Chem. 264:1551-1557(1989).
 CC -!- FUNCTION: Troponin I is the actomyosin ATPase inhibitory subunit
 CC present in the thin filament regulatory complex.
 CC -!- MISCELLANEOUS: There is a 30 residue long N-terminal tail that
 CC does not occur in skeletal muscle Tni's, but is present in cardiac
 CC muscle Tni's.
 CC -!- SIMILARITY: Belongs to the troponin I family.
 DR InterPro; IPR001978; Troponin.
 DR Pfam; PF00992; Troponin; 1.
 KW Methylation; Actin-binding; Acetylation.
 FT MOD_RES 1 1 ACETYLATION (PROBABLE).
 FT MOD_RES 142 142 METHYLATION (TRI-).
 FT MOD_RES 146 146 METHYLATION (TRI-).
 FT DOMAIN 108 117 TROPONIN T-INTERACTION.
 FT DOMAIN 135 148 ACTIN-BINDING.
 SQ SEQUENCE 201 AA; 23490 MW; 47595EB56DB88A65 CRC64;

Query Match 4.2%; Score 6; DB 1; Length 201;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 120 KKKEFE 125
 DB 175 KKKEFE 180

RESULT 41

ZFP_IRV6 STANDARD; PRT; 208 AA.
 ID ZFP_IRV6
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Zinc finger protein.
 OS Chilo iridescent virus (CIV) (Insect iridescent virus type 6).
 CC Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Iridovirus.
 OX NCBI_TaxID=10488;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92196996; PubMed=1549908;
 RA Handermann M., Schnitzler P., Roesen-Wolff A.P., Raab K.,
 Sontag K.C., Darai G.;
 RT "Identification and mapping of origins of DNA replication within the
 RT DNA sequences of the genome of insect iridescent virus type 6";
 RL Virus Genes 6:19-32(1992).
 CC [2]

CC REVISIONS TO C-TERMINUS.
 RA Jakob N.J., Mueller K., Bahr U., Darai G.;
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Contains 1 BIR repeat.
 CC -!- SIMILARITY: Contains 1 RING-type zinc finger.

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DR EMBL; AF303741; AAB94481.1; --
 DR HSSP; O15392; 1B31.
 DR InterPro; IPR001370; BIR.
 DR InterPro; IPR001841; Znf_ring.
 DR Pfam; PF00653; BIR; 1.
 DR Pfam; PF00097; zf-C3HC4; 1.
 DR SMART; SMO0238; BIR; 1.
 DR SMART; SMO0184; RING; 1.
 DR PROSITE; PS01282; BIR_REPEAT_1; FALSE_NEG.
 DR PROSITE; PS50143; BIR_REPEAT_2; 1.
 DR PROSITE; PS00516; ZF_RING_1; FALSE_NEG.
 DR PROSITE; PS50089; ZF_RING_2; 1.
 KW Zinc-finger; Repeat.
 FT REPEAT 37 108 BIR.
 FT DOMAIN 134 151 3 X 6 AA TANDEM REPEATS.
 FT REPEAT 134 139 1.
 FT REPEAT 140 145 2.
 FT REPEAT 146 151 3.
 FT ZN_FING 163 197 RING-TYPE.
 SQ SEQUENCE 208 AA; 24142 MW; 41A2E2FC18833390 CRC64;

Query Match 4.2%; Score 6; DB 1; Length 208;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 BEHKKH 80
 DB 92 BEHKKH 97

RESULT 42

CYB6_EUGGR STANDARD; PRT; 214 AA.
 ID CYB6_EUGGR
 AC P31480;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Cytochrome b6.
 GN PETE.
 OS Euglena gracilis.


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RESULT 44
YG30 YEAST
ID_YG30 YEAST STANDARD; PRT; 217 AA.
AC P48238;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical 25.2 kDa protein in RSRI-CYS4 intergenic region.
GN YGR153W OR G6661.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=96158062; PubMed=8585325;
RA Skala J., Nawrocki A., Goffeau A.;
RT "The sequence of a 27 kb segment on the right arm of chromosome VII
from Saccharomyces cerevisiae reveals MOLI, NAT2, RPL30B, RSRI, CYS4,
PEM1/CHC2, NSRI genes and ten new open reading frames.";
RL Yeast 11:1421-1427(1995).
CC
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CC
CC
CC EMBL; X85807; CAA59810.1; -;
CC EMBL; Z72938; CAA97167.1; -;
CC PIR; S60443; S60443.
CC Germline; 141465; -.
CC SGD; S0003385; TOS10.
CC KW Hypothetical protein.
CC SEQUENCE 217 AA; 25213 MW; E507C7EBC095CED0 CRC64;
CC
CC
CC Query Match 4.2%; Score 6; DB 1; Length 217;
CC Best Local Similarity 100.0%; Pred. No. 1.1e+02;
CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 60 CFEKE 65
CC Db 160 CFEKE 165
CC
CC
CC RESULT 45
CC YMS1 ARCFU
CC ID_YMS1 ARCFU STANDARD; PRT; 229 AA.
CC AC Q28033;
CC DT 16-OCT-2001 (Rel. 40, Created)
CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
CC DE Hypothetical protein AF2251.
CC GN AF2251.
CC OS Archaeoglobus fulgidus.
CC OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
CC OC Archaeoglobaceae; Archaeoglobus.
CC OX NCBI_TaxID=2234;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
CC RX MEDLINE=98049343; PubMed=9389475;
CC RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
CC Ketchum K.A., Dodson R.J., Winn M., Hickey E.K., Peterson J.D.,
CC Richardson D.L., Kurlavsky A.R., Graham D.E., Kyrpides N.C.,
CC Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
CC Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
CC Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
CC Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
CC Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,

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SA dow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
RL Nature 390:364-370(1997).
CC -!- SIMILARITY: Belongs to the cinA family.
CC
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CC
CC
CC EMBL; AE00949; AAB89006.1; -;
CC PIR; C69531; C69531.
CC TIGR; AF2251; -.
CC HAMAP; MF_00226; -; 1.
CC InterPro; IPR001453; MOCF_biosynth.
CC Pfam; PF00994; MOCF_biosynth; 1.
CC ProDom; PD002460; MOCF_biosynth; 1.
CC TIGRFAMs; TIGR00177; molyb_syn; 1.
CC KW Hypothetical protein; Complete proteome.
CC SEQUENCE 229 AA; 25521 MW; DPF623780665EC81 CRC64;
CC
CC
CC Query Match 4.2%; Score 6; DB 1; Length 229;
CC Best Local Similarity 100.0%; Pred. No. 1.2e+02;
CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 91 KQFEEL 96
CC Db 219 KQFEEL 224
CC
CC
CC RESULT 46
CC YG61 FUSNN
CC ID_YG61 FUSNN STANDARD; PRT; 249 AA.
CC AC Q8E1E0;
CC DT 10-OCT-2003 (Rel. 42, Created)
CC DT 10-OCT-2003 (Rel. 42, Last sequence update)
CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
CC DE Hypothetical UPF0082 protein FN1661.
CC GN FN1661.
CC OS Fusobacterium nucleatum (subsp. nucleatum).
CC OC Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;
CC OC Fusobacterium.
CC OX NCBI_TaxID=76856;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=ATCC 25586;
CC RX MEDLINE=21886394; PubMed=11899109;
CC RA Kapatal V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
CC Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
CC Vasileva O., Chu L., Kogan I., Chaga O., Goltzman E., Bernal A.,
CC Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
CC Fonstein M., Kyrpides N., Overbeek R.;
CC RT "Genome sequence and analysis of the oral bacterium Fusobacterium
CC nucleatum strain ATCC 25586."
CC RL J. Bacteriol. 184:2005-2018(2002).
CC -!- SIMILARITY: Belongs to the UPF0082 family.
CC
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CC
CC
CC EMBL; AE010472; AAL93776.1; -;
CC HAMAP; MF_00693; -; 1.

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DR InterPro: IPR002876; DUF28.
DR Pfam: PF01709; DUF28; 1.
DR ProDom: PD004323; DUF28; 1.
DR TIGRFAMs: TIGR01033; TIGR01033; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 249 AA; 27768 MW; FC721F033467208A CRC64;

Query Match 4.2%; Score 6; DB 1; Length 249;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 126 ETAKKV 131
   |||||
Db 213 ETAKKV 218

RESULT 47
PUR7_SYNXPX STANDARD; PRT; 250 AA.
AC Q7U8Q9;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Phosphoribosylaminoimidazole-succinocarboxamide synthase (EC 6.3.2.6)
DE (SAICAR synthetase).
DE (SAICAR synthetase).
GN PURC OR SYNW0554.
OS Synechococcus sp. (strain WH8102).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=84588;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22825697; PubMed=12917641;
RA Palenik B., Brahamsha B., Latimer F.W., Land M., Hauser L., Chain P.,
RA Lamerdin J., Regala W., Allen E.E., McCarren J., Paulsen I.,
RA Dufresne A., Partensky F., Webb E.A., Waterbury J.;
RT "The genome of a motile marine Synechococcus."
RL Nature 424:1037-1042(2003).
CC -!- CATALYTIC ACTIVITY: ADP + 5-amino-1-(5-phospho-D-
CC ribosyl)imidazole-4-carboxylate + L-aspartate = ADP + phosphate +
CC (S)-2-[5-amino-1-(5-phospho-D-ribosyl)imidazole-4-
CC carboxamido]succinate.
CC -!- PATHWAY: De novo purine biosynthesis; seventh step.
CC -!- SIMILARITY: Belongs to the SAICAR synthetase family.
CC
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CC
CC EMBL; BX569690; CAE07069.1; -
CC HAMAP; MF 00137; -; 1.
CC InterPro: IPR001636; SAICAR synt.
CC Pfam; PF01259; SAICAR synt; 1.
CC ProDom; PD003043; SAICAR synt; 1.
CC TIGRFAMs; TIGR00081; purC; 1.
CC PROSITE; PS01057; SAICAR SYNTHETASE 1; 1.
CC PROSITE; PS01058; SAICAR SYNTHETASE 2; FALSE NEG.
KW Purine biosynthesis; Ligase; Complete proteome.
SQ SEQUENCE 250 AA; 28002 MW; 8E2B604EF31CBAF2 CRC64;

Query Match 4.2%; Score 6; DB 1; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 AIEQLA 139
   |||||
Db 152 AIEQLA 157

RESULT 48
LIVG_ARCFU STANDARD; PRT; 257 AA.
ID LIVG_ARCFU
AC O28881;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable branched-chain amino acid transport ATP-binding protein livg.
DE LIVG OR AF1390.
OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;

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OC Archaeoglobaceae; Archaeoglobus.
OX NCBI_TaxID=2234;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; PubMed=9389475;
RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
RA Richardson D.L., Krelage A.S., Graham D.E., Kyrpides N.C.,
RA Fleischmann R.D., Kerkubush J., Lee N.H., Sutton G.G., Gill S.,
RA Kirnesh E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA Peterson S., Reich C.I., McNeill L.K., Badger J.H., Glodek A., Zhou L.,
RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Uterback T.,
RA Cotton M.D., Spriggs T., Artchik P., Kane B.P., Sykes S.M.,
RA Sadow P.W., D'Andrea K.J., Bowman C., Fujii C., Garland S.A.,
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
RT reducing archaeon Archaeoglobus fulgidus."
RL Nature 390:364-370(1997).
CC -!- FUNCTION: Probable component of a branched-chain amino-acid
CC transport system.
CC -!- SIMILARITY: Belongs to the ABC transporter family.
CC
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CC
CC -----
CC EMBL; AF001008; AAB89855.1; ALT_INIT.
CC TIGR; AF1390; -.
CC InterPro; IPR003593; AAA ATPase.
CC InterPro; IPR003439; ABC transporter.
CC Pfam; PF00005; ABC_tran; 1.
CC ProDom; PD000006; ABC transporter; 1.
CC SMART; SM00382; AAA; 1.
CC PROSITE; PS00811; ABC_TRANSPORTER_1; 1.
CC PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
CC Amino-acid transport; Transport; ATP-binding; Complete proteome.
KW NP BIND 36 43 ATP (POTENTIAL).
FT SEQUENCE 257 AA; 28854 MW; A8D8397E0F3BB491 CRC64;
SQ
Query Match 4.2%; Score 6; DB 1; Length 257;
Best Local Similarity 100.0%; Pred.No.1.3e+02; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;
QY 100 EFLKLD 105
DB 134 EFLKLD 139
ID _SPRC_CABEL STANDARD; PRT; 264 AA.
AC P34714;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE SPARC precursor (Secreted protein acidic and rich in cysteine)
DE (Osteonectin) (ON) (Basement membrane protein BM-40).
DE OST-1 OR SPARC OR C4B12.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=94080020; PubMed=8257796;

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RA Schwarzbauer J.E., Spencer C.S.;
RT "The Caenorhabditis elegans homologue of the extracellular calcium
RT binding protein SPARC/osteonectin affects nematode body morphology
RT and mobility."
RL Mol. Biol. Cell 4:941-952(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX Tin-Wollam A.;
RA Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: HAS A HIGH AFFINITY FOR COLLAGEN. AFFECTS NEMATODE
CC BODY MORPHOLOGY AND MOBILITY. ESSENTIAL FOR C. ELEGANS DEVELOPMENT
CC AND MUSCLE FUNCTION. THE CYSTEINE-RICH REGION COULD HAVE PROTEASE
CC INHIBITORY ACTIVITY OR MAY PROVIDE THE FRAMEWORK FOR A PROTEIN
CC BINDING MODULE. PROBABLE ROLE IN SKELETAL MORPHOGENESIS.
CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC -!- TISSUE SPECIFICITY: EXPRESSED BY BODY WALL AND SEX MUSCLE CELLS.
CC PROBABLE ASSOCIATION WITH BASEMENT MEMBRANES.
CC -!- DEVELOPMENTAL STAGE: FIRST EXPRESSED IN UNHATCHED LARVAE;
CC CONTINUOUS THROUGHOUT SUBSEQUENT LARVAL STAGES AND IN ADULTS.
CC -!- SIMILARITY: Contains 1 osteonectin-like domain.
CC -!- SIMILARITY: Contains 1 Kazal-like domain.
CC -!- SIMILARITY: Contains 1 EF-hand calcium-binding domain.
CC
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CC
CC -----
CC EMBL; L21758; AAA16827.1; -.
CC EMBL; AF036692; AAB88325.1; -.
CC PIR; A47737; A47737.
CC HSPSP; P09486; ISRA.
CC WormPep; C44B12.2; CE08703.
CC InterPro; IPR002048; EF-hand.
CC InterPro; IPR003645; FcIn.
CC InterPro; IPR002350; Kazal.
CC InterPro; IPR001999; Osteonectin.
CC Pfam; PF00050; Kazal; 1.
CC SMART; SM00274; FcIn; 1.
CC SMART; SM00280; KAZAL; 1.
CC PROSITE; PS00018; EF_HAND; 1.
CC PROSITE; PS00612; OSTONECTIN_1; 1.
CC PROSITE; PS00613; OSTONECTIN_2; 1.
CC Extracellular matrix; Glycoprotein; Calcium-binding; Copper; Signal;
KW Developmental protein; Basement membrane.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 264 SPARC.
FT DOMAIN 75 135 KAZAL-LIKE.
FT CA_BIND 237 248 EF-HAND (BY SIMILARITY).
FT DISULFID 53 64 BY SIMILARITY.
FT DISULFID 58 74 BY SIMILARITY.
FT DISULFID 76 110 BY SIMILARITY.
FT DISULFID 80 103 BY SIMILARITY.
FT DISULFID 92 135 BY SIMILARITY.
FT DISULFID 141 228 BY SIMILARITY.
FT DISULFID 236 252 BY SIMILARITY.
FT CARBOHYD 96 96 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 243 243 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 264 AA; 30172 MW; 2F952056B466E18F CRC64;
Query Match 4.2%; Score 6; DB 1; Length 264;
Best Local Similarity 100.0%; Pred.No.1.4e+02; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;
QY 26 PFLEGC 31
DB 231 PFLEGC 236

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RESULT 51
TRY6_ANOGA
ID TRY6_ANOGA STANDARD; PRT; 273 AA.
AC P35040;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE TRYPsin 6 precursor (EC 3.4.21.4)
GN TRYP6.
OS Anopheles gambiae (African malaria mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
OX NCBI_TaxID=7165;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=Suakoko; TISSUE=Midgut;
RX MEDLINE=9332779; PubMed=8335004;
RA Mueller H.M., Crampton J.M., della Torre A., Sinden R., Crisanti A.;
RT "Members of a trypsin gene family in Anopheles gambiae are induced in
RT the gut by blood meal";
RL EMBO J. 12:2891-2900(1993).
CC -!- FUNCTION: Major function may be to aid in digestion of the blood
CC meal.
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lys-|-Xaa.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Midgut.
CC -!- SIMILARITY: Belongs to peptidase family S1.
CC -!- CAUTION: As this protein has Gly-222 in the position that
CC determines the specificity of the enzyme instead of the Asp found
CC in trypsins, it could have a chymotrypsin-like activity.
CC
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CC
CC EMBL: Z22930; CA80513.1; -.
CC PIR: S40003; S40003.
CC DR PIR: S40003; S40003.
CC HSP: P00761; 1EPT.
CC
CC MEROPS: S01.112; -.
CC
CC InterPro: IPR009003; Cys_Ser_trypsin.
CC DR InterPro: IPR001254; Peptidase_S1.
CC DR InterPro: IPR001314; Peptidase_S1A.
CC Pfam: PF00089; trypsin; 1.
CC PRINTS: PR00722; CHYMOTRYPSIN.
CC SMART: SM00020; TRYP_SPC; 1.
CC PROSITE: PSS00240; TRYPsin DOM; 1.
CC DR PROSITE: PS00134; TRYPsin HIS; 1.
CC DR PROSITE: PS00135; TRYPsin SER; FALSE NEG.
CC KW Hydroxylase; Serine protease; Signal; Zymogen; Digestion;
CC Multigene family.
CC FT SIGNAL 1 22 POTENTIAL.
CC FT PROPEP 23 46 ACTIVATION PEPTIDE.
CC FT CHAIN 47 273 TRYPsin 6.
CC FT ACT_SITE 87 87 CHARGE RELAY SYSTEM (BY SIMILARITY).
CC FT ACT_SITE 132 132 CHARGE RELAY SYSTEM (BY SIMILARITY).
CC FT ACT_SITE 228 228 CHARGE RELAY SYSTEM (BY SIMILARITY).
CC FT DISULFID 72 88 BY SIMILARITY.
CC FT DISULFID 197 213 BY SIMILARITY.
CC FT DISULFID 224 248 BY SIMILARITY.
CC FT SITE 222 222 REQUIRED FOR SPECIFICITY (BY SIMILARITY).
CC SQ SEQUENCE 273 AA; 29373 MW; 83ED22152BFD2D66 CRC64;

Query Match 4.2%; Score 6; DB 1; Length 273;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 DDPFEE 76
DB 157 DDPFEE 162

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RESULT 52
SPEE_PYRFU
ID SPEE_PYRFU STANDARD; PRT; 281 AA.
AC Q8U4G1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Probable spermidine synthase (EC 2.5.1.16) (Putrescine
DE aminopropyltransferase) (SPDSV).
GN SPEE OR PF0127.
OS Pyrococcus furiosus.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=2261;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=Vc1 / DSM 3638 / ATCC 43587 / JCM 8422;
RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
RT "The complete sequence of the Pyrococcus furiosus genome.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: S-adenosylmethionine + putrescine = 5'-
CC methylthioadenosine + spermidine.
CC -!- PATHWAY: Spermidine biosynthesis; fifth (last) step.
CC -!- SIMILARITY: Belongs to the spermidine/spermine synthase family.
CC
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CC
CC EMBL: AB010139; AAL80251.1; -.
CC PDB: 1MJF; 18-SEP-02.
CC DR HAMAP: MF_00198; -.
CC DR InterPro: IPR000051; SAM_bind.
CC DR InterPro: IPR001045; Spermine synthase.
CC Pfam: PF01564; Spermine synth; 1.
CC DR TIGRFAMs: TIGR00417; speE; 1.
CC DR PROSITE: PS01330; SPERMIDINE SYNTHASE; 1.
CC KW Spermidine biosynthesis; Transferase; Complete proteome; 3D-structure.
CC FT DOMAIN 77 117 BINDING TO DECARBOXYLATED SAM
CC FT POTENTIAL.
CC SQ SEQUENCE 281 AA; 32334 MW; 72C97AE45BE1C487 CRC64;

Query Match 4.2%; Score 6; DB 1; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 DREKAK 110
DB 247 DREKAK 252

RESULT 53
Y765_HAEIN
ID Y765_HAEIN STANDARD; PRT; 282 AA.
AC Q57125; C05033;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical glycosyl transferase HI0765 (EC 2.---).
GN HI0765.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=Rd / KW20 / ATCC 51907;

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RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerkvliet R.A., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT Rd.";
RL Science 269:496-512(1995).
CC -!- SIMILARITY: Belongs to the glycosyltransferase family 25.
CC -----
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CC -----
CC EMBL: U32760; AAC22423.1; -.
CC PIR: F64091; F64091.
CC TIGR: H10765; -.
CC InterPro: IPR002654; Glyco_transf_25; 1.
CC Pfam: PF01755; Glyco_transf_25; 1.
CC KW Hypothetical protein; Transferase; Glycosyltransferase;
CC Complete proteome.
CC SEQUENCE 282 AA; 32481 MW; D962E402AA207A18 CRC64;
CC -----
CC Query Match 4.2%; Score 6; DB 1; Length 282;
CC Best Local Similarity 100.0%; Pred. No. 1.4e+02;
CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC -----
QY 125 BETAXK 130
DB 72 BETAXK 77
CC -----
RESULT 54
FPG_STRCO STANDARD; PRT; 286 AA.
AC Q9ZB06;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Formamidopyrimidine-DNA glycosylase (EC 3.2.2.23) (FAPY-DNA
DE glycosylase).
GN MUTM OR FPG OR SC05573 OR SC7A1.17.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinovitch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wierzbicki A., Woodward J., Barrall B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
CC -!- FUNCTION: This enzyme may play a significant role in processes
CC leading to recovery from mutagenesis and/or cell death by

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CC alkylating agents (By similarity).
CC -!- CATALYTIC ACTIVITY: Hydrolysis of DNA containing ring-opened N(7)-
CC methylguanine residues, releasing 2,6-diamino-4-hydroxy-5-(N-
CC methyl)formamidopyrimidine.
CC -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC -!- SIMILARITY: Belongs to the FPG family.
CC -----
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CC -----
CC EMBL: AJ939124; CAA22416.1; -.
CC PIR: T35657; T35657.
CC HSP: OS0606; 1EES.
CC HAMAP: MF 00103; -.
CC InterPro: IPR000191; Fapy DNA glyco.
CC InterPro: IPR000214; Fapy_DNAG_Zn_BS.
CC Pfam: PF01149; Fapy_DNA_glyco; 1.
CC ProDom: PD003680; Fapy_DNA_glyco; 1.
CC TIGRFAMS: TIGR00577; fpg; 1.
CC PROSITE: PS01242; FPG; 1.
CC KW DNA repair; Hydrolase; Glycosidase; Zinc; Zinc-finger;
CC Complete proteome. 278 POTENTIAL.
CC ZN FING 255
CC ET ZN FING 286 AA; 32511 MW; C98F08045A9F386B CRC64;
CC SQ SEQUENCE 286 AA; 32511 MW; C98F08045A9F386B CRC64;
CC -----
CC Query Match 4.2%; Score 6; DB 1; Length 286;
CC Best Local Similarity 100.0%; Pred. No. 1.5e+02;
CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC -----
QY 14 LKDHRI 19
DB 48 LKDHRI 53
CC -----
RESULT 55
SGBU_HAEIN STANDARD; PRT; 286 AA.
AC P44990;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Putative hexulose-6-phosphate isomerase (EC 5.-.-.-) (HUMPI).
GN SGBU OR H1026.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerkvliet R.A., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT Rd.";
RL Science 269:496-512(1995).
CC -!- FUNCTION: Isomerization of D-arabino-6-hexulose 3-phosphate to D-
CC fructose 6-phosphate.
CC -!- PATHWAY: Probably part of a sugar metabolic pathway along with
CC sgbH.
CC -!- SIMILARITY: BELONGS TO THE HUMPI FAMILY.

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DR EMBL; U32783; AAC22686.1; -
 DR PIR; G64164; G64164.
 DR TIGR; H1026; -

DR InterPro; IPR004560; Hx16Piso_put.
 DR Pfam; PF03809; Hx16Piso_put; 1.
 DR TIGRFAMs; TIGR00542; hx16Piso_put; 1.
 KW isomerase; Complete proteome.
 SQ SEQUENCE 286 AA; 33062 MW; 689543EBDE5E89BB CRC64;

Query Match 4.2%; Score 6; DB 1; Length 286;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 94 BELTIG 99
 DB 196 BELTIG 201

RESULT 56
 NOLT_RHIFR
 ID NOLT_RHIFR STANDARD; PRT; 289 AA.
 AC P33209;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Nodulation protein NOLT precursor.
 GN NOLT
 OS Rhizobium fredii (Sinorhizobium fredii).
 OG Plasmid sym.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
 OX NCBI_TaxID=380;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=USDA 257;
 RX MEDLINE=94018604; PubMed=8412662;
 RA Meinhardt L.W., Krishnan H.B., Balatti P.A., Pueppke S.G.;
 RT "Molecular cloning and characterization of a symb plasmid locus that
 RT regulates cultivar-specific nodulation of soybean by Rhizobium fredii
 RT USDA257";
 RL Mol. Microbiol. 9:17-29(1993).

CC -!- FUNCTION: Regulates cultivar-specific nodulation of soybean.
 CC -!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
 CC anchor (Probable).
 CC -!- INDUCTION: By flavonoid signal compounds.
 CC -!- SIMILARITY: Belongs to the yscJ lipoprotein family.

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DR EMBL; L12251; AAB17677.1; -
 DR PIR; S35022; S35022.
 DR InterPro; IPR000437; Prok_lipoprot_S.
 DR InterPro; IPR003282; SecTIQMPK.
 DR InterPro; IPR006182; YscJ_Flip.
 DR Pfam; PF01514; YscJ_Flip; 1.
 DR PRINTS; PR01338; TYE30MKPROT.
 DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; FALSE NEG.
 KW Plasmid; Outer membrane; Signal; Lipoprotein; Nodulation;

KW Transmembrane; Palmitate.
 FT SIGNAL 1 33
 FT CHAIN 34 289
 FT LIPID 34 34
 FT LIPID 34 34
 FT LIPID 34 34
 FT TRANSMEM 233 253
 SQ SEQUENCE 289 AA; 31241 MW; 5944DE5C9A60DB2B CRC64;

Query Match 4.2%; Score 6; DB 1; Length 289;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 EPDLAQ 56
 DB 216 EPDLAQ 221

RESULT 57

CHIA_CUCSA
 ID CHIA_CUCSA STANDARD; PRT; 292 AA.
 AC P17541;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Acidic endochitinase precursor (EC 3.2.1.14).
 OS Cucumis sativus (Cucumber).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
 OX NCBI_TaxID=3659;
 RN [1]
 RP SEQUENCE FROM N.A.; AND PARTIAL SEQUENCE.
 RC STRAIN=cv Wisconsin SMR-58;
 RX MEDLINE=89128884; PubMed=2915985;
 RA Mettraux J.P., Burkhardt W., Moyer M., Dancher S., Middlesteadt W.,
 RA Williams S., Payne G., Carnes M., Ryals J.;
 RT "Isolation of a complementary DNA encoding a chitinase with
 RT structural homology to a bifunctional lysozyme/chitinase";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:896-900(1989).
 RN [2]
 RP SEQUENCE FROM N.A.

CC TISSUE=Leaf;
 CC MEDLINE=94220741; PubMed=8167370;
 RA Lawton K., Beck J., Potter S., Ward E., Ryals J.;
 RT "Regulation of cucumber class III chitinase gene expression";
 RL Mol. Plant Microbe Interact. 7:48-57(1994).
 CC -!- FUNCTION: This protein functions as a defense against chitin
 CC containing fungal pathogens.
 CC -!- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages of N-
 CC acetyl-D-glucosamine polymers of chitin.
 CC -!- SUBCELLULAR LOCATION: Extracellular.
 CC -!- INDUCTION: By salicylate and upon tobacco necrosis virus
 CC infection.
 CC -!- SIMILARITY: Belongs to chitinase class II (family 18 of glycosyl
 CC hydrolases).

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DR EMBL; M24365; AAC33120.1; -
 DR EMBL; M84214; AAC37395.1; -
 DR PIR; A31455; A31455.
 DR HGSP; P23472; 2HVM
 DR InterPro; IPR001223; Glyco_hydro_18.
 DR InterPro; IPR001579; Glyco_hydro_18AS.
 DR Pfam; PF00704; Glyco_hydro_18; 1.
 DR PROSITE; PS01095; CHITINASE_18; 1.
 KW Hydrolyase; Glycosidase; Chitin degradation; Signal.


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FT SIGNAL 1 25
FT CHAIN 26 292
FT DISULFID 45 92
FT DISULFID 75 82
FT DISULFID 180 209
FT ACT SITE 152 152
SQ SEQUENCE 292 AA; 30774 MW; 2DE39D42BDBE0093 CRC64;

Query Match 4.2%; Score 6; DB 1; Length 292;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 GC AFLS 88
Db 81 GC AFLS 86

RESULT 58
ENGC_BACAA STANDARD; PRT; 293 AA.
AC Q81WH7;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DE Probable GTPase engC (EC 3.6.1.-).
GN ENGC OR BA3999
OS Bacillus anthracis (strain Ames).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=198094;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22608414; PubMed=12721629;
RA Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapfel E.K., Ostad O.A., Helgason E., Ristone J., Wu M.,
RA Kolonay J.F., Beaman M.J., Dodson R.J., Brinkac L.M., Gwinn M.,
RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.L., Mahmoud Y., Jiang L., Harce I.R., Weidman J.F.,
RA Barry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L.,
RA Thomson B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,
RA Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria."
RL Nature 423:81-86(2003).
CC -1- FUNCTION: Unusual circularly permuted GTPase that catalyzes rapid
CC hydrolysis of GTP with a slow catalytic turnover (By similarity).
CC -1- SUBUNIT: Monomer (Probable).
CC -1- SIMILARITY: Contains 1 engC GTPase domain.
CC -----
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CC -----
CC ENBL; A017036; AAP27727.1; -.
CC TIGR; BA3999; -.
CC HAMAP; MF_01820; -.
CC InterPro; IPR004881; DUF258.
CC Pfam; PF03193; DUF258; 1.
CC TIGRFAMs; TIGR00157; TIGR00157; 1.
CC PROSITE; PS50936; ENGC_GTPASE; 1.
CC Hydrolase; GTP-binding; Complete proteome.
FT DOMAIN 72 221
FT DONAIN 112 115
FT NP BIND 166 173
FT NP BIND 166 173
FT NP BIND 247 260
FT SITE 293 AA; 33132 MW; 315FD5AF9645E875 CRC64;
SQ SEQUENCE 293 AA; 33132 MW; 315FD5AF9645E875 CRC64;

Query Match 4.2%; Score 6; DB 1; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 96 LTLGEF 101
Db 190 LTLGEF 195

RESULT 60
Y680.HAEIN STANDARD; PRT; 298 AA.
AC Q57389; O05030;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein HI0680.
GN HI0680.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

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RA McKenney X., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodok A., Kelley J.M.,
RA Wetman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudok D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagan N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.,
RA "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT Rd.",
RL Science 269:496-512(1995).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (potential).
CC -!- SIMILARITY: Belongs to the eamA transporter family.
CC
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CC
CC EMBL: U32750; AAC22339.1; -.
CC PIR: I64085; I64085.
CC TIGR: H10680; -.
CC InterPro: IPR000620; DUF6.
CC InterPro: IPR004626; RAR.
CC Pfam: PF00892; DUF6; 1.
CC TIGRFAMs: TIGR00688; rarD; 1.
CC Hypothetical protein; Transport; Transmembrane; Complete proteome.
KW
FT TRANSMEM 5 23
FT TRANSMEM 33 52
FT TRANSMEM 72 91
FT TRANSMEM 101 120
FT TRANSMEM 127 145
FT TRANSMEM 149 166
FT TRANSMEM 175 194
FT TRANSMEM 207 229
FT TRANSMEM 238 260
FT TRANSMEM 265 284
FT TRANSMEM 298 346; 33463 MW; 65DC2A9EB8F9EF02 CRC64;
SQ SEQUENCE 298 AA; 33463 MW; 65DC2A9EB8F9EF02 CRC64;

Query Match 4.2%; Score 6; DB 1; Length 298;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 RISTFK 23
DB 123 RISTFK 128

RESULT 61
LXD2 PHOLE
ID LXD2 PHOLE STANDARD; PRT; 305 AA.
AC Q06878;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Acyl transferase (EC 2.3.1.-) (ACT) (Myristoyl-ACP-specific
DE thioesterase).
DE LUXD.
GN LUXD.
OS Photobacterium leiognathi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Photobacterium.
OX NCBI_TaxID=658;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=741;
RX MEDLINE=93321531; PubMed=8472957;
RA Chao Y.-F., Weng S.-F., Lin J.-W.;
RT "Sequence of the luxD gene encoding acyltransferase of the lux operon
RT from Photobacterium leiognathi."
RL Gene 126:155-156(1993).
CC -!- FUNCTION: ACYL TRANSFERASE IS PART OF THE FATTY ACID REDUCTASE

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CC SYSTEM REQUIRED FOR ALDEHYDE BIOSYNTHESIS; IT PRODUCES FATTY
CC ACIDS FOR THE LUMINESCENT REACTION.
CC -!- PATHWAY: Bioluminescent fatty acid reduction system;; first step.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: X65612; CAA46563.1; -.
CC PIR: JN0518; JN0518.
CC HSP: P05531; 1THT.
CC InterPro: IPR003157; Acyl transf.
CC Pfam: PF02773; Acyl_transf_2; 1.
CC Luminescence; Transferase; Acyltransferase.
KW SEQUENCE 305 AA; 34384 MW; 0BDAA76D08913164 CRC64;
SQ SEQUENCE 305 AA; 34384 MW; 0BDAA76D08913164 CRC64;

Query Match 4.2%; Score 6; DB 1; Length 305;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 KNKIAK 115
DB 296 KNKIAK 301

RESULT 62
OTCC MYCCC
ID OTCC MYCCC STANDARD; PRT; 312 AA.
AC P59779;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ornithine carbamoyltransferase, catabolic (EC 2.1.3.3) (OTCase).
DE ARCS.
GN Mycoplasma capricolum subsp. capripneumoniae.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=40480;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GL100;
RA Freyraud A., Thiaucourt F.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-ornithine = phosphate
CC + L-citrulline.
CC -!- PATHWAY: Arginine degradation; arginine deiminase pathway; second
CC step.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- SIMILARITY: Belongs to the Arcase/OTCase family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AY282502; AAP38180.1; -.
CC HAMAP: MF_01109; -.
CC InterPro: IPR006130; Asp/Orn Cotransf.
CC InterPro: IPR002292; Orn carbtransf.
CC InterPro: IPR006131; OTCase_O.
CC InterPro: IPR006132; OTCase_P.
CC Pfam: PF00185; OTCase; 1.
CC Pfam: PF02729; OTCase_N; 1.
CC PRINTS: PR00100; AOTCASE.
CC TIGRFAMs: TIGR00658; orn carb tr; 1.
CC PROSITE: PS00097; CARBAMOYLTRANSFERASE; 1.

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KW Arginine metabolism; Transferase.
FT SITE 32 32 IMPORTANT FOR STRUCTURAL INTEGRITY (BY
FT SITE 57 61 CARBAMOYLPHOSPHATE BINDING (BY
FT SITE 108 108 CARBAMOYLPHOSPHATE BINDING (BY
FT SITE 135 135 CARBAMOYLPHOSPHATE BINDING (BY
FT SITE 148 148 CARBAMOYLPHOSPHATE BINDING (BY
FT SITE 271 274 ORNITHINE BINDING (BY SIMILARITY).
FT SITE 312 AA; 35026 MW; 3761P407593F4DDB CRC64;
SQ SEQUENCE 312 AA; 35026 MW; 3761P407593F4DDB CRC64;
Query Match 4.2%; Score 6; DB 1; Length 312;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 113 IAKETN 118
DB 204 IAKETN 209
RESULT 63
PANE_LACLA STANDARD; PRT; 312 AA.
AC Q9CFI8; 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Putative 2-dehydropantoate 2-reductase (EC 1.1.1.169) (Ketopantoate
DE reductase) (KPA reductase) (KPR).
GN L11323.
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1360;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21235186; PubMed=11337471;
RA Bolotin A.; Wincker P.; Mauger S.; Jaillon O.; Malarne K.,
RA Weissbach J., Ehrlich S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium Lactococcus
RT lactis ssp. lactis IL1403."
RL Genome Res. 11:731-753(2001).
CC -!- FUNCTION: Catalyzes the NADPH-dependent reduction of ketopantoate
CC into pantoic acid (By similarity).
CC -!- CATALYTIC ACTIVITY: (R)-pantoate + NADP(+) = 2-dehydropantoate +
CC NADPH.
CC -!- PATHWAY: Pantothenate biosynthesis.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- SIMILARITY: Belongs to the ketopantoate reductase family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AE006364; AAK05421.1; -.
DR PIR; C86790.
DR InterPro; IPR008927; 6DGDH_C_like.
DR TrEMBL; P02558; Apba; 1.
DR TrEMBL; TIGR00745; apba_pane; 1.
KW Hypothetical protein; Pantothenate biosynthesis; Oxidoreductase; NADP;
Complete proteome.
FT NP_BIND 7 12 NADP (POTENTIAL).
FT ACT_SITE 187 187 BY SIMILARITY.
FT ACT_SITE 273 273 BY SIMILARITY.
SQ SEQUENCE 312 AA; 34443 MW; 1C7FC4547F081BAD CRC64;

KW Arginine metabolism; Transferase.
FT SITE 32 32 IMPORTANT FOR STRUCTURAL INTEGRITY (BY
FT SITE 57 61 CARBAMOYLPHOSPHATE BINDING (BY
FT SITE 108 108 CARBAMOYLPHOSPHATE BINDING (BY
FT SITE 135 135 CARBAMOYLPHOSPHATE BINDING (BY
FT SITE 148 148 CARBAMOYLPHOSPHATE BINDING (BY
FT SITE 271 274 ORNITHINE BINDING (BY SIMILARITY).
FT SITE 312 AA; 35026 MW; 3761P407593F4DDB CRC64;
SQ SEQUENCE 312 AA; 35026 MW; 3761P407593F4DDB CRC64;
Query Match 4.2%; Score 6; DB 1; Length 312;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 113 IAKETN 118
DB 204 IAKETN 209
RESULT 63
PANE_LACLA STANDARD; PRT; 312 AA.
AC Q9CFI8; 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Putative 2-dehydropantoate 2-reductase (EC 1.1.1.169) (Ketopantoate
DE reductase) (KPA reductase) (KPR).
GN L11323.
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1360;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21235186; PubMed=11337471;
RA Bolotin A.; Wincker P.; Mauger S.; Jaillon O.; Malarne K.,
RA Weissbach J., Ehrlich S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium Lactococcus
RT lactis ssp. lactis IL1403."
RL Genome Res. 11:731-753(2001).
CC -!- FUNCTION: Catalyzes the NADPH-dependent reduction of ketopantoate
CC into pantoic acid (By similarity).
CC -!- CATALYTIC ACTIVITY: (R)-pantoate + NADP(+) = 2-dehydropantoate +
CC NADPH.
CC -!- PATHWAY: Pantothenate biosynthesis.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- SIMILARITY: Belongs to the ketopantoate reductase family.
CC
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CC
CC EMBL; AE006364; AAK05421.1; -.
DR PIR; C86790.
DR InterPro; IPR008927; 6DGDH_C_like.
DR TrEMBL; P02558; Apba; 1.
DR TrEMBL; TIGR00745; apba_pane; 1.
KW Hypothetical protein; Pantothenate biosynthesis; Oxidoreductase; NADP;
Complete proteome.
FT NP_BIND 7 12 NADP (POTENTIAL).
FT ACT_SITE 187 187 BY SIMILARITY.
FT ACT_SITE 273 273 BY SIMILARITY.
SQ SEQUENCE 312 AA; 34443 MW; 1C7FC4547F081BAD CRC64;

Query Match 4.2%; Score 6; DB 1; Length 312;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 125 EETAKK 130
DB 157 EETAKK 162
RESULT 64
CPKA_PYRAB STANDARD; PRT; 314 AA.
AC Q9UNF8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Carbamate kinase (EC 2.7.2.2) (Carbamate kinase-like
DE carbamoylphosphate synthetase).
GN CPKA OR CPA OR PYRAB0820 OR PAB0593.
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococci; Thermococcaceae; Thermococcaceae;
OX Pyrococcus.
OX NCBI_TaxID=29292;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=GES / Orsay;
RX MEDLINE=22511545; PubMed=11523892;
RA Pucarea C.; Herve G.; Cunin R.; Evans D.R.;
RA Poch O.; Prieur D.; Querellou J.; Ripp R.; Thierry J.-C.;
RA Van der Oost J.; Weissbach J.; Zivanovic Y.; Forterre P.;
RT "An integrated analysis of the genome of the hyperthermophilic
RT archaeon Pyrococcus abyssi."
RL Mol. Microbiol. 47:1495-1512(2003).
CC -!- CATALYTIC ACTIVITY: ATP + NH(3) + CO(2) = ADP + carbamoyl
CC phosphate.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the carbamate kinase family.
CC
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CC
CC EMBL; AF081680; AAF23075.1; -.
DR EMBL; AJ248285; CAB49796.1; -.
DR PIR; C75135; C75135.
DR HSP; P95474; 1E19.
DR InterPro; IPR001048; Aa_kinase.
DR InterPro; IPR003964; Bac_carb_kinase.
DR Pfam; PF00696; aak_kinase; 1.
DR PRINTS; PR01469; CARBMTKINASE.
DR TIGR; TIGR00746; arcC; 1.
KW Transferase; Kinase; Complete proteome.
SQ SEQUENCE 314 AA; 34355 MW; 85DED486A01A8B2 CRC64;
Query Match 4.2%; Score 6; DB 1; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 125 EETAKK 130

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Db 139 BETAKK 144
|||||
RESULT 65
NIA CHLVU
ID_NIA CHLVU STANDARD; PRT; 318 AA.
AC Q01170;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Nitrate reductase [NADH] (EC 1.7.1.1) (NR) (Fragment).
OS Chlorella vulgaris.
OC Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;
OC Chlorellaceae; Chlorella.
OX NCBI_TaxID=3077;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=91354204; PubMed=1883330;
RX Cannons A.C., Iida N., Solomonson L.P.;
RT "Expression of a cDNA clone encoding the haem-binding domain of
RT Chlorella nitrate reductase."
RL Biochem. J. 278:203-209(1991).
CC -!- FUNCTION: Nitrate reductase is a key enzyme involved in the first
CC step of nitrate assimilation in plants, fungi and bacteria.
CC -!- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate + NADH.
CC -!- COFACTOR: Each subunit of the enzyme contains 1 equivalent of FAD,
CC heme iron, and molybdenum-pterin as prosthetic groups. The heme
CC group is called cytochrome b-557.
CC -!- SUBUNIT: Homodimer.
CC -!- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
CC N-TERMINAL DOMAIN.
CC -!- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
CC -!- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
CC C-TERMINAL DOMAIN.
CC
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CC
CC EMBL; X56771; CAA40090.1; -
CC PIR; S17197; S17197.
CC HSSP; P04166; 1BSM.
CC InterPro; IPR001199; Cyt B5.
CC InterPro; IPR008135; Euk_Mb_oxred.
CC InterPro; IPR007110; Ig-I_Lk6.
CC InterPro; IPR005066; Mo-co_dimer.
CC InterPro; IPR000572; Oxidored_molyb.
CC Pfam; PF00173; heme_1; 1.
CC Pfam; PF03404; Mo-co_dimer; 1.
CC PRINTS; PR00363; CYTOCHROME_B5.
CC PRINTS; PR00407; EUMOPTERIN.
CC PRODOM; PD000612; Cyt_B5; 1.
CC PROSITE; PS00191; CYTOCHROME_B5_1; 1.
CC PROSITE; PS0255; CYTOCHROME_B5_2; 1.
CC PROSITE; PS00559; MOLYBDOPTERIN_EUK; PARTIAL.
CC Oxidoreductase; Flavoprotein; FAD; NAD; Heme; Molybdenum;
KW Nitrate assimilation.
FT NON_TER 1
FT METAL 251 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT METAL 274 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT NON_TER 318
SQ SEQUENCE 318 AA; 34830 NW; E60D82FE1E98292A CRC64;

Query Match 4.2%; Score 6; DB 1; Length 318;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 12 PFLKDH 17
|||||
Db 139 BETAKK 144
|||||
RESULT 65
NIA CHLVU
ID_NIA CHLVU STANDARD; PRT; 318 AA.
AC Q01170;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Nitrate reductase [NADH] (EC 1.7.1.1) (NR) (Fragment).
OS Chlorella vulgaris.
OC Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;
OC Chlorellaceae; Chlorella.
OX NCBI_TaxID=3077;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=91354204; PubMed=1883330;
RX Cannons A.C., Iida N., Solomonson L.P.;
RT "Expression of a cDNA clone encoding the haem-binding domain of
RT Chlorella nitrate reductase."
RL Biochem. J. 278:203-209(1991).
CC -!- FUNCTION: Nitrate reductase is a key enzyme involved in the first
CC step of nitrate assimilation in plants, fungi and bacteria.
CC -!- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate + NADH.
CC -!- COFACTOR: Each subunit of the enzyme contains 1 equivalent of FAD,
CC heme iron, and molybdenum-pterin as prosthetic groups. The heme
CC group is called cytochrome b-557.
CC -!- SUBUNIT: Homodimer.
CC -!- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
CC N-TERMINAL DOMAIN.
CC -!- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
CC -!- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
CC C-TERMINAL DOMAIN.
CC
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CC
CC EMBL; X56771; CAA40090.1; -
CC PIR; S17197; S17197.
CC HSSP; P04166; 1BSM.
CC InterPro; IPR001199; Cyt B5.
CC InterPro; IPR008135; Euk_Mb_oxred.
CC InterPro; IPR007110; Ig-I_Lk6.
CC InterPro; IPR005066; Mo-co_dimer.
CC InterPro; IPR000572; Oxidored_molyb.
CC Pfam; PF00173; heme_1; 1.
CC Pfam; PF03404; Mo-co_dimer; 1.
CC PRINTS; PR00363; CYTOCHROME_B5.
CC PRINTS; PR00407; EUMOPTERIN.
CC PRODOM; PD000612; Cyt_B5; 1.
CC PROSITE; PS00191; CYTOCHROME_B5_1; 1.
CC PROSITE; PS0255; CYTOCHROME_B5_2; 1.
CC PROSITE; PS00559; MOLYBDOPTERIN_EUK; PARTIAL.
CC Oxidoreductase; Flavoprotein; FAD; NAD; Heme; Molybdenum;
KW Nitrate assimilation.
FT NON_TER 1
FT METAL 251 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT METAL 274 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT NON_TER 318
SQ SEQUENCE 318 AA; 34830 NW; E60D82FE1E98292A CRC64;

Query Match 4.2%; Score 6; DB 1; Length 318;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 12 PFLKDH 17
|||||
Db 246 PFLKDH 251
|||||
RESULT 66
K6PF OCEIH
ID_K6PF OCEIH STANDARD; PRT; 319 AA.
AC Q8EFD6;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 6-phosphofructokinase (EC 2.7.1.11) (Phosphofructokinase)
DE 6-phosphohexokinase).
DE PFKA OR PFK OR OB2172.
GN Oceanobacillus iheyensis.
OS Oceanobacillus iheyensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
OX NCBI_TaxID=182710;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=HTE831 / DSM 14371 / JCM 11309;
RX MEDLINE=2220767; PubMed=12235376;
RA Takami H., Takaki Y., Uchiyama I.;
RT "Genome sequence of Oceanobacillus iheyensis isolated from the Iheya
RT Ridge and its unexpected adaptive capabilities to extreme
RT environments."
RL Nucleic Acids Res. 30:3927-3935(2002).
CC -!- CATALYTIC ACTIVITY: ATP + D-fructose 6-phosphate = ADP + D-
CC fructose 1,6-bisphosphate.
CC -!- PATHWAY: Key control step of glycolysis.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the phosphofructokinase family.
CC
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CC
CC EMBL; AP004600; BAC14128.1; -
CC HAMAP; MF_00339; 1.
CC InterPro; IPR000023; PpfFructKinase.
CC Pfam; PF00365; PFK; 1.
CC PRINTS; PR00476; PPFRTKINASE.
CC PRODOM; PD000707; PpfFructKinase; 1.
CC PROSITE; PS00433; PHOSPHOFRUCTOKINASE; 1.
CC Kinase; Transferase; Glycolysis; Complete proteome.
KW SEQUENCE 319 AA; 34576 NW; 32DD7454310A7086 CRC64;
SQ SEQUENCE 319 AA; 34576 NW; 32DD7454310A7086 CRC64;

Query Match 4.2%; Score 6; DB 1; Length 319;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 133 RAEQL 138
|||||
Db 84 RAEQL 89
|||||
RESULT 67
ODPB_BACST
ID_ODPB_BACST STANDARD; PRT; 324 AA.
AC P21874;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pyruvate dehydrogenase E1 component, beta subunit (EC 1.2.4.1).
DE PDHB.
GN Bacillus stearothermophilus.
OS Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
OX NCBI_TaxID=1422;
RN [1]
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
```

RC STRAIN=NCA 1503;
RX MEDLINE=90345939; PubMed=2200674;
RA Hawkins C.F., Borges A., Perham R.N.;
RT "Cloning and sequence analysis of the genes encoding the alpha and
RT beta subunits of the E1 component of the pyruvate dehydrogenase
RT multienzyme complex of Bacillus stearothermophilus.";
RL Eur. J. Biochem. 191:337-346(1990).
CC -!- FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall
CC conversion of pyruvate to acetyl-CoA and CO(2). It contains
CC multiple copies of three enzymatic components: pyruvate
CC dehydrogenase (E1), dihydrolipoamide acetyltransferase (E2) and
CC lipoamide dehydrogenase (E3).
CC -!- CATALYTIC ACTIVITY: Pyruvate + lipoamide = S-
CC acetyldihydrolipoamide + CO(2).
CC -!- COFACTOR: Thiamine pyrophosphate.
CC -!- SUBUNIT: Heterodimer of an alpha and a beta chain.
CC
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CC
CC EMBL: X53560; CAA37629.1; -
CC FIR; S14230; S14230.
CC HSP; P09061; I0S0.
CC InterPro: IPR009014; Transketo_C like.
CC InterPro: IPR005476; Transketolase_C.
CC InterPro: IPR005475; Transketolase_CR.
CC Pfam: PF02779; transket_pyr; 1.
CC Pfam: PF02780; transketolase_C; 1.
CC Glycolysis; Oxidoreductase; Flavoprotein; Thiamine pyrophosphate.
FT INIT MET 0
SQ SEQUENCE 324 AA; 35328 MW; F7C6085E33371384 CRC64;

Query Match 4.2%; Score 6; DB 1; Length 324;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 126 ETAKKV 131
Db 316 ETAKKV 321

RESULT 68
K6PF MYCPU STANDARD; PRT; 326 AA.
AC Q98PF8;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 6-phosphofructokinase (EC 2.7.1.11) (Phosphofructokinase)
DE (phosphohexokinase).
GN PFKA OR MYPU 6010.
OS Mycoplasma pulmonis.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2107;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UAB CTIP;
RX MEDLINE=21267165; PubMed=11353084;
RA Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Galieson F.,
RA Mosser I., Dybvig K., Wroblewski H., Viari A., Rocha E.P.C.,
RA Blanchard A.;
RT "The complete genome sequence of the murine respiratory pathogen
RT Mycoplasma pulmonis.";
RL Nucleic Acids Res. 29:2145-2153(2001).
CC -!- CATALYTIC ACTIVITY: ATP + D-fructose 6-phosphate = ADP + D-
CC fructose 1,6-bisphosphate.
CC -!- PATHWAY: Key control step of glycolysis.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

CC -!- SIMILARITY: Belongs to the phosphofructokinase family.
CC
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CC
CC EMBL: AL445565; CAC13774.1; -
CC FIR; A9587; A9587.
CC Mypulist; MTPU_6010; -
CC HAMAP; MF 00339; -; 1.
CC InterPro: IPR000023; Ppfruckinase.
CC Pfam; PF00365; PFK; 1.
CC PRINTS; PR00476; PPFRTKINASE.
CC ProDom; PD000707; Ppfruckinase; 1.
CC PROSITE; PS00433; PHOSPHOFRUCTOKINASE; FALSE NEG.
CC Kinase; Transferase; Glycolysis; Complete proteome.
SQ SEQUENCE 326 AA; 35832 MW; 14AD0F5B3F956EC5 CRC64;

Query Match 4.2%; Score 6; DB 1; Length 326;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 89 VKQOF 94
Db 206 VKQOF 211

RESULT 69
HUR STRAU STANDARD; PRT; 340 AA.
AC Q00923;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Hydroxyurea phosphotransferase (EC 2.7.-.-) (Hydroxyurea resistance
DE protein).
GN HUR.
OS Streptomyces aureofaciens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1894;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 10762 / CCM 3239;
RX MEDLINE=92267374; PubMed=1316866;
RA Kormanec J., Farkasovsky M., Potuchkova L., Godar S.;
RT "A gene (hur) from Streptomyces aureofaciens, conferring resistance
RT to hydroxyurea, is related to genes encoding streptomycin
RT phosphotransferase.";
RL Gene 114:133-137(1992).
CC -!- FUNCTION: THIS IS A POTENTIAL PHOSPHOTRANSFERASE THAT INACTIVATES
CC HYDROXYUREA BY PHOSPHORYLATION OF THE HYDROXY GROUP IN THE
CC HYDROXYLAMINE MOIETY.
CC -!- SIMILARITY: TO AMINOGLYCOSIDE PHOSPHOTRANSFERASES.
CC
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CC
CC EMBL: M81739; AAA26767.1; -
CC FIR; JC1125; JC1125.
CC InterPro: IPR006748; APH_6_hur.
CC Pfam: PF04655; APH_6_hur; 1.
CC Transferase; Kinase; ATP-binding.
CC DOMAIN 172 184 AMINOGLYCOSIDE BINDING (BY SIMILARITY).

FT ACT SITE 240 240 BY SIMILARITY.
SQ SEQUENCE 340 AA; 36049 MW; 7D16C52D350BB3E9 CRC64;
Query Match 4.2%; Score 6; DB 1; Length 340;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 104 LDRERA 109
|||||
DB 296 LDRERA 301
|||||
RESULT 70
RECA_MYCGE STANDARD; PRT; 340 AA.
ID RECA_MYCGE
AC P47581; O49512;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE RecA protein (Recombinase A).
GN RECA OR MG339.
OS Mycoplasma genitalium.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmatataceae; Mycoplasma.
OX NCBI_TaxID=2097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33530 / G-37;
RX MEDLINE=96026346; PubMed=7569993;
RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
RA Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
RA Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhmann J.L.,
RA Nguyen D.T., Uterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
RA Tomb J.-F., Dougherty B.A., Bitt K.F., Hu P.-C., Lucier T.S.,
RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
RA "The minimal gene complement of Mycoplasma genitalium.";
RL Science 270:397-403(1995).
RN [2]
RP SEQUENCE OF 32-124 FROM N.A.
RC STRAIN=ATCC 33530 / G-37;
RX MEDLINE=94075230; PubMed=8253680;
RA Peterson S.N., Hu P.-C., Bitt K.F., Hutchison C.A. III;
RA "A survey of the Mycoplasma genitalium genome by using random
RT sequencing.";
RL J. Bacteriol. 175:7918-7930(1993).
CC -!- FUNCTION: Can catalyze the hydrolysis of ATP in the presence of
CC single-stranded DNA, the ATP-dependent uptake of single-stranded
CC DNA by duplex DNA, and the ATP-dependent hybridization of
CC homologous single-stranded DNAs. It interacts with lexA causing
CC its activation and leading to its autocatalytic cleavage.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the recA family.

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CC ENBL; U39715; AAC71564.1; -;
CC EMBL; U01704; AAB01016.1; -;
CC PIR; E64237; E64237.
CC HSP; P03017; 2REB.
CC TIGR; MG339; -;
CC HAMAP; MF 00268; -; 1.
CC InterPro; IPR003593; AAA_ATPase.
CC InterPro; IPR001553; RecA.
CC Pfam; PF00154; recA; 1.
CC PRINTS; PR00142; RECA.
CC ProDom; PD000229; RecA; 1.
CC SMART; SM00382; AAA; 1.
CC PROSITE; PS00321; RECA_1; 1.

DR PROSITE; PS00162; RECA_2; 1.
DR PROSITE; PS00163; RECA_3; 1.
KW DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding;
KW Complete proteome.
FT NP_BIND 67 74 ATP (BY SIMILARITY).
FT CONFLICT 32 36 AKNS -> CKEKH (IN REF. 2).
SQ SEQUENCE 340 AA; 37430 MW; 0957B712CD2125C0 CRC64;
Query Match 4.2%; Score 6; DB 1; Length 340;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 110 KXKIAK 115
|||||
DB 250 KXKIAK 255
|||||
RESULT 71
VANB_ENTFA STANDARD; PRT; 342 AA.
ID VANB_ENTFA
AC Q06893; O47821; Q57112;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Vancomycin B-type resistance protein vanB (EC 6.3.2.-) (VanB ligase)
DE (D-alanine--D-lactate ligase).
GN VANB OR VANB2 OR EF2294.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=V583 / ATCC 700802;
RX MEDLINE=94171087; PubMed=8125347;
RA Evers S., Reynolds P.E., Courvalin P.;
RA "Sequence of the vanB and ddl genes encoding D-alanine:D-lactate and
RT D-alanine:D-alanine ligases in vancomycin-resistant Enterococcus
RL faecalis V583.";
RL Gene 140:97-102(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=V583 / ATCC 700802;
RX MEDLINE=96200099; PubMed=8631706;
RA Evers S., Courvalin P.;
RA "Regulation of vanB-type vancomycin resistance gene expression by the
RT vanS(B)-vanR(B) two-component regulatory system in Enterococcus
RL faecalis V583.";
RL J. Bacteriol. 178:1302-1309(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=V583 / ATCC 700802;
RX MEDLINE=22550857; PubMed=12663927;
RA Paulsen I.T., Banerjee L., Myers G.S.A., Nelson K.E., Seshadri R.,
RA Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
RA Tettelin H., Dodson R.J., Umayam L., Brinkac L., Beanan M.,
RA Dougherty S., DeBoy R.T., Durkin S., Kolonay J., Madupu R., Nelson W.,
RA Vanamthavan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H.,
RA Uterback T., Radtke D., Ketchum K.A., Dougherty B.A., Fraser C.M.;
RT "Role of mobile DNA in the evolution of vancomycin-resistant
RT Enterococcus faecalis.";
RL Science 299:2071-2074(2003).
RN [4]
RP SEQUENCE OF 110-305 FROM N.A.
RC STRAIN=V583 / ATCC 700802.
RX MEDLINE=93178969; PubMed=8440477;
RA Evers S., Salm D.F., Courvalin P.;
RA "The vanB gene of vancomycin-resistant Enterococcus faecalis V583 is
RT structurally related to genes encoding D-Ala:D-Ala ligases and
RT glycopeptide-resistance proteins VanA and VanC.";
RL Gene 124:143-144(1993).
RN [5]
RP SEQUENCE OF 103-312 FROM N.A.
RC STRAIN=SF300;


```

CC CC -!- CATALYTIC ACTIVITY: UDP-N-acetylmuramate + NADP(+) = UDP-N-
CC CC acetyl-3-O-(1-carboxyvinyl)-D-glucosamine + NADPH.
CC CC -!- COFACTOR: FAD (By similarity).
CC CC -!- PATHWAY: Peptidoglycan biosynthesis.
CC CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC CC -!- SIMILARITY: Belongs to the murB family.
CC CC -----
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CC CC -----
CC CC EMBL; AE004120; AAF93491.1; ALT_INIT.
CC CC PIR; D82337; D82337.
CC CC HSP; P08373; 2MR.
CC CC TIGR; VC0318; -.
CC CC HAMAP; MF_00037; -.
CC CC InterPro; IPR003170; MurB.
CC CC InterPro; IPR006094; Oxid FAD bind.
CC CC Pfam; PF01565; FAD binding_4; 1.
CC CC Pfam; PF02873; MurB_C; 1.
CC CC TIGRFAMs; TIGR00179; murB; 1.
CC CC Oxidoreductase; NADP; Flavoprotein; FAD; Cell wall; Cell division;
CC CC Peptidoglycan synthesis; Complete proteome.
CC CC KW Peptidoglycan synthesis; Complete proteome.
CC CC SQ SEQUENCE 347 AA; 38271 MW; C4758B7E14A31CD6 CRC64;

Query Match 4.2%; Score 6; DB 1; Length 347;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 135 IEQLAA 140
DB 17 IEQLAA 22
|||||
|||||

RESULT 74
SYFA_STRPN
ID SYFA_STRPN STANDARD; PRT; 348 AA.
AC Q97836;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phenylalanine-tRNA synthetase alpha chain (EC 6.1.1.20)
DE (Phenylalanine--tRNA ligase alpha chain) (PHERS).
GN PHERS OR SP0579.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OC NCBI_TaxID=1313;
OX [1]
RN SEQUENCE FROM N.A.
RC STRAIN=ATCC BAA-334 / TIGR4;
RX MEDLINE=21357209; PubMed=11463916;
RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
RA Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
RA Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
RA McDonald L.A., Feldblyum T.V., Anguoli S., Dickinson T., Hickey E.K.,
RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
RA "Complete genome sequence of a virulent isolate of Streptococcus
RA pneumoniae".
RL Science 293:498-506(2001).
CC -!- CATALYTIC ACTIVITY: ATP + L-phenylalanine + tRNA(Phe) = AMP +
CC CC diphosphate + L-phenylalanyl-tRNA(Phe).
CC CC -!- COFACTOR: Binds 2 magnesium ions per tetramer (By similarity).
CC CC -!- SUBUNIT: Tetramer of two alpha and two beta chains (By
CC CC similarity).
CC CC -!- SUBCELLULAR LOCATION: Cytoplasmic.

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CC CC -!- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
CC CC Pre-CRNA synthetase alpha chain subfamily 1.
CC CC -----
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CC CC -----
CC CC EMBL; AE007368; AAK74733.1; -.
CC CC PIR; D95067; D95067.
CC CC TIGR; SP0579; -.
CC CC HAMAP; MF_00281; -.
CC CC InterPro; IPR004188; Phe_tRNA_synth_N.
CC CC InterPro; IPR004529; PheS.
CC CC InterPro; IPR002319; tRNA-synt 2d.
CC CC InterPro; IPR006195; tRNA ligase II.
CC CC Pfam; PF02912; Phe tRNA-synt N; 1.
CC CC Pfam; PF01409; tRNA-synt 2d_1.
CC CC TIGRFAMs; TIGR00468; PheS; 1.
CC CC PROSITE; PS50862; AA tRNA_LIGASE II; 1.
CC CC Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
CC CC KW Metal-binding; Magnesium; Complete proteome.
CC CC FT METAL 262 262 MAGNESIUM (BY SIMILARITY).
CC CC SQ SEQUENCE 348 AA; 39101 MW; 7762B76B5627652D CRC64;

Query Match 4.2%; Score 6; DB 1; Length 348;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 FEETAK 129
DB 77 FEETAK 82
|||||
|||||

RESULT 75
EGSA_SULTO
ID EGSA_SULTO STANDARD; PRT; 350 AA.
AC P58460;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glycerol-1-phosphate dehydrogenase [NAD(P)] (EC 1.1.1.261) (Sn-
DE glycerol-1-phosphate dehydrogenase) (G-1-P dehydrogenase)
DE (Enantiomeric glycerophosphate synthase).
GN EGSA OR ST0344.
OS Sulfolobus tokodaii.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OC NCBI_TaxID=111955;
OX [1]
RN SEQUENCE FROM N.A.
RC STRAIN=JCM 10545 / 7;
RX MEDLINE=21456156; PubMed=11572479;
RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
RA Sekine M., Baba S.-I., Ankaï A., Kosugi H., Hosoyama A., Fukui S.,
RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kishida N., Oguchi A.,
RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
RA Oshima T., Kikuchi H.;
RA "Complete genome sequence of an aerobic thermoacidophilic
RA Crenarchaeon, Sulfolobus tokodaii strain 7."
RL DNA Res. 8:123-140(2001).
CC -!- FUNCTION: Responsible for the formation of archaea-specific
CC CC glycerophosphate backbone of phospholipids, G-1-P, from
CC CC dihydroxyacetonephosphate (DHAP) (By similarity).
CC CC -!- CATALYTIC ACTIVITY: Sn-glycerol-1-phosphate + NAD(P)(+) =
CC CC glycerone phosphate + NAD(P)H.
CC CC -!- PATHWAY: De novo phospholipid biosynthesis.
CC CC -!- SUBUNIT: Tetramer of two alpha and two beta chains (By
CC CC similarity).
CC CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC CC -!- SIMILARITY: Belongs to the glycerol-1-phosphate dehydrogenase

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CC family.
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CC -----
DR EMBL; AP000982; BAB65322.1; -.
DR HAMAP; MF 00457; -. 1.
DR InterPro; IPR001670; Fe-ADH.
DR Pfam; PF00465; Fe-ADH; 1.
KW Phospholipid biosynthesis; Oxidoreductase; NADP; Complete proteome.
SQ SEQUENCE 350 AA; 37792 MW; 539461CC2F6BD310 CRC64;
Query Match 4.2%; Score 6; DB 1; Length 350;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 112 KIAXET 117
Db 341 KIAXET 346

```

Search completed: August 11, 2004, 14:24:15
Job time : 15 secs

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OM protein - protein search, using sw model

Run on: August 11, 2004, 14:21:17 ; Search time 39 seconds
(without alignments)

1148.810 Million cell updates/sec

Title: US-09-690-825-34

Perfect score: 142

Sequence: 1 MGAPLPPAWOPFLKDHRS.....EFETAKVRRRAIEQLAAMD 142

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database :

SPREMBL.25.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriaph.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	106	74.6	142	6	Q81009
2	58	40.8	142	6	Q9GLN5
3	41	28.9	121	11	Q923F7
4	13	9.2	157	13	Q804H7
5	12	8.5	135	13	Q90ZNO
6	12	8.5	142	13	Q9DDK0
7	12	8.5	160	13	Q8JG75
8	12	8.5	160	13	Q8JG75
9	12	8.5	160	13	Q8JG75
10	9	6.3	59	13	Q90VY6
11	9	6.3	128	13	Q90WU8
12	8	5.6	142	13	Q90WU9
13	8	5.6	195	10	Q94EC5
14	8	5.6	197	16	Q82VH3
15	8	5.6	234	2	Q9F8X4
16	8	5.6	491	5	Q95TA6

17	8	5.6	706	16	P72747
18	8	5.6	875	5	O18265
19	8	5.6	1621	5	O81LL7
20	8	5.6	1822	2	Q07290
21	7	4.9	66	2	Q57137
22	7	4.9	102	16	Q8DS63
23	7	4.9	118	16	Q8PKK9
24	7	4.9	125	12	Q91CW7
25	7	4.9	130	5	O18231
26	7	4.9	130	12	Q91CX3
27	7	4.9	149	12	Q8QXX8
28	7	4.9	152	16	Q8ZUX0
29	7	4.9	152	16	Q8ZOV6
30	7	4.9	155	16	Q89DB1
31	7	4.9	171	12	Q9QBX0
32	7	4.9	175	2	Q84F94
33	7	4.9	178	16	Q8XKR3
34	7	4.9	182	16	Q834K3
35	7	4.9	199	2	Q9JMX3
36	7	4.9	199	16	O25261
37	7	4.9	219	16	Q9ZLV1
38	7	4.9	219	16	Q8D904
39	7	4.9	224	16	Q7U7M6
40	7	4.9	228	17	O58403
41	7	4.9	228	17	Q9UY11
42	7	4.9	248	9	Q37965
43	7	4.9	250	16	Q822K6
44	7	4.9	253	16	Q92TM2
45	7	4.9	255	16	Q8EBM3
46	7	4.9	265	10	Q9M521
47	7	4.9	271	17	O28569
48	7	4.9	308	10	Q9M526
49	7	4.9	308	10	Q9M522
50	7	4.9	308	10	Q9M525
51	7	4.9	308	10	O81651
52	7	4.9	308	10	Q91L41
53	7	4.9	309	10	Q9M520
54	7	4.9	310	10	Q9SD20
55	7	4.9	312	12	Q67551
56	7	4.9	313	10	Q9LD14
57	7	4.9	314	10	Q9LD00
58	7	4.9	343	3	O59708
59	7	4.9	353	16	Q7USB6
60	7	4.9	374	5	Q9TXL0
61	7	4.9	379	16	Q9BTR2
62	7	4.9	393	16	Q91253
63	7	4.9	405	13	Q8AVV0
64	7	4.9	427	10	Q9SCQ5
65	7	4.9	442	5	Q26582
66	7	4.9	467	16	Q89ZX8
67	7	4.9	501	16	Q8P9W0
68	7	4.9	525	16	Q97E19
69	7	4.9	546	16	Q87YV7
70	7	4.9	579	10	Q9LD30
71	7	4.9	609	16	Q87FL8
72	7	4.9	625	17	Q8PZW5
73	7	4.9	671	16	Q8EJ00
74	7	4.9	673	11	Q91VK6
75	7	4.9	698	16	Q8ZJ11
76	7	4.9	731	16	Q7UMT4
77	7	4.9	762	10	Q943W8
78	7	4.9	778	16	Q8RIK8
79	7	4.9	788	16	O81126
80	7	4.9	885	16	O55683
81	7	4.9	932	10	O49680
82	7	4.9	966	16	Q89PV0
83	7	4.9	1032	3	Q8WZ22
84	7	4.9	1042	16	Q7VUJ9
85	7	4.9	1084	16	Q8XJX8
86	7	4.9	1098	5	O19149
87	7	4.9	1205	5	Q9V8B7
88	7	4.9	1770	5	O813A3
89	7	4.9	1924	12	Q67654

P72747	synchocyst
O18265	caenorhabdi
O81LL7	plasmodium
Q07290	streptococc
Q57137	paracoccus
Q8DS63	streptococc
Q8PKK9	xanthomonas
Q91CW7	kalanchoe 1
Q18231	caenorhabdi
Q91CX3	kalanchoe 1
Q8QXX8	garlic late
Q8ZUX0	salmonella
Q8ZOV6	salmonella
Q89DB1	bradyrhizob
Q9QBX0	lily latenz
Q84F94	myxococcus
O8XKR3	clostridium
O834K3	enterococcu
Q9JMX3	helicobacte
O25261	helicobacte
Q9ZLV1	helicobacte
Q8D904	vibrio vuln
Q7U7M6	synchococc
O58403	pyrococcus
Q9UY11	pyrococcus
Q37965	bacterioph
Q822K6	enterococcu
Q92TM2	rhizobium m
Q8EBM3	shewanella
Q9M521	tsuga heter
Q9M526	tsuga heter
Q9M522	tsuga heter
O81651	pinus taeda
Q91L41	pinus taeda
Q9M520	tsuga heter
Q9SD20	glycine max
O67551	garlic late
Q9LD14	thuja plica
Q9LD00	thuja plica
O59708	schizosacch
Q7USB6	rhodopirell
Q9TXL0	caenorhabdi
Q9BTR2	deinococcus
Q91253	pseudomonas
Q8AVV0	xenopus lae
Q9SCQ5	arabidopsis
Q26582	schistosoma
Q89ZX8	bacteroides
Q8P9W0	leptospiro
Q97E19	clostridium
Q87YV7	pseudomonas
Q9LD30	cryptocodi
Q87FL8	vibrio para
Q8PZW5	methanosarc
Q8EJ00	mycoplasma
Q91VK6	mus muscucu
O8ZJ11	versinia pe
Q7UMT4	rhodopirell
Q943W8	oryza sativ
Q8RIK8	fusobacteri
O81126	bacillus ce
O55683	synchocyst
O49680	arabidopsis
Q89PV0	bradyrhizob
Q8WZ22	neurospora
Q7VUJ9	helicobacte
Q8XJX8	clostridium
O19149	caenorhabdi
Q9V8B7	drosophila
O813A3	plasmodium
Q67654	garlic late

90 Q8QY8 garlic late
 91 Q65652 blueberry s
 92 Q96171 plasmidium
 93 Q812C4 plasmidium
 94 Q94657 plasmidium
 95 Q64046 bacteriophage
 96 Q31976 bacillus su
 97 P90580 plasmidium
 98 Q81640 plasmidium
 99 Q81640 plasmidium
 100 Q97R96 streptococc

7 4.9 1924 12 Q8QY8
 7 4.9 1967 12 Q65652
 7 4.9 2010 5 Q96171
 7 4.9 2203 5 Q812C4
 7 4.9 2212 5 Q94657
 7 4.9 2285 9 Q64046
 7 4.9 2285 16 Q31976
 7 4.9 2647 5 P90580
 7 4.9 2860 5 Q81640
 7 4.9 3384 5 Q81640
 6 4.2 35 16 Q97R96

ALIGNMENTS

RESULT 1

Q81009 PRELIMINARY; PRT; 142 AA.
 AC Q81009;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Survivin.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Inoue C., Yamazaki J., Kano R., Hasegawa A.;
 RT "Canis familiaris mRNA for survivin-protein, complete cds."
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB095108; BAC22748.2; -.
 DR GO; GO:0005622; C:intracellular; IEA.
 DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
 DR GO; GO:0006916; P:anti-apoptosis; IEA.
 DR InterPro; IPR001370; BIR.
 DR SMART; SM00238; BIR; 1.
 DR PROSITE; PS50143; BIR_REPEAT_2; 1.
 SQ SEQUENCE 142 AA; 16375 MW; E960DC9DE6D36792 CRC64;

Query Match 74.6%; Score 106; DB 6; Length 142;
 Best Local Similarity 100.0%; Pred. No. 3e-104;
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 RMAEAGTHCPTNEPDLAQCFKCEGWEPPDDPIEHHKHSGCCAFSLSVKKQFEEL 96
 DB 37 RMAEAGTHCPTNEPDLAQCFKCEGWEPPDDPIEHHKHSGCCAFSLSVKKQFEEL 96
 QY 97 TLGFLKLDREARAKNIATETNNKKKFEETAKKVRRAIEQLAMD 142
 DB 97 TLGFLKLDREARAKNIATETNNKKKFEETAKKVRRAIEQLAMD 142

RESULT 2

Q9GLN5 PRELIMINARY; PRT; 142 AA.
 AC Q9GLN5;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Apoptosis inhibitor survivin.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=21328903; PubMed=11435714;
 RX Cirera S., Fredholm M.;
 RT "Isolation and mapping the pig homologs survivin (BIRC5) and effector

RT cell protease receptor 1 (EPRI) genes.";
 RL Cytogenet. Cell Genet. 92:351-352 (2001).
 DR EMBL; AF195781; AAG17540.1; -.
 DR HSSP; O15392; IE31.
 DR GO; GO:0005622; C:intracellular; IEA.
 DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
 DR GO; GO:0006916; P:anti-apoptosis; IEA.
 DR InterPro; IPR001370; BIR.
 DR Pfam; PF00653; BIR; 1.
 DR SMART; SM00238; BIR; 1.
 DR PROSITE; PS50143; BIR_REPEAT_2; 1.
 SQ SEQUENCE 142 AA; 16297 MW; 56BAV53E651F4F2C CRC64;

Query Match 40.8%; Score 58; DB 6; Length 142;
 Best Local Similarity 100.0%; Pred. No. 3e-53;
 Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 AGFIHCPTNEPDLAQCFKCEGWEPPDDPIEHHKHSGCCAFSLSVKKQFEEL 98
 DB 41 AGFIHCPTNEPDLAQCFKCEGWEPPDDPIEHHKHSGCCAFSLSVKKQFEEL 98

RESULT 3

Q923F7 PRELIMINARY; PRT; 121 AA.
 ID Q923F7;
 AC Q923F7;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Baculoviral IAP repeat-containing 5.
 GN BIRC5.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC004702; AA04702.1; -.
 DR MGD; MGI:1203517; Birc5.
 DR GO; GO:0005737; C:cytoplasm; IEA.
 DR GO; GO:0008189; F:apoptosis inhibitor activity; IMP.
 DR GO; GO:0006916; P:anti-apoptosis; IMP.
 DR InterPro; IPR001370; BIR.
 DR Pfam; PF00653; BIR; 1.
 DR SMART; SM00238; BIR; 1.
 DR PROSITE; PS50143; BIR_REPEAT_2; 1.
 SQ SEQUENCE 121 AA; 14154 MW; 1E0ECT7E01BA65585 CRC64;

Query Match 28.9%; Score 41; DB 11; Length 121;
 Best Local Similarity 100.0%; Pred. No. 3e-35;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 CACTPERMAEAGTHCPTNEPDLAQCFKCEGWEPPDD 71
 DB 31 CACTPERMAEAGTHCPTNEPDLAQCFKCEGWEPPDD 71

RESULT 4

Q804H7 PRELIMINARY; PRT; 157 AA.
 ID Q804H7;
 AC Q804H7;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE SIX.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]

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RP SEQUENCE FROM N.A.
RA Song K.-H., Kim H.-J., Kim H.-J., Kim H.-H., Kwon H.-B.,
RA Kim W.-S., Choi H.-S.;
RT "Molecular cloning and characterization of a novel inhibitor of
RT apoptosis protein from Xenopus laevis.";
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY174765; AAC00085.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 1.
DR SMART; SM00238; BIR; 1.
DR PROSITE; PS0143; BIR REPEAT 2; 1.
SQ SEQUENCE 157 AA; 18311 MW; 1ED9COA65C6ED627 CRC64;

Query Match      9.5%; Score 13; DB 13; Length 157;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 CACTPERVAAGF 43
Db 44 CACTPERVAAGF 56

RESULT 5
Q90ZNO PRELIMINARY; PRT; 135 AA.
AC Q90ZNO;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Survivin delta.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Langer J.S., Bridgham J.T., Johnson A.L.;
RT "Molecular cloning and characterization of novel chicken survivin
RT splicing variants.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF377323; AK56308.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 1.
DR SMART; SM00238; BIR; 1.
DR PROSITE; PS0143; BIR REPEAT 2; 1.
SQ SEQUENCE 135 AA; 14995 MW; 60D205839B465C3C CRC64;

Query Match      8.5%; Score 12; DB 13; Length 135;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 KELEGWEPDDDP 73
Db 64 KELEGWEPDDDP 75

RESULT 6
Q9DDKO PRELIMINARY; PRT; 142 AA.
AC Q9DDKO;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Survivin.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Langer J.S., Johnson A.L., Bridgham J.T.;
RT "Molecular cloning and characterization of chicken survivin.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF322051; AAG42494.1; -.
DR HSP; O15392; IE31.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 1.
DR SMART; SM00238; BIR; 1.
DR PROSITE; PS0143; BIR REPEAT 2; 1.
SQ SEQUENCE 142 AA; 15955 MW; 1323CCBD5ER2F551 CRC64;

Query Match      8.5%; Score 12; DB 13; Length 142;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 KELEGWEPDDDP 73
Db 64 KELEGWEPDDDP 75

RESULT 7
Q8JG75 PRELIMINARY; PRT; 160 AA.
AC Q8JG75;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Survivin.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Bolton M.A., Lan W., Powers S.E., McClelland M.L., Kuang J.,
RA Stukenberg P.T.;
RT "Aurora B kinase exists in a complex with survivin and INCENP and its
RT kinase activity is stimulated by survivin binding and
RT phosphorylation.";
RL Mol. Biol. Cell 0:0-0(2002).
DR EMBL; AY115553; AAM76714.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 1.
DR SMART; SM00238; BIR; 1.
DR PROSITE; PS0143; BIR REPEAT 2; 1.
SQ SEQUENCE 160 AA; 18677 MW; B7C32E02119DC61E CRC64;

Query Match      8.5%; Score 12; DB 13; Length 160;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 KELEGWEPDDDP 73
Db 71 KELEGWEPDDDP 82

RESULT 8
Q8JGN5 PRELIMINARY; PRT; 160 AA.
AC Q8JGN5;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)

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DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DE 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Survivin/XBIR1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Losada A., Hirano M., Hirano T.;
RT "Aurora B and polo kinases cooperate to establish metaphase chromosome
structure with bi-oriented sister chromatids."
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY1005639; AAM44085.1;
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 1.
DR SMART; SM00238; BIR; 1.
DR PROSITE; PS0143; BIR_REPEAT_2; 1.
SQ SEQUENCE 160 AA; 18686 MW; 9AC32E02119DC609 CRC64;

Query Match 8.5%; Score 12; DB 13; Length 160;
Best Local Similarity 100.0%; Pred.No. 0.00024;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 KELEGWEPDDDP 73
DB 71 KELEGWEPDDDP 82

RESULT 9
Q8AXI6 PRELIMINARY; PRT; 160 AA.
AC Q8AXI6;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Survivin.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Murphy C.R., Sabel J.L., Sandler A.D., Dagle J.M.;
RT "Survivin mRNA is down-regulated during early Xenopus laevis
embryogenesis."
RL Dev. Dyn. 225:597-601(2002).
DR EMBL; AF424292; AAN76690.1;
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 1.
DR SMART; SM00238; BIR; 1.
DR PROSITE; PS0143; BIR_REPEAT_2; 1.
SQ SEQUENCE 160 AA; 18812 MW; 57538991C6190F4B CRC64;

Query Match 8.5%; Score 12; DB 13; Length 160;
Best Local Similarity 100.0%; Pred.No. 0.00024;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 KELEGWEPDDDP 73
DB 71 KELEGWEPDDDP 82

RESULT 10
Q8AXI6 PRELIMINARY; PRT; 160 AA.
AC Q8AXI6;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Survivin.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Murphy C.R., Sabel J.L., Sandler A.D., Dagle J.M.;
RT "Survivin mRNA is down-regulated during early Xenopus laevis
embryogenesis."
RL Dev. Dyn. 225:597-601(2002).
DR EMBL; AF424292; AAN76690.1;
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 1.
DR SMART; SM00238; BIR; 1.
DR PROSITE; PS0143; BIR_REPEAT_2; 1.
SQ SEQUENCE 160 AA; 18812 MW; 57538991C6190F4B CRC64;

Query Match 8.5%; Score 12; DB 13; Length 160;
Best Local Similarity 100.0%; Pred.No. 0.00024;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 KELEGWEPDDDP 73
DB 71 KELEGWEPDDDP 82

RESULT 11
Q90WU8 PRELIMINARY; PRT; 128 AA.
AC Q90WU8;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Survivin 2.
GN BIR5B.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20373792; PubMed=10917738;
RA Inohara N., Nunez G.;
RT "Genes with homology to mammalian apoptosis regulators identified in
zebrafish."
RL Cell Death Differ. 7:509-510(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Inohara N., Nunez G.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY057058; AAL18251.1;
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 1.
DR SMART; SM00238; BIR; 1.
DR PROSITE; PS0143; BIR_REPEAT_2; 1.
SQ SEQUENCE 128 AA; 15294 MW; A8496849082DDC66 CRC64;

Query Match 6.3%; Score 9; DB 13; Length 128;
Best Local Similarity 100.0%; Pred.No. 0.31;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 ELEGWEPDD 71
DB 52 ELEGWEPDD 60

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Q90VY6 PRELIMINARY; PRT; 59 AA.
AC Q90VY6;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Survivin gamma (Survivin short).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Langer J.S., Brigham J.T., Johnson A.L.;
RT "Molecular cloning and characterization of novel chicken survivin
splicing variants."
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF377324; AAK56309.1;
DR EMBL; AF377322; AAK56307.1;
DR SEQUENCE 59 AA; 5716 MW; 79F59B7DA6C2A2CA CRC64;

Query Match 6.3%; Score 9; DB 13; Length 59;
Best Local Similarity 100.0%; Pred.No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 EGCACTPER 37
DB 31 EGCACTPER 39

RESULT 11
Q90WU8 PRELIMINARY; PRT; 128 AA.
AC Q90WU8;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Survivin 2.
GN BIR5B.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20373792; PubMed=10917738;
RA Inohara N., Nunez G.;
RT "Genes with homology to mammalian apoptosis regulators identified in
zebrafish."
RL Cell Death Differ. 7:509-510(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Inohara N., Nunez G.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY057058; AAL18251.1;
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 1.
DR SMART; SM00238; BIR; 1.
DR PROSITE; PS0143; BIR_REPEAT_2; 1.
SQ SEQUENCE 128 AA; 15294 MW; A8496849082DDC66 CRC64;

Query Match 6.3%; Score 9; DB 13; Length 128;
Best Local Similarity 100.0%; Pred.No. 0.31;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 ELEGWEPDD 71
DB 52 ELEGWEPDD 60

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RESULT 12
Q90WU9 PRELIMINARY; PRT; 142 AA.
AC Q90WU9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Survivin 1.
GN BIRSA.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2037392; PubMed=10917738;
RA Inohara N., Nunez G.;
RT "Genes with homology to mammalian apoptosis regulators identified in
RT zebrafish."
RL Cell Death Differ. 7:509-510(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Inohara N., Nunez G.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY057057; AL18250.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0008916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 1.
DR SMART; SM00238; BIR; 1.
DR PROSITE; PS0143; BIR REPEAT 2; 1.
DR SEQUENCE 142 AA; 16412 MW; 71AED23945235C78 CRC64;

Query Match 5.6%; Score 8; DB 13; Length 142;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 KELEGWEP 69
DB 61 KELEGWEP 68

RESULT 13
Q94EC5 PRELIMINARY; PRT; 195 AA.
AC Q94EC5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE P002B05.14 protein.
GN P002B05.14.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA) genomic DNA, chromosome 1, PAC
RT clone:P002B05."
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF003141; BAB63494.1; -.
DR Gramene; Q94EC5; -.
SQ SEQUENCE 195 AA; 21153 MW; CD2BFC4B9D005A1A CRC64;

Query Match 5.6%; Score 8; DB 10; Length 195;
Best Local Similarity 100.0%; Pred. No. 5;

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Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 135 IEQLAMD 142
DB 41 IEQLAMD 48

RESULT 14
Q82YH3 PRELIMINARY; PRT; 197 AA.
ID Q82YH3
AC Q82YH3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN SAPI_7.
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=33903;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4880 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=22608306; PubMed=12692562;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermitilis.";
RL Nat. Biotechnol. 21:526-531(2003).
DR GO; GO:0005645; BAC75291.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
KW Hypothetical protein; Plasmid; Complete proteome.
SQ SEQUENCE 197 AA; 21399 MW; 059D770B58CA2F75 CRC64;

Query Match 5.6%; Score 8; DB 16; Length 197;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2 GAPTLPFA 9
DB 113 GAPTLPFA 120

RESULT 15
Q9F8X4 PRELIMINARY; PRT; 234 AA.
ID Q9F8X4
AC Q9F8X4;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE TrER.
GN TrER.
OS Pseudomonas fluorescens.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=294;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 17400;
RX MEDLINE=98027372; PubMed=9361421;
RA Gaballa A., Abeysinghe P.D., Ulrich G., Matthijs S., De Greve H.,
RA Cornelis P., Koedam N.;
RT "Trehalose induces antagonism towards Pythium debaryanum in
RT Pseudomonas fluorescens ATCC 17400."
RL Appl. Environ. Microbiol. 63:4340-4345(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 17400;
RX MEDLINE=21030915; PubMed=11191810;
RA Matthijs S.L.C., Koedam N., Cornelis P., De Greve H.;
RT "The trehalose operon of Pseudomonas fluorescens ATCC 17400."
RL Res. Microbiol. 151:845-851(2000).

```

CC -!- SIMILARITY: BELONGS TO THE GNTR FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.

DR EMBL: AF229829; AAG31030.1; -.
DR GO: GO:0005822; C:intracellular; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO: GO:0006350; P:transcription; IEA.
DR InterPro: IPR000524; HTH_GNTR.
DR Pfam: PF00392; gntr; 1.
DR PRINTS: PR00035; HTHGNTR.
DR SMART: SM00345; HTH_GNTR; 1.
DR DNA-binding; Transcription; Transcription regulation.
KW DNA-binding; Transcription; Transcription regulation.
SQ SEQUENCE 234 AA; 26716 MW; 538FC11BFBD2C32B CRC64;

Query Match 5.6%; Score 8; DB 2; Length 234;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 131 VRRRAIEQL 138
Db 43 VRRRAIEQL 50
|||||

RESULT 16

Q95YA6 PRELIMINARY; PRT; 491 AA.
AC Q95YA6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein F41G4.5.
GN F41G4.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
DE Hypothetical protein F41G4.5.
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA Wilson R.;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Miller N., Gattung S.;
RT "The sequence of C. elegans cosmid F41G4.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.H.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
[5]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
[6]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
[7]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;

RA Waterston R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
[8]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
[9]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
[10]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC006638; AAK85485.2; -.
KW Hypothetical protein.
SQ SEQUENCE 491 AA; 56030 MW; C1C08713B0A88486 CRC64;

Query Match 5.6%; Score 8; DB 5; Length 491;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GAPTLPFA 9
Db 392 GAPTLPFA 399
|||||

RESULT 17

P72747 PRELIMINARY; PRT; 706 AA.
ID P72747
AC P72747;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein slr1103.
GN SLR1103.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
DE Hypothetical protein slr1103.
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hiroseawa M., Sugita M., Sasanoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA Shimpou S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
DR EMBL: D90900; BAA16762.1; -.
DR PIR: S74610; S74610.
DR InterPro: IPR001633; EAL.
DR InterPro: IPR00253; FHA.
DR InterPro: IPR00160; GGDEF.
DR InterPro: IPR008984; SMAD_FHA.
DR Pfam: PF00563; EAL; 1.
DR Pfam: PF00498; FHA; 1.
DR Pfam: PF00590; GGDEF; 1.
DR SMART: SM00267; DUF1; 1.
DR SMART: SM00052; DUF2; 1.
DR SMART: SM00240; FHA; 1.
DR TIGRfams: TIGR00254; GGDEF; 1.
DR PROSITE: PS50883; EAL; 1.
DR PROSITE: PS50006; FHA DOMAIN; 1.
DR PROSITE: PS50867; GGDEF; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 706 AA; 79830 MW; 5B909B4AA5DAC300 CRC64;

Query Match 5.6%; Score 8; DB 16; Length 706;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 132 RRAIQOLA 139

Db 585 RRAIQOLA 592

RESULT 18

O18265 PRELIMINARY; PRT; 875 AA.

AC O18265;

DT 01-JAN-1998 (TREMBLrel. 05, Created)

DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE ZC15.1 protein.

GN ZC15.1.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

OC Rhabditidae; Feloderinae; Caenorhabditis.

OX NCBI_TaxID=6239;

PN [1]

RP SEQUENCE FROM N.A.

RA Basham V.M.;

RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=99069613; PubMed=9851916;

RA none;

RT "Genome sequence of the nematode C.elegans: A platform for

RT investigating biology.";

RT Science 282:2012-2016(1998).

DR EMBL; Z93396; CA807709.1; -.

DR PIR; T27495; T27495.

DR WormPep; ZC15.1; CE16683.

DR GO; GO:0003676; F:nucleic acid binding; IEA.

DR InterPro; IPR001878; Znf CCHC.

DR SMART; SM00343; Znf C2HC; 1.

SQ SEQUENCE 875 AA; 100139 MW; 9812345834B6AB84 CRC64;

Query Match

Best Local Similarity 5.6%; Score 8; DB 5; Length 875;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GAPTLPAA 9

Db 433 GAPTLPAA 440

RESULT 19

Q8ILL7

AC Q8ILL7 PRELIMINARY; PRT; 1621 AA.

DT 01-MAR-2003 (TREMBLrel. 23, Created)

DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)

DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

DE Hypothetical protein.

GN PF14_0226.

OS Plasmodium falciparum (isolate 3D7).

OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

OX NCBI_TaxID=36329;

PN [1]

RP SEQUENCE FROM N.A.

RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,

RA MEDLINE=22255705; PubMed=12368864;

RA Carlton J.N., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,

RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,

RA Chan M.-S., Nene V., Shallow S.J., Suh B., Peterson J., Angiuoli S.,

RA Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,

RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,

RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,

RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
 RA Fraser C.M., Barrell B.;

RT "Genome sequence of the human malaria parasite Plasmodium

RT falciparum";

RL Nature 419:498-511(2002).

DR EMBL; AE014819; AAN36839.1; -.

DR InterPro; IPR001646; Septide_repeat.

DR Pfam; PF00805; Pentapeptide; 2.

KW Hypothetical protein.

SQ SEQUENCE 1621 AA; 192605 MW; B4492093FDAD3A4E CRC64;

Query Match

Best Local Similarity 5.6%; Score 8; DB 5; Length 1621;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 75 EEHKGSS 82

Db 1019 EEHKGSS 1026

RESULT 20

Q07290

ID Q07290 PRELIMINARY; PRT; 1822 AA.

AC Q07290;

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

DE Epi* protein.

GN EPI*.

OS Streptococcus suis.

OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

OC Streptococcus.

OX NCBI_TaxID=1307;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=1890;

RA Smith H.E., Reek F.H., Vecht U., Gielkens A.L.J., Smits M.A.;

RT "Repeats in an extracellular protein of weakly pathogenic strains of

RT Streptococcus suis type 2 are absent in pathogenic strains.";

RL Infect. Immun. 61:3318-3326(1993).

DR EMBL; X71880; CAA50714.1; -.

DR PIR; S33441; S33441.

DR GO; GO:0016020; C:membrane; IEA.

DR InterPro; IPR005877; Gpos YSIRK.

DR Pfam; PF04650; YSIRK signal; 1

DR TIGRFAMs; TIGR01168; YSIRK signal; 1.

SQ SEQUENCE 1822 AA; 192632 MW; 3838960C77641D7D CRC64;

Query Match

Best Local Similarity 5.6%; Score 8; DB 2; Length 1822;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 109 AKNKIAKE 116

Db 1057 AKNKIAKE 1064

RESULT 21

Q57137

ID Q57137 PRELIMINARY; PRT; 66 AA.

AC Q57137;

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE Hypothetical protein.

OS Paracoccus denitrificans.

OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;

OC Rhodobacteraceae; Paracoccus.

OX NCBI_TaxID=266;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=95370157; PubMed=7642505;

RA Van Spanning R.J., Reijnders W.N., Stouthamer A.H.;
 RT "Integration of heterologous DNA into the genome of *Paracoccus*
 RT *denitrificans* is mediated by a family of IS1248-related elements and a
 RT second type of integrative recombination event."
 RL J. Bacteriol. 177:4772-4778 (1995).
 DR ENBL; U08856; AAA82147.1; -
 DR ENBL; U08864; AAC43508.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 66 AA; 7025 MW; 1865DD2D0F8316EC3 CRC64;

Query Match 4.9%; Score 7; DB 2; Length 66;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 APTLPPA 9
 |||||
 Db 33 APTLPPA 39

RESULT 22
 Q8DS63 PRELIMINARY; PRT; 102 AA.
 AC Q8DS63;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Conserved hypothetical protein.
 GN SMO.1972C.
 OS Streptococcus mutans.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1309;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=UAI59 / ATCC 700610 / Serotype C;
 RX MEDLINE=22295063; PubMed=12397186;
 RA Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
 RA Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S., Qian Y.,
 RA Li S., Zhu H., Najjar F., Lai H., White J., Roe B.A., Ferretti J.J.;
 RT "Genome sequence of *Streptococcus* mutans UAI59, a cariogenic dental
 RT pathogen".
 RL Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439 (2002).
 DR ENBL; AE015020; AAN59577.1; -
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 102 AA; 11678 MW; E4B1AA4265E0F554 CRC64;

Query Match 4.9%; Score 7; DB 16; Length 102;
 Best Local Similarity 100.0%; Pred. No. 34;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 89 VKQFEE 95
 |||||
 Db 27 VKQFEE 33

RESULT 23
 Q8PKK9 PRELIMINARY; PRT; 118 AA.
 AC Q8PKK9;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Hypothetical protein XAC2162.
 GN XAC2162.
 OS Xanthomonas axonopodis (pv. citri).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 OC Xanthomonadaceae; Xanthomonas.
 OX NCBI_TaxID=92829;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=306 / ATCC 13902 / XV 101;
 RX MEDLINE=22022145; PubMed=12024217;
 RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
 RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
 RA Camarotte G., Cannavan F., Cardozo J., Chamberg F., Ciapina L.P.,
 RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
 RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
 RA Formighieri E.F., Franco M.C., Gregio C.C., Gruber A.,
 RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
 RA Locati E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
 RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
 RA Moreira L.M., Novo M.I.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
 RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
 RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
 RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
 RA Setubal J.C., Kitajima J.P.;
 RT "Comparison of the genomes of two Xanthomonas pathogens with differing
 RT host specificities".
 RL Nature 417:459-463 (2002).
 DR ENBL; AE011853; AAM37015.1; -
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 118 AA; 12295 MW; DCEC804DDB651B0 CRC64;

Query Match 4.9%; Score 7; DB 16; Length 118;
 Best Local Similarity 100.0%; Pred. No. 38;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 APTLPPA 9
 |||||
 Db 44 APTLPPA 50

RESULT 24
 Q9ICW7 PRELIMINARY; PRT; 125 AA.
 AC Q9ICW7;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE RNA replicase (fragment).
 OS Kalanchoe latent virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Carlaviruses.
 OX NCBI_TaxID=132477;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PV-0290;
 RX MEDLINE=21342909; PubMed=11450944;
 RA Nicolaissen M., Nielsen S.L.;
 RT "Analysis of the triple gene block and coat protein sequences of two
 RT strains of Kalanchoe latent Carlavirus."
 RL Virus Genes 22:265-270 (2001).
 DR ENBL; AJ293571; CAB97502.1; -
 DR GO; GO:0003723; F:RNA binding; IEA.
 DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
 DR GO; GO:0006350; P:transcription; IEA.
 DR InterPro; IPR001788; RNA_dep_RNAPol2.
 DR Pfam; PF00978; RNA_dep_RNAPol2; 1.
 FT NON_TER
 SQ SEQUENCE 125 AA; 14327 MW; 20867AB30B7BA945 CRC64;

Query Match 4.9%; Score 7; DB 12; Length 125;
 Best Local Similarity 100.0%; Pred. No. 40;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 113 IAKETNN 119
 |||||
 Db 57 IAKETNN 63

RESULT 25
 Q18231 PRELIMINARY; PRT; 130 AA.
 ID Q18231
 AC Q18231;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

Query Match	Best Local Similarity	Score	DB	Length
Matches	7; Conservative	0; Mismatches	0; Indels	0; Gaps
QY	113 IAKETNN 119			
DB	62 IAKETNN 68			
SEQUENCE	130 AA; 14842 MW; 770B214D0D6CD7A0 CRC64;			
Query Match	4.9%;	Score	7; DB	12; Length
Best Local Similarity	100.0%;	Pred. No.	42;	
Matches	7; Conservative	0; Mismatches	0; Indels	0; Gaps
QY	113 IAKETNN 119			
DB	62 IAKETNN 68			
SEQUENCE	130 AA; 14842 MW; 770B214D0D6CD7A0 CRC64;			
Query Match	4.9%;	Score	7; DB	12; Length
Best Local Similarity	100.0%;	Pred. No.	46;	
Matches	7; Conservative	0; Mismatches	0; Indels	0; Gaps
QY	113 IAKETNN 119			
DB	81 IAKETNN 87			
SEQUENCE	149 AA; 17307 MW; BE6E5747657A7F54 CRC64;			
Query Match	4.9%;	Score	7; DB	12; Length
Best Local Similarity	100.0%;	Pred. No.	46;	
Matches	7; Conservative	0; Mismatches	0; Indels	0; Gaps
QY	113 IAKETNN 119			
DB	81 IAKETNN 87			
SEQUENCE	149 AA; 17307 MW; BE6E5747657A7F54 CRC64;			
Query Match	4.9%;	Score	7; DB	12; Length
Best Local Similarity	100.0%;	Pred. No.	46;	
Matches	7; Conservative	0; Mismatches	0; Indels	0; Gaps
QY	113 IAKETNN 119			
DB	81 IAKETNN 87			
SEQUENCE	149 AA; 17307 MW; BE6E5747657A7F54 CRC64;			
Query Match	4.9%;	Score	7; DB	12; Length
Best Local Similarity	100.0%;	Pred. No.	46;	
Matches	7; Conservative	0; Mismatches	0; Indels	0; Gaps
QY	113 IAKETNN 119			
DB	81 IAKETNN 87			
SEQUENCE	149 AA; 17307 MW; BE6E5747657A7F54 CRC64;			
Query Match	4.9%;	Score	7; DB	12; Length
Best Local Similarity	100.0%;	Pred. No.	46;	
Matches	7; Conservative	0; Mismatches	0; Indels	0; Gaps
QY	113 IAKETNN 119			
DB	81 IAKETNN 87			
SEQUENCE	149 AA; 17307 MW; BE6E5747657A7F54 CRC64;			
Query Match	4.9%;	Score	7; DB	12; Length
Best Local Similarity	100.0%;	Pred. No.	46;	
Matches	7; Conservative	0; Mismatches	0; Indels	0; Gaps
QY	113 IAKETNN 119			
DB	81 IAKETNN 87			
SEQUENCE	149 AA; 17307 MW; BE6E5747657A7F54 CRC64;			
Query Match	4.9%;	Score	7; DB	12; Length
Best Local Similarity	100.0%;	Pred. No.	46;	
Matches	7; Conservative	0; Mismatches	0; Indels	0; Gaps
QY	113 IAKETNN 119			
DB	81 IAKETNN 87			
SEQUENCE	149 AA; 17307 MW; BE6E5747657A7F54 CRC64;			
Query Match	4.9%;	Score	7; DB	12; Length
Best Local Similarity	100.0%;	Pred. No.	46;	
Matches	7; Conservative	0; Mismatches	0; Indels	0; Gaps
QY	113 IAKETNN 119			
DB	81 IAKETNN 87			
SEQUENCE	149 AA; 17307 MW; BE6E5747657A7F54 CRC64;			
Query Match	4.9%;	Score	7; DB	12; Length
Best Local Similarity	100.0%;	Pred. No.	46;	
Matches	7; Conservative	0; Mismatches	0; Indels	0; Gaps
QY	113 IAKETNN 119			
DB	81 IAKETNN 87			
SEQUENCE	149 AA; 17307 MW; BE6E5747657A7F54 CRC64;			
Query Match	4.9%;	Score	7; DB	12; Length
Best Local Similarity	100.0%;	Pred. No.	46;	
Matches	7; Conservative	0; Mismatches	0; Indels	0; Gaps
QY	113 IAKETNN 119			
DB	81 IAKETNN 87			
SEQUENCE	149 AA; 17307 MW; BE6E5747657A7F54 CRC64;			
Query Match	4.9%;	Score	7; DB	12; Length
Best Local Similarity	100.0%;	Pred. No.	46;	
Matches	7; Conservative	0; Mismatches	0; Indels	0; Gaps
QY	113 IAKETNN 119			
DB	81 IAKETNN 87			
SEQUENCE	149 AA; 17307 MW; BE6E5747657A7F54 CRC64;			
Query Match	4.9%;	Score	7; DB	12; Length

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RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Ngwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.,
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
  LT2."
RL Nature 413:852-856(2001).
RL EMBL; AE008914; AAL23367.1; -.
DR InterPro; IPR007214; YbaK.
DR Pfam; PF04073; YbaK; 1.
DR Hypothetical protein; Complete proteome.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 152 AA; 16273 MW; 1DE1B508E10C8653 CRC64;

Query Match 4.9%; Score 7; DB 16; Length 152;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 TPERMAE 40
DB 135 TPERMAE 141
|||||
RESULT 29
Q8ZOV6 PRELIMINARY; PRT; 152 AA.
AC Q8ZOV6
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein STY4902.
GN STY4902 OR T4592.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrall B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
  enterica serovar Typhi CT18."
RL Nature 413:848-852(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Ty2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=12644504;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodoyanni V., Schwartz D.C., Blattner F.R.;
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
  and CT18."
RL J. Bacteriol. 195:2330-2337(2003).
DR EMBL; AL627284; CA003387.1; -.
DR EMBL; AE016849; AA002027.1; -.
DR InterPro; IPR007214; YbaK.
DR Pfam; PF04073; YbaK; 1.
DR Hypothetical protein; Complete proteome.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 152 AA; 16229 MW; 1DE1B3B833EB3202 CRC64;

Query Match 4.9%; Score 7; DB 16; Length 152;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 TPERMAE 40
DB 135 TPERMAE 141
|||||

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DB 135 TPERMAE 141
RESULT 30
Q89D81 PRELIMINARY; PRT; 155 AA.
AC Q89D81
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE BLR7561 protein.
GN BLR7561.
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobiium.
OX NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USDA 110;
RX MEDLINE=22484998; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashina K.,
RA Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
  Bradyrhizobium japonicum USDA110."
RL DNA Res. 9:189-197(2002).
DR EMBL; AP005982; BAC52826.1; -.
DR InterPro; IPR007214; YbaK.
DR Pfam; PF04073; YbaK; 1.
KW Complete proteome.
SQ SEQUENCE 155 AA; 16422 MW; 469A81F631A1A17F CRC64;

Query Match 4.9%; Score 7; DB 16; Length 155;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 TPERMAE 40
DB 135 TPERMAE 141
|||||
RESULT 31
Q9QBX0 PRELIMINARY; PRT; 171 AA.
AC Q9QBX0
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Replicase (Fragment).
GN REP.
OS Lily latent virus (LiLV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Carlavirus.
OX NCBI_TaxID=92693;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Lilv-KK;
RA Ryu J.H., Park H.W., Park W.M., Lee S.Y., Ryu K.H.;
RT "Molecular analysis of the 3'-terminal region of lily latent
  Carlavirus from Lilium lancitolum."
RL J. Plant Pathol. 16:231-235(2000).
DR EMBL; AJ131812; CAB57958.1; -.
DR GO; GO:0003723; rRNA binding; IEA.
DR GO; GO:0003968; rRNA-directed RNA polymerase activity; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR GO; GO:0019079; P:Viral genome replication; IEA.
DR InterPro; IPR001788; RNA_dep_RNAPol2.
DR InterPro; IPR007094; RNA_pol_Psvir.
DR Pfam; PF00978; RNA_dep_RNAPol2; 1.
FT NON_TER
SQ SEQUENCE 171 AA; 19849 MW; 246D7C9729465F8 CRC64;

Query Match 4.9%; Score 7; DB 12; Length 171;

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Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 TAKETNN 119
Db 103 TAKETNN 109
|||||

RESULT 32
Q84F94 PRELIMINARY; PRT; 175 AA.
AC Q84F94;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE HslV-like protein.
OS Myxococcus xanthus.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
OC Cybacterineae; Myxococcaceae; Myxococcus.
OX NCBI_TaxID=34;
RN [1]
RP SEQUENCE FROM N.A.
RA Hartzell P.L., Youderian P.A.;
RT "Identification of genes required for adventurous gliding motility in
RT Myxococcus xanthus with the transposable element mariner.";
RL Submitted (DEC-2002) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AY204472; AAC22924.1; -
DR GO; GO:0005839; C:proteasome core complex (sensu Eukarya); IEA.
DR GO; GO:0004175; F:endorpeptidase activity; IEA.
DR GO; GO:0006511; P:ubiquitin-dependent protein catabolism; IEA.
DR InterPro; IPR001353; Peptidase_T1.
DR Pfam; PF00227; Proteasome; 1.
SQ SEQUENCE 127 AA; 19060 MW; D72BFCB837A6950A CRC64;

Query Match 4.9%; Score 7; DB 2; Length 175;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 TAKKVR 133
Db 34 TAKKVR 40
|||||

RESULT 33
Q8XKR3 PRELIMINARY; PRT; 178 AA.
AC Q8XKR3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Rubrerythrin.
GN RUBY OR CPE1331.
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=13 / Type A;
RX MEDLINE=21664373; PubMed=11792842;
RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
RT flesh-eater.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
DR EMBL; AF001190; BAB81037.1; -
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR009040; Ferritin like.
DR InterPro; IPR004039; Rubredox.
DR InterPro; IPR003251; Rubrerythrin.
DR Pfam; PF02915; Rubrerythrin; 1.
DR ProDom; PD006196; Rubrerythrin; 1.

DR PROSITE; PS50905; FERRITIN LIKE; 1.
DR PROSITE; PS50903; RUBREDOXIN LIKE; 1.
KW Complete proteome.
SQ SEQUENCE 178 AA; 21033 MW; F55A85ADB0F56A01 CRC64;

Query Match 4.9%; Score 7; DB 16; Length 178;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 122 KEFEETA 128
Db 91 KEFEETA 97
|||||

RESULT 34
Q834K3 PRELIMINARY; PRT; 182 AA.
ID Q834K3
AC Q834K3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Heat shock protein HslV.
GN HSLV OR EF1647.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=V583 / ATCC 700802;
RX MEDLINE=22550857; PubMed=12663927;
RA Paulsen I.T., Banerjee L., Myers G.S.A., Nelson K.E., Seshadri R.,
RA Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
RA Tettelin H., Dodson R.J., Umayam L., Brinkac L., Beanan M.,
RA Vamathevan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H.,
RA Utterback T., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M.;
RT "Role of mobile DNA in the evolution of vancomycin-resistant
RT Enterococcus faecalis.";
RL Science 299:2071-2074(2003).
DR EMBL; AE016952; AAC81425.1; -
DR TIGR; EF1647; -
DR GO; GO:0005839; C:proteasome core complex (sensu Eukarya); IEA.
DR GO; GO:0004175; F:endorpeptidase activity; IEA.
DR GO; GO:0003773; F:heat shock protein activity; IEA.
DR GO; GO:0006511; P:ubiquitin-dependent protein catabolism; IEA.
DR InterPro; IPR001353; Peptidase_T1.
DR Pfam; PF00227; Proteasome; 1.
DR Heat shock; Complete proteome.
KW Heat shock; Complete proteome.
SQ SEQUENCE 182 AA; 19712 MW; 76C1D6ABA7DE2237 CRC64;

Query Match 4.9%; Score 7; DB 16; Length 182;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 TAKKVR 133
Db 39 TAKKVR 45
|||||

RESULT 35
Q9JMX9 PRELIMINARY; PRT; 199 AA.
ID Q9JMX9
AC Q9JMX9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Cag-Z.
GN CAG-Z.
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN [1]


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AC Q07UM6;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical.
GN SYN0955.
OS Synechococcus sp. (strain WH8102).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=84588;
RN [1]
RP SEQUENCE FROM N.A. PubMed=12917641;
RX MEDLINE=22825697;
RA Palenik B., Brahamsha B., Larimer F.W., Land M., Hauser L., Chain P.,
RA Lamerdin J., Regala W., Allen E.E., McCarrren J., Paulsen I.,
RA Dufresne A., Partensky F., Webb E.A., Waterbury J.;
RT "The genome of a motile marine Synechococcus.";
RL Nature 424:1037-1042(2003).
DR EMBL; EX569691; CAB07470.1; -;
KW Hypothetical protein; Signal; Complete proteome.
FT SIGNAL 224 224
SQ SEQUENCE 224 AA; 25402 MW; D22937524F061D2B CRC64;

Query Match 4.9%; Score 7; DB 16; Length 224;
Best Local Similarity 100.0%; Pred. No. 65; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

OY 104 LDRERAK 110
DB 92 LDRERAK 98
|||||

RESULT 40
O58403 PRELIMINARY; PRT; 228 AA.
AC O58403;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE 228AA long hypothetical aspartate racemase.
GN PH0670.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=53953;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98344137; PubMed=9679194;
RA Kwarabavasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamanoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
RL DNA Res. 5:55-76(1998).
DR EMBL; AF000003; BAA29761.1; -;
DR PIR; G71112; G71112.
DR PDB; 1JFL; 25-DEC-02.
DR GO; GO:0016855; F:racemase and epimerase activity, acting on . . .; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR001920; Asp/Glu_race.
DR InterPro; IPR004380; Asp_race.
DR Pfam; PF01177; Asp_Glu_race; 1.
DR TIGRFAMs; TIGR00035; asp_race; 1.
DR PROSITE; PS00923; ASP_GLU_RACEMASE_1; 1.
DR PROSITE; PS00924; ASP_GLU_RACEMASE_2; 1.
KW Complete proteome.
SQ SEQUENCE 228 AA; 25157 MW; DD42CBEB39682CF CRC64;

Query Match 4.9%; Score 7; DB 17; Length 228;
Best Local Similarity 100.0%; Pred. No. 66; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

OY 125 BETAKKV 131
DB 105 BETAKKV 111
|||||

RESULT 42
Q37965 PRELIMINARY; PRT; 248 AA.
AC Q37965;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Antiterminator.
DR Q OR GENE 40.
OS Bacteriophage N15.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
OC Lambda-like viruses.
OX NCBI_TaxID=40631;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=N15CMI;
RX MEDLINE=96213032; PubMed=8631680;
RA Lobočka M.B., Svarchevsky A.N., Rybchin V.N., Yarmolinsky M.B.;
RT "Characterization of the primary immunity region of the Escherichia
RT coli linear plasmid prophage N15.";
RL J. Bacteriol. 178:2902-2910(1996).
RN [2]

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Best Local Similarity 100.0%; Pred. No. 66; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

OY 125 BETAKKV 131
DB 105 BETAKKV 111
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RESULT 41
Q9JUY1 PRELIMINARY; PRT; 228 AA.
AC Q9JUY1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Aspartate racemase.
GN RACD-1 OR PYRAB13760 OR PAB0912.
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=29292;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=GS / Orsay;
RA Heilig R.;
RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
RT structure and evolution.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ248287; CAB50281.1; -;
DR PIR; D75048; D75048.
DR GO; GO:0016855; F:racemase and epimerase activity, acting on . . .; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR001920; Asp/Glu_race.
DR InterPro; IPR004380; Asp_race.
DR Pfam; PF01177; Asp_Glu_race; 1.
DR TIGRFAMs; TIGR00035; asp_race; 1.
DR PROSITE; PS00923; ASP_GLU_RACEMASE_1; 1.
DR PROSITE; PS00924; ASP_GLU_RACEMASE_2; 1.
KW Complete proteome.
SQ SEQUENCE 228 AA; 25097 MW; 88B261B57A1D18C6 CRC64;

Query Match 4.9%; Score 7; DB 17; Length 228;
Best Local Similarity 100.0%; Pred. No. 66; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

OY 125 BETAKKV 131
DB 105 BETAKKV 111
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RP SEQUENCE FROM N.A.
RC STRAIN=N15CML;
RA Loboeka M.B.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Hendrix R.W., Ravin V.K., Casjens S.R., Ford M.E., Ravin N.V.,
RA Smirnov I.K.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; U45242; AB881658.1; -.
DR EMBL; AF064539; AAC19067.1; -.
DR PIR; T13126; T13126.
DR GO; GO:0005743; C:Mitochondrial inner membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001993; Mitoch carrier.
DR PROSITE; PS00215; MITOCH CARRIER; 1.
SQ SEQUENCE 246 AA; 28817 MW; 3CBEA8CC0388C7D3 CRC64;

Query Match 4.9%; Score 7; DB 9; Length 248;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 RRAIEQL 138
DB 91 RRAIEQL 97

RESULT 43
Q822K6 PRELIMINARY; PRT; 250 AA.
ID Q822K6
AC Q822K6
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Phosphosugar-binding transcriptional regulator, RpiR family,
DE putative.
GN EF3049.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=V583 / ATCC 700802;
RX MEDLINE=22550857; PubMed=12663927;
RA Paulsen I.T., Banerjee L., Myers G.S.A., Nelson K.E., Seshadri R.,
RA Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
RA Tettelin H., Dodson R.J., Umayam L., Brinkac L., Beanan M.,
RA Dougherty S., DeBoy R.T., Durkin S., Kolonay J., Madupu R.,
RA Vamathevan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H.,
RA Utterback T., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M.;
RT "Role of mobile DNA in the evolution of vancomycin-resistant
RT Enterococcus faecalis";
RL Science 299:2071-2074 (2003).
DR EMBL; AE016956; AAC82731.1; -.
DR TIGR; BF3049; -.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR001347; SIS.
DR Pfam; PF01360; SIS; 1.
DR Complete proteome.
RW
SQ SEQUENCE 250 AA; 28455 MW; 7C37D6590E2BC9AC CRC64;

Query Match 4.9%; Score 7; DB 16; Length 250;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EETAKKV 131
DB 158 EETAKKV 164

RESULT 44

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Q92TW2 PRELIMINARY; PRT; 253 AA.
ID Q92TW2
AC Q92TW2
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative proteocatechuate 3,4-dioxygenase beta chain protein (EC
DE 1.13.11.3).
GN PCAH OR R81489 OR SM320577.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21395508; PubMed=11481431;
RA Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P.,
RA Vorholter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J.,
RA Golding B., Puchler A.;
RT "The complete sequence of the 1.683-kb pSymB megaplasmid from the N2-
RT fixing endosymbiont Sinorhizobium meliloti";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894 (2001).
DR EMBL; AL603647; CAC49889.1; -.
DR PIR; A96028; A96028.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR GO; GO:0008199; F:ferric iron binding; IEA.
DR GO; GO:0016702; F:oxidoreductase activity, acting on single d. . .; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006725; P:aromatic compound metabolism; IEA.
DR InterPro; IPR000627; Dioxigenase.
DR Pfam; PF00775; Dioxigenase; 1.
DR PROSITE; PS00083; INTRADIOL_DIOXYGENAS; 1.
DE Dioxigenase; Oxidoreductase; Plasmid; Hypothetical protein;
DE Complete proteome.
RW
SQ SEQUENCE 253 AA; 28522 MW; 8D3A91173A144606 CRC64;

Query Match 4.9%; Score 7; DB 16; Length 253;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 RRAIEQL 138
DB 209 RRAIEQL 215

RESULT 45
Q8EBM3 PRELIMINARY; PRT; 255 AA.
ID Q8EBM3
AC Q8EBM3
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Transcriptional regulator, AraC/XylS family.
GN SO3488.
OS Shewanella oneidensis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Alteromonadaceae; Shewanella.
OX NCBI_TaxID=70863;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MR-1;
RX MEDLINE=22297686; PubMed=12368813;
RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
RA Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A.,
RA Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Dougherty S.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,
RA Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M.,
RA Vamathevan J., Weidman J., Imprim M., Lee K., Berry K., Lee C.,
RA Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A.,
RA Feldblyum T.V., Smith H.O., Venter J.C., Nealeon K.H., Fraser C.M.;
RT "Genome sequence of the dissimilatory metal ion-reducing bacterium

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RT Shewanella oneidensis";
RL Nat. Biotechnol. 20:1118-1123(2002).
DR EMBL; AF015785; AAN56481.1; -.
DR TIGR; SO3488; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; E:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR003313; Arac_binding.
DR InterPro; IPR000005; HTHARAC.
DR Pfam; PF02311; Arac_binding; 1.
DR Pfam; PF00165; HTH Arac; 2.
DR PRINTS; PR00032; HTHARAC.
DR SMART; SM00342; HTH ARAC; 1.
DR PROSITE; PS00041; HTH ARAC FAMILY 1; 1.
DR PROSITE; PS01124; HTH_ARAC_FAMILY_2; 1.
DR Complete proteome.
SQ SEQUENCE 255 AA; 28737 MW; B22E48B542E4235E CRC64;

Query Match 4.9%; Score 7; DB 16; Length 255;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 AIEQLAA 140
DB 213 AIEQLAA 219

RESULT 46
Q9M521 PRELIMINARY; PRT; 265 AA.
AC Q9M521;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Pinorea l-aricresinol reductase TH1.
OS Tsuga heterophylla (Western hemlock).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Tsuga.
OX NCBI_TaxID=3359;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stem;
RX MEDLINE=99167523; PubMed=10066819;
RA Gang D.R., Kasahara H., Xia Z.Q., Vander Mijnsbrugge K., Bauw G.,
RA Boerjan W., Van Montagu M., Davin L.B., Lewis N.G.;
RA "Evolution of plant defense mechanisms. Relationships of
RT phenylcoumaran benzylic ether reductases to pinorea l-aricresinol
RT and isoflavone reductases.";
RL J. Biol. Chem. 274:7516-7527(1999).
[2]

Query Match 4.9%; Score 7; DB 10; Length 265;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 KVRRAIE 136
DB 93 KVRRAIE 99

RESULT 47
O28569 PRELIMINARY; PRT; 271 AA.
ID O28569
AC O28569;
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DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein AF1704.
GN AF1704.
OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
OC Archaeoglobaceae; Archaeoglobus.
OX NCBI_TaxID=2234;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; PubMed=9389475;
RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
RA Richardson D.L., Karlavage A.R., Graham D.E., Kyripides N.C.,
RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Uterback T.,
RA Cotton M.D., Spriggs T., Artlich P., Kaine B.P., Sykes S.M.,
RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA Venter J.C.;
RA "The complete genome sequence of the hyperthermophilic, sulphate-
RT reducing archaeon Archaeoglobus fulgidus.";
RL Nature 390:364-370(1997).
DR EMBL; AE000986; AAB89546.1; -.
DR PIR; G69462; G69462.
DR TIGR; AF1704; -.
DR InterPro; IPR003794; DUF191.
DR Pfam; PF02642; DUF191; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 271 AA; 30820 MW; 5FA452411B211D36 CRC64;

Query Match 4.9%; Score 7; DB 17; Length 271;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 LDRERAK 110
DB 220 LDRERAK 226

RESULT 48
Q9M526 PRELIMINARY; PRT; 308 AA.
AC Q9M526;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Phenylcoumaran benzylic ether reductase homolog TH1.
OS Tsuga heterophylla (Western hemlock).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Tsuga.
OX NCBI_TaxID=3359;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stem;
RX MEDLINE=99167523; PubMed=10066819;
RA Gang D.R., Kasahara H., Xia Z.Q., Vander Mijnsbrugge K., Bauw G.,
RA Boerjan W., Van Montagu M., Davin L.B., Lewis N.G.;
RA "Evolution of plant defense mechanisms. Relationships of
RT phenylcoumaran benzylic ether reductases to pinorea l-aricresinol
RT and isoflavone reductases.";
RL J. Biol. Chem. 274:7516-7527(1999).
[2]

Query Match 4.9%; Score 7; DB 10; Length 265;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 KVRRAIE 136
DB 93 KVRRAIE 99

RESULT 47
O28569 PRELIMINARY; PRT; 271 AA.
ID O28569
AC O28569;
```

RT InterPro; IPR003866; Isoflav reduct.
RT Pfam; PF02716; Isoflavone redu; 1.
SQ SEQUENCE 308 AA; 33464 MW; F3CF7A3D123D0251 CRC64;

Query Match 4.9%; Score 7; DB 10; Length 308;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 KVRRAIE 136
Db 136 KVRRAIE 142
|||||

RESULT 49
Q9M522 PRELIMINARY; PRT; 308 AA.

ID Q9M522 AC
Q9M522; AC
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Phenylcoumaran benzylic ether reductase homolog TH7.
OS Tsuga heterophylla (Western hemlock).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Tsuga.
NCBI_TaxID=3359;
RX [1]
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stem;
RX MEDLINE=99167523; PubMed=10066819;
RA Gang D.R., Kasahara H., Xia Z.Q., Vander Mijnsbrugge K., Bauw G.,
RA Boerjan W., Van Montagu M., Davin L.B., Lewis N.G.;
RA "Evolution of plant defense mechanisms. Relationships of
RT phenylcoumaran benzylic ether reductases to pinosresinol-lariciresinol
RT and isoflavone reductases";
RL J. Biol. Chem. 274:7516-7527(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Stem;
RX MEDLINE=99167523; PubMed=10066819;
RA Gang D.R., Kasahara H., Xia Z.Q., Davin L.B., Lewis N.G.;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF242498; AAF64182.1; -
GO; GO:0003824; F:catalytic activity; IEA.
DR InterPro; IPR003866; Isoflav reduct.
DR Pfam; PF02716; Isoflavone redu; 1.
SQ SEQUENCE 308 AA; 33849 MW; DIA3FE2515A26DD CRC64;

Query Match 4.9%; Score 7; DB 10; Length 308;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 KVRRAIE 136
Db 136 KVRRAIE 142
|||||

RESULT 50
Q9M525 PRELIMINARY; PRT; 308 AA.

ID Q9M525 AC
Q9M525; AC
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Phenylcoumaran benzylic ether reductase homolog TH4.
OS Tsuga heterophylla (Western hemlock).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Tsuga.
NCBI_TaxID=3359;
RX [1]
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stem;
RX MEDLINE=99167523; PubMed=10066819;
RA Gang D.R., Kasahara H., Xia Z.Q., Vander Mijnsbrugge K., Bauw G.,
RA Boerjan W., Van Montagu M., Davin L.B., Lewis N.G.;
RA "Evolution of plant defense mechanisms. Relationships of
RT phenylcoumaran benzylic ether reductases to pinosresinol-lariciresinol
RT and isoflavone reductases";
RL J. Biol. Chem. 274:7516-7527(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Stem;
RX MEDLINE=99167523; PubMed=10066819;
RA Gang D.R., Kasahara H., Xia Z.Q., Davin L.B., Lewis N.G.;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF242498; AAF64182.1; -
GO; GO:0003824; F:catalytic activity; IEA.
DR InterPro; IPR003866; Isoflav reduct.
DR Pfam; PF02716; Isoflavone redu; 1.
SQ SEQUENCE 308 AA; 33849 MW; DIA3FE2515A26DD CRC64;

Query Match 4.9%; Score 7; DB 10; Length 308;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 KVRRAIE 136
Db 136 KVRRAIE 142
|||||

RESULT 51
Q9M525 PRELIMINARY; PRT; 308 AA.

ID Q9M525 AC
Q9M525; AC
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Phenylcoumaran benzylic ether reductase.
OS Pinus taeda (loblolly pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
NCBI_TaxID=3352;
RX [1]
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stem;
RX MEDLINE=99167523; PubMed=10066819;
RA Gang D.R., Kasahara H., Davin L.B., Lewis N.G.;
RA "Cloning of phenylcoumaran benzylic ether reductase from Pinus taeda
RT and heterologous expression of its recombinant protein in E. coli.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF081678; AAC32591.1; -
GO; GO:0003824; F:catalytic activity; IEA.
DR InterPro; IPR003866; Isoflav reduct.
DR Pfam; PF02716; Isoflavone redu; 1.
SQ SEQUENCE 308 AA; 33565 MW; 07F9DD1F2CC8B134 CRC64;

Query Match 4.9%; Score 7; DB 10; Length 308;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 KVRRAIE 136
Db 136 KVRRAIE 142
|||||

RESULT 52
Q9LL41 PRELIMINARY; PRT; 308 AA.

ID Q9LL41 AC
Q9LL41; AC
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Phenylcoumaran benzylic ether reductase PT1.
OS Pinus taeda (loblolly pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
NCBI_TaxID=3352;
RX [1]
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stem;
RX MEDLINE=99167523; PubMed=10066819;
RA Boerjan W., Van Montagu M., Davin L.B., Lewis N.G.;
RA "Evolution of plant defense mechanisms. Relationships of
RT phenylcoumaran benzylic ether reductases to pinosresinol-lariciresinol
RT and isoflavone reductases";
RL J. Biol. Chem. 274:7516-7527(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Stem;
RX MEDLINE=99167523; PubMed=10066819;
RA Gang D.R., Kasahara H., Xia Z.Q., Davin L.B., Lewis N.G.;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF242498; AAF64182.1; -
GO; GO:0003824; F:catalytic activity; IEA.
DR InterPro; IPR003866; Isoflav reduct.
DR Pfam; PF02716; Isoflavone redu; 1.
SQ SEQUENCE 308 AA; 33464 MW; F3CF7A3D123D0251 CRC64;

Query Match 4.9%; Score 7; DB 10; Length 308;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 KVRRAIE 136
Db 136 KVRRAIE 142
|||||

RESULT 53
Q9M525 PRELIMINARY; PRT; 308 AA.

ID Q9M525 AC
Q9M525; AC
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Phenylcoumaran benzylic ether reductase homolog TH4.
OS Tsuga heterophylla (Western hemlock).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Tsuga.
NCBI_TaxID=3359;
RX [1]
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stem;
RX MEDLINE=99167523; PubMed=10066819;
RA Gang D.R., Kasahara H., Xia Z.Q., Vander Mijnsbrugge K., Bauw G.,
RA Boerjan W., Van Montagu M., Davin L.B., Lewis N.G.;
RA "Evolution of plant defense mechanisms. Relationships of
RT phenylcoumaran benzylic ether reductases to pinosresinol-lariciresinol
RT and isoflavone reductases";
RL J. Biol. Chem. 274:7516-7527(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Stem;
RX MEDLINE=99167523; PubMed=10066819;
RA Gang D.R., Kasahara H., Xia Z.Q., Davin L.B., Lewis N.G.;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF242498; AAF64182.1; -
GO; GO:0003824; F:catalytic activity; IEA.
DR InterPro; IPR003866; Isoflav reduct.
DR Pfam; PF02716; Isoflavone redu; 1.
SQ SEQUENCE 308 AA; 33849 MW; DIA3FE2515A26DD CRC64;

Query Match 4.9%; Score 7; DB 10; Length 308;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 KVRRAIE 136
Db 136 KVRRAIE 142
|||||

RESULT 54
Q9M525 PRELIMINARY; PRT; 308 AA.

ID Q9M525 AC
Q9M525; AC
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Phenylcoumaran benzylic ether reductase homolog TH4.
OS Tsuga heterophylla (Western hemlock).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Tsuga.
NCBI_TaxID=3359;
RX [1

RA Gang D.R., Kasahara H., Xia Z.Q., Vander Mijnsbrugge K., Bauw G.,
 RA Boerjan W., Van Montagu M., Davin L.B., Lewis N.G.;
 RT "Evolution of plant defense mechanisms. Relationships of
 RT phenylcoumaran benzylic ether reductases to pinorensinol-lariciresinol
 RT and isoflavone reductases."; J. Biol. Chem. 274:7516-7527 (1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Gang D.R., Kasahara H., Xia Z.Q., Davin L.B., Lewis N.G.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF242490; AAF64173.2; -;
 DR GO; GO:0003824; F:catalytic activity; IEA.
 DR InterPro; IPR003866; Isoflav_reduct.
 DR Pfam; PF02716; Isoflavone_redu; 1.
 SQ SEQUENCE 308 AA; 33524 MW; E93FA4456C7854SF CRC64;

Query Match 4.9%; Score 7; DB 10; Length 308;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 130 KVRRAIE 136
 |||||
 Db 136 KVRRAIE 142

RESULT 53

Q9SM520 PRELIMINARY; PRT; 309 AA.

ID Q9SM520
 AC Q9SM520;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Pinorensinol-lariciresinol reductase TH2.
 OS Tsuga heterophylla (Western hemlock).
 CC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 CC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Tsuga.
 OX NCBI_TaxID=3359;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Stem;
 RX MEDLINE=99167523; PubMed=10066819;
 RA Gang D.R., Kasahara H., Xia Z.Q., Vander Mijnsbrugge K., Bauw G.,
 RA Boerjan W., Van Montagu M., Davin L.B., Lewis N.G.;
 RT "Evolution of plant defense mechanisms. Relationships of
 RT phenylcoumaran benzylic ether reductases to pinorensinol-lariciresinol
 RT and isoflavone reductases."; J. Biol. Chem. 274:7516-7527 (1999).
 RL J. Biol. Chem. 274:7516-7527 (1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Stem;
 RA Gang D.R., Kasahara H., Xia Z.Q., Davin L.B., Lewis N.G.;
 RL Submitted (Mar-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF242502; AAF64185.1; -;
 DR GO; GO:0003824; F:catalytic activity; IEA.
 DR InterPro; IPR003866; Isoflav_reduct.
 DR Pfam; PF02716; Isoflavone_redu; 1.
 SQ SEQUENCE 309 AA; 34814 MW; 5ADB69A362E3F3E1 CRC64;

Query Match 4.9%; Score 7; DB 10; Length 309;
 Best Local Similarity 100.0%; Pred. No. 85;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 130 KVRRAIE 136
 |||||
 Db 137 KVRRAIE 143

RESULT 54

Q9SD20 PRELIMINARY; PRT; 310 AA.

ID Q9SD20
 AC Q9SD20;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Isoflavone reductase homolog 2.
 GN IPR2;
 OS Glycine max (Soybean).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 CC Eumetazoa; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 OX NCBI_TaxID=3847;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tran M.H., Kufli K., Gijzen M.;
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF202184; AAF1578.1; -;
 DR GO; GO:0003824; F:catalytic activity; IEA.
 DR InterPro; IPR003866; Isoflav_reduct.
 DR Pfam; PF02716; Isoflavone_redu; 1.
 SQ SEQUENCE 310 AA; 33939 MW; 2E76DFPA1BA199B0 CRC64;

Query Match 4.9%; Score 7; DB 10; Length 310;
 Best Local Similarity 100.0%; Pred. No. 85;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 130 KVRRAIE 136
 |||||
 Db 137 KVRRAIE 143

RESULT 55

Q67551 PRELIMINARY; PRT; 312 AA.

ID Q67551
 AC Q67551;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE RNA replicase (Fragment).
 OS Garlic latent virus.
 CC Viruses; ssRNA positive-strand viruses, no DNA stage; Carlaviruses.
 OX NCBI_TaxID=12458;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tsuneyoshi T., Sumi S.;
 RT "Differentiation among garlic viruses in mixed infections based on RT-
 RT PCR procedures and direct tissue blotting immunoassays."; J. Phytopathology 86:253-259 (1996).
 DR EMBL; D11161; BAA01931.1; -;
 DR GO; GO:0003723; F:RNA binding; IEA.
 DR GO; GO:0003688; F:RNA-directed RNA polymerase activity; IEA.
 DR GO; GO:0006350; P:transcription; IEA.
 DR GO; GO:0019079; P:viral genome replication; IEA.
 DR InterPro; IPR001788; RNA_dep_RNAPol2.
 DR InterPro; IPR007095; RNA_pol_DS_PS.
 DR InterPro; IPR007094; RNA_pol_PSVir.
 DR Pfam; PF00978; RNA_dep_RNAPol2; 1.
 FT NON_TER
 SQ SEQUENCE 312 AA; 36230 MW; C79E6563DA488175 CRC64;

Query Match 4.9%; Score 7; DB 12; Length 312;
 Best Local Similarity 100.0%; Pred. No. 85;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 113 IAKETNN 119
 |||||
 Db 244 IAKETNN 250

RESULT 56

Q9LD14
ID Q9LD14 PRELIMINARY; PRT; 313 AA.
AC Q9LD14;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Pinorexinol-lariciresinol reductase.
OS Thuja plicata (Giant arborvitae).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Cupressaceae; Thuja.
OX NCBI_TaxID=3316;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stem;
RX MEDLINE=99091594; PubMed=9872995;
RA Fujita M., Gang D.R., Davin L.B., Lewis N.G.;
RT "Recombinant pinorexinol-lariciresinol reductases from western red
cedar (Thuja plicata) catalyze opposite enantiospecific conversions.";
RL J. Biol. Chem. 274:618-627(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Stem;
RX MEDLINE=99091594; PubMed=9872995;
RA Fujita M., Gang D.R., Davin L.B., Lewis N.G.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF242503; AAF63507.1; -
DR GO; GO:0003824; F:catalytic activity; IEA.
DR InterPro; IPR003866; Isoflav reduct.
DR Pfam; PF02716; Isoflavone reduct; 1.
SQ SEQUENCE 313 AA; 35580 MW; 3D3178ACE73E8B57 CRC64;
Query Match 4.9%; Score 7; DB 10; Length 313;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 130 KVRRAIE 136
Db 140 KVRRAIE 146
RESULT 57
Q9LD00
ID Q9LD00 PRELIMINARY; PRT; 314 AA.
AC Q9LD00;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Phenylcoumaran benzylic ether reductase homolog Tpl (Pinorexinol-
lariciresinol reductase).
OS Thuja plicata (Giant arborvitae).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Cupressaceae; Thuja.
OX NCBI_TaxID=3316;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Young Stem;
RX MEDLINE=99167523; PubMed=10066819;
RA Gang D.R., Kasahara H., Xia Z.Q., Vander Mijnsbrugge K., Bauw G.,
Boerjan W., Van Montagu M., Davin L.B., Lewis N.G.;
RT "Evolution of plant defense mechanisms. Relationships of
phenylcoumaran benzylic ether reductases to pinorexinol-lariciresinol
and isoflavone reductases.";
RL J. Biol. Chem. 274:7516-7527(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Young Stem;
RX MEDLINE=99091594; PubMed=9872995;
RA Fujita M., Gang D.R., Davin L.B., Lewis N.G.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Young Stem;
RX MEDLINE=99091594; PubMed=9872995;
RA Fujita M., Gang D.R., Davin L.B., Lewis N.G.;
RT "Recombinant pinorexinol-lariciresinol reductases from western red

cedar (Thuja plicata) catalyze opposite enantiospecific conversions.";
RL J. Biol. Chem. 274:618-627(1999).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Young Stem;
RX Fujita M., Gang D.R., Davin L.B., Lewis N.G.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF242500; AAF64183.1; -
DR EMBL; AF242505; AAF63509.1; -
DR GO; GO:0003824; F:catalytic activity; IEA.
DR InterPro; IPR003866; Isoflav reduct.
DR 2fam; PF02716; Isoflavone reduct; 1.
SQ SEQUENCE 314 AA; 35408 MW; 64BA4ED27EF6E8CB CRC64;
Query Match 4.9%; Score 7; DB 10; Length 314;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 130 KVRRAIE 136
Db 140 KVRRAIE 146
RESULT 58
OS9708
ID OS9708 PRELIMINARY; PRT; 343 AA.
AC OS9708;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein.
GN SPEC36.11.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97Zh-;
RA Lyne M., Wood V., Rajandream M.A., Barrell B.G., Hilbert H.,
Moestl D., Duesterhoeft A;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL023589; CAA19059.1; -
DR PIR; T40306; T40306.
DR GeneDB; Spombe; SPBC36.11; -
KW Hypothetical protein.
SQ SEQUENCE 343 AA; 37741 MW; A04C84F8C55DD5FF CRC64;
Query Match 4.9%; Score 7; DB 3; Length 343;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 75 BEHKHS 81
Db 330 BEHKHS 336
RESULT 59
Q7USB6
ID Q7USB6 PRELIMINARY; PRT; 353 AA.
AC Q7USB6;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein.
GN R54603.
OS Rhodospirillum rubrum.
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Pirellula.
OX NCBI_TaxID=117;
RN [-]
RP SEQUENCE FROM N.A.

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RC STRAIN=1;
RX MEDLINE=22735913; PubMed=12835416;
RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot I.,
RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
RA Schleener H., Anann R., Reinhardt R.;
RT "Complete genome sequence of the marine planctomycete Pirellula sp.
RL strain 1."; Acad. Sci. U.S.A. 100:8298-8303 (2003).
DR EMBL; BX294140; CAD73881.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 353 AA; 39090 MW; 48EDB8240A95B44C CRC64;

Query Match 4.9%; Score 7; DB 16; Length 353;
Best Local Similarity 100.0%; Pred. No. 95; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

Qy 136 EQLAAMD 142
Db 241 EQLAAMD 247

RESULT 50
Q9TXLO PRELIMINARY; PRT; 374 AA.
AC Q9TXLO;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN K04F1.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
[1]
RC SEQUENCE FROM N.A.
RP STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RA "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018 (1998).
[2]
RC SEQUENCE FROM N.A.
RP STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RA "The sequence of C. elegans cosmid K04F1.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
[3]
RC SEQUENCE FROM N.A.
RP STRAIN=Bristol N2;
RX Waterston R.;
RA "Direct Submission.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF106575; AAC78165.1; -.
DR PIR; G88955; G88955.
DR WormPep; K04F1.6; CE19957.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005006; F:epidermal growth factor receptor activity; IEA.
DR InterPro; IPR000494; EGFR_L domain.
DR Pfam; PF01030; Recep_L domain; I.
KW Hypothetical protein.
SQ SEQUENCE 374 AA; 43106 MW; 42BBE75C5ADBED10 CRC64;

Query Match 4.9%; Score 7; DB 5; Length 374;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 92 QFELTL 98
Db 236 QFELTL 242

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RESULT 61
Q9RT2 PRELIMINARY; PRT; 379 AA.
AC Q9RT2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein DR1694.
GN DR1694.
OS Deinococcus radiodurans.
OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=1299;
[1]
RC SEQUENCE FROM N.A.
RP STRAIN=R1 / ATCC 13939 / DSM 20539 / NCIB 9279;
RX MEDLINE=20036896; PubMed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
RA Makarova K.S., Aravind L., Daly M.J., Miron K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
RL radiodurans R1.";
RL Science 286:1571-1577 (1999).
DR EMBL; AE002011; ABF11251.1; -.
DR PIR; E75364; E75364.
DR TIGR; DR1694; -.
DR GO; GO:0008757; F:S-adenosylmethionine-dependent methyltransf. .; IEA.
DR InterPro; IPR000051; SAM bind.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 379 AA; 41459 MW; 83459F87DEABDC4C CRC64;

Query Match 4.9%; Score 7; DB 16; Length 379;
Best Local Similarity 100.0%; Pred. No. 1e+02; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

Qy 134 AIEQLAA 140
Db 262 AIEQLAA 268

RESULT 62
Q9I253 PRELIMINARY; PRT; 393 AA.
AC Q9I253;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Probable pyridoxal-phosphate dependent enzyme.
GN PA2062.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
[1]
RC SEQUENCE FROM N.A.
RP STRAIN=ATCC 15692 / PAO1;
RX MEDLINE=20437337; PubMed=10984043;
RA Stever C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Raizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
RL opportunistic pathogen.";
RL Nature 406:959-964 (2000).
DR EMBL; AE004633; AAG05450.1; -.
DR PIR; C83387; C83387.
DR GO; GO:0008483; F:transaminase activity; IEA.

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DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR000192; AminoTrans_V.
DR Pfam; PF00266; aminotran_5; 1.
DR PROSITE; PS00595; AA_TRANSER_CLASS_5; 1.
DR Complete proteome.
KW
SQ SEQUENCE 393 AA; 41520 MW; 38099C516ECSEBBSB CRC64;

Query Match
Best Local Similarity 4.9%; Score 7; DB 16; Length 393;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PAWQPF 14
DB 381 PAWQPF 387

RESULT 63
Q9AVV0 PRELIMINARY; PRT; 405 AA.
AC Q8AVV0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to splicing factor 3a, subunit 2, 66kDa.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.; to the EMBL/GenBank/DBJ databases.
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC041254; AA41254.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR000690; Znf_matriin.
DR SMART; SMO0451; ZNF_U1.
DR PROSITE; PSS0171; ZF_MATRIIN; 1.
SQ SEQUENCE 405 AA; 43673 MW; 2D91D3FCF2BFDFA60 CRC64;

Query Match
Best Local Similarity 4.9%; Score 7; DB 13; Length 405;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 APTLPPA 9
DB 220 APTLPPA 226

RESULT 64
Q9SCQ5 PRELIMINARY; PRT; 427 AA.
AC Q8SCQ5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN T3A5.90.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC
RA Bloembergen H., Mewes H.W., Lemcke K., Mayer K.F.X., Quetier F.,
RA Salanoubat M.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.

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RA EU Arabidopsis sequencing project;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL132979; CAB62440.1; -.
DR PIR; T46148; T46148.
DR InterPro; IPR001810; F-box.
DR InterPro; IPR006566; FBD.
DR InterPro; IPR001092; HLH_basic.
DR InterPro; IPR008945; SKI1_Skp2.
DR Pfam; PF00646; F-box; 1.
DR SMART; SMO0579; FBD; 1.
DR SMART; SMO0256; FBOX; 1.
DR PROSITE; PS00038; HLH_1; 1.
KW Hypothetical protein.
SQ SEQUENCE 427 AA; 49869 MW; DD61F344D0D2C003 CRC64;

Query Match
Best Local Similarity 4.9%; Score 7; DB 10; Length 427;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 DDPIEEH 77
DB 339 DDPIEEH 345

RESULT 65
Q26582 PRELIMINARY; PRT; 442 AA.
AC Q26582;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Heat shock protein 86 (fragment).
OS Schistosoma mansoni (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatoidea; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6183;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90043865; PubMed=2509907;
RA Johnson K.S., Wells K., Bock J.V., Nene V., Taylor D.W.,
RA Cordingley J.S.;
RT "the 86 kDa antigen from Schistosoma mansoni is a heat shock protein
RL homologous to yeast HSP-90.";
RL Mol. Biochem. Parasitol. 36:19-28(1989).
DR EMBL; J04017; AAA29899.1; -.
DR PIR; A45529; A45529.
DR GO; GO:0003754; F:chaperone activity; IEA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001404; Hsp90.
DR Pfam; PF00183; HSP90; 1.
DR InterPro; IPR00209; Peptidase_S8.
DR PROSITE; PS00136; SUBTILASE_ASP; 1.
FT NON_TER
SQ SEQUENCE 442 AA; 50996 MW; 48B83001936D6DBB CRC64;

Query Match
Best Local Similarity 4.9%; Score 7; DB 5; Length 442;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 90 KQOFEEL 96
DB 269 KQOFEEL 275

RESULT 66
Q89ZX8 PRELIMINARY; PRT; 467 AA.
AC Q89ZX8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative oxidoreductase (Putative secreted protein).

```

```
GN BT4243.
OS Bacteroides thetaiotaomicron.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=818;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=VPI-5482 / ATCC 29148;
RX MEDLINE=22550859; PubMed=12663928;
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
RA Chiang H.C., Hooper L.V., Gordon J.I.;
RA "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
RL Science 299:2074-2076(2003).
DR EMBL; AE016944; AA079348.1; -.
DR GO; GO:0016431; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000683; GFO_IDH_MocA.
DR Pfam; PF01408; GFO_IDH_MocA; 1.
KW Complete proteome.
SQ SEQUENCE 467 AA; 52831 MW; E0CE1286819FC2FB CRC64;

Query Match 4.9%; Score 7; DB 16; Length 467;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 125 EETAKV 131
Db 387 EETAKV 393

RESULT 67
Q8F9W0 PRELIMINARY; PRT; 501 AA.
AC Q8F9W0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Conserved hypothetical protein.
GN LA0078.
OS Leptospira interrogans.
OC Bacteria; Spirochaetes.
OC Bacteriia; Spirochaetales; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=173;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
RA Ren S.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE011199; AA047277.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 501 AA; 57403 MW; 46A887E1E8AA34DD CRC64;

Query Match 4.9%; Score 7; DB 16; Length 501;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 100 EFLKLD 106
Db 185 EFLKLD 191

RESULT 68
Q97E19 PRELIMINARY; PRT; 525 AA.
AC Q97E19;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Spore germination protein GerKA, membrane protein.
GN CAC3300.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1488;

[1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=11466286;
RA Noelling J., Breton G., Omeichenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
RA Bennett G.N., Koonin E.V., Smith D.R.;
RA "Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium acetobutylicum.";
RL J. Bacteriol. 183:4823-4839(2001).
DR EMBL; AE007827; AA081233.1; -.
DR PIR; F97305; F97305.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0009847; P:spore germination; IEA.
DR InterPro; IPR004995; GerA.
DR Pfam; PF03323; GerA; 1.
KW Complete proteome.
SQ SEQUENCE 525 AA; 58570 MW; BA2B14BF1818C4EA CRC64;

Query Match 4.9%; Score 7; DB 16; Length 525;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 94 BELTGE 100
Db 183 BELTGE 189

RESULT 69
Q87YV7 PRELIMINARY; PRT; 546 AA.
AC Q87YV7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Methyl-accepting chemotaxis protein.
GN PSPT03685.
OS Pseudomonas syringae (pv. tomato).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=323;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=DC3000;
RA Buell R., Joardar V., Khouri H., Fedorova N., Tran B., Russell D.,
RA Berry K., Utterback T., Van Aken S., Feldblyum T., Gwinn M.,
RA Dodson R., DeBoy R., Durkin A., Kolonay J., Madupu R., Daugherty S.,
RA Brinkac L., Beanan M., Haft D., Selengut J., Nelson W., Davidson T.,
RA White O., Fraser C., Collier A.;
RA "Complete sequence of Pseudomonas syringae.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE016869; AA057154.1; -.
DR TIGR; PSPT03685; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006935; P:chemotaxis; IEA.
DR GO; GO:0007165; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR004089; Chmtaxis_trans.
DR InterPro; IPR003660; HAMF.
DR InterPro; IPR000005; HTHARAC.
DR InterPro; IPR004090; Me_chemotaxis.
DR Pfam; PF00672; HAMF; 1.
DR PRINTS; PR00260; MCPsignal; 1.
DR PROSITE; PS00111; CHEMTAXIS_TRANSUC_2; 1.
DR PROSITE; PS00041; HTH_ARAC_FAMILY_1; 1.
KW Complete proteome.
SQ SEQUENCE 546 AA; 58319 MW; CD58FF6BE35AC1A0 CRC64;
```

Query Match 4.9%; Score 7; DB 16; Length 546;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 AIEQLAA 140
Db 350 AIEQLAA 356

RESULT 70
Q9LD30 PRELIMINARY; PRT; 579 AA.
AC Q9LD30;
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DE 01-OCT-2000 (TREMELrel. 15, Last annotation update)
DE Dipl-associated protein G (fragment).
GN DAPG.
OS Cryptocodium cohnii (Dinoflagellate).
OC Eukaryota; Alveolata; Dinophyceae; Gonyaulacales; Cryptocodiaceae;
OC Cryptocodium.
OX NCBI_TaxID=2866;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9305750; PubMed=10377987;
RA Bhaid Y., Geraud M.L., Ausseil J., Sayer-Gobillard M.O., Moreau H.;
RT "Cyclic expression of a nuclear protein in a dinoflagellate.";
RL J. Eukaryot. Microbiol. 46:259-267(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Gullebault D., Moreau H.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
FT EMBL; AF255447; AAF78929.1; -;
FT NON_TER 1
FT NON_TER 579 579
SQ SEQUENCE 579 AA; 65085 MW; FOC05B3CE5AE58AE CRC64;

Query Match 4.9%; Score 7; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PTLPPAW 10
Db 160 PTLPPAW 166

RESULT 71
Q87FL8 PRELIMINARY; PRT; 609 AA.
AC Q87FL8;
DT 01-JUN-2003 (TREMELrel. 24, Created)
DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)
DE 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Putative AcSD.
GN VPA1661.
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RIMD 2210633 / Serotype O3:k6;
RX MEDLINE=22508454; PubMed=12620739;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shingawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism distinct from that of V. cholerae.";
RL Lancet 361:743-749(2003).
DR EMBL; AP005089; BAC63004.1; -;
DR GO; GO:0015343; F:siderochrome-iron transporter activity; IEA.
DR GO; GO:0019290; P:siderochrome biosynthesis; IEA.
DR InterPro; IPR007310; IucA_lucc.

DR Pfam; PF04183; IucA_lucC; 1.
KW Complete proteome.
SQ SEQUENCE 609 AA; 69486 MW; 148CA003AAF2099E CRC64;

Query Match 4.9%; Score 7; DB 16; Length 609;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 VRAIEQ 137
Db 262 VRAIEQ 268

RESULT 72
Q8PZW5 PRELIMINARY; PRT; 625 AA.
AC Q8PZW5;
DT 01-OCT-2002 (TREMELrel. 22, Created)
DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
DE 01-OCT-2002 (TREMELrel. 22, Last annotation update)
DE Conserved protein.
GN MW0374.
OS Methanosarcina mazei (Methanosarcina frisia).
OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
OC Methanosarcinales; Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2209;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Goel / GO1 / ATCC BAA-199 / DSM 3647 / OCM 88;
RX MEDLINE=22120827; PubMed=12125824;
RA Deppenmeier U., Johann A., Hartsch T., Merkl R., Schmitz R.A.,
RA Martinez-Arias R., Henne A., Wierzer A., Baumer S., Jacobi C.,
RA Bruggemann H., Lienard T., Christmann A., Boencke M., Steckel S.,
RA Bhattacharya A., Lykdis A., Overbeek R., Klenk H.-P., Gunsalus R.P.,
RA Fritz H.-J., Gottschalk G.;
RT "The genome of Methanosarcina mazei: evidence for lateral gene transfer between Bacteria and Archaea.";
RL J. Mol. Microbiol. Biotechnol. 4:453-461(2002).
DR EMBL; AE013262; AAM30070.1; -;
KW Complete proteome.
SQ SEQUENCE 625 AA; 68028 MW; 811CFB57502DA3A1 CRC64;

Query Match 4.9%; Score 7; DB 17; Length 625;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 LKLDRE 108
Db 40 LKLDRE 46

RESULT 73
Q8EUJ0 PRELIMINARY; PRT; 671 AA.
AC Q8EUJ0;
DT 01-MAR-2003 (TREMELrel. 23, Created)
DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Phosphate ABC transporter permease PstA.
GN MYPE9360.
OS Mycoplasma penetrans.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=28227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HF-2;
RX MEDLINE=22354719; PubMed=12466555;
RA Sasaki Y., Ishikawa J., Yamashita A., Oshima K., Kenri T., Furuya K.,
RA Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.;
RT "The complete genomic sequence of Mycoplasma penetrans, an intracellular bacterial pathogen in humans.";
RL Nucleic Acids Res. 30:5293-5300(2002).
DR EMBL; AP004174; BAC44723.1; -;

DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000515; BPD transp.
DR Pfam; PF00528; BPD transp; 2.
KW Complete proteome.
SQ SEQUENCE 671 AA; 74044 MW; BBFC521F4CC311A3 CRC64;

Query Match 4.9%; Score 7; DB 16; Length 671;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 109 AKNKIAK 115
Db 452 AKNKIAK 458
|||||

RESULT 74
Q91VK6 PRELIMINARY; PRT; 673 AA.
AC Q91VK6
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast tumor;
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC012871; AAH12871.1; -
DR InterPro; IPR004018; RPEL_repeat.
DR Pfam; PF02755; RPEL; 4.
DR SMART; SM00707; RPEL; 4.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 673 AA; 73270 MW; 3D938DC6A2505820 CRC64;

Query Match 4.9%; Score 7; DB 11; Length 673;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 36 ERMAEAG 42
Db 46 ERMAEAG 52
|||||

RESULT 75
Q8ZJ11 PRELIMINARY; PRT; 698 AA.
AC Q8ZJ11
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE 4-alpha-glucanotransferase (EC 2.4.1.25) (Amylomaltase).
GN MALQ OR YPO0126 OR Y3902.
OS Versinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11596350;
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Parraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,

RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague."
RL Nature 413:523-527(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=KIM5 / Biovar Mediaevalis;
RX MEDLINE=22137863; PubMed=12142430;
RA Dang W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
RA Straley S.C., McDonough K.A., Milles M.L., Matson J.S., Blattner F.R.,
RA Perry R.D.;
RT "Genome sequence of Yersinia pestis KIM."
RL J. Bacteriol. 194:4601-4611(2002).
DR EMBL; AJ414141; CAC88989.1; -
DR EMBL; AE013995; AAM87446.1; -
DR PIR; AC0016; AC0016.
DR GO; GO:0004134; F:4-alpha-glucanotransferase activity; IEA.
DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR003385; Glyco_hydro_77.
DR Pfam; PF02446; 4A_glucoamylins; 1.
DR TIGRFAMs; TIGR00217; malQ.1.
KW Glycosyltransferase; Transferase; Complete proteome.
SQ SEQUENCE 698 AA; 78553 MW; 685512C27B2A682 CRC64;

Query Match 4.9%; Score 7; DB 16; Length 698;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 LDRERAK 110
Db 586 LDRERAK 592
|||||

Search completed: August 11, 2004, 14:25:06
Job time : 42 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 11, 2004, 14:17:41 ; Search time 54 Seconds
(without alignments)
742.995 Million cell updates/sec

Title: US-09-690-825-34
Perfect score: 142
Sequence: 1 NGATLPPAWOPFLKDHRS.....EFETAKVRRRAIQLAAMD 142

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 0
Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Listing first 100 summaries
Database : A_Geneseq_29Jan04: *
1: Geneseq1980s: *
2: Geneseq1990s: *
3: Geneseq2000s: *
4: Geneseq2001s: *
5: Geneseq2002s: *
6: Geneseq2003as: *
7: Geneseq2003bs: *
8: Geneseq2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	142	100.0	142	2	Aaw61359 Survivin
2	142	100.0	142	2	Aay49080 Human Sur
3	142	100.0	142	4	Aag65360 Human Her
4	142	100.0	142	5	Aau74571 Human sur
5	142	100.0	142	5	Aao14948 Survivin-
6	142	100.0	142	6	Abp72162 Human Sur
7	142	100.0	142	7	Abf61582 Human sur
8	142	100.0	143	4	Aau29999 Novel hum
9	132	93.0	142	5	Aau74573 Human mut
10	129	90.8	141	6	Abu56477 Lung canc
11	125	88.0	125	5	Aau74582 Human del
12	108	76.1	142	5	Aau74574 Human mut
13	96	67.6	142	5	Aau74577 Human mut
14	88	62.0	142	5	Aau74572 Human mut
15	87	61.3	142	5	Aau74578 Human mut
16	87	61.3	142	5	Aau74579 Human mut
17	82	57.7	142	5	Aau74580 Human mut
18	82	57.7	142	5	Aau74581 Human mut
19	79	55.6	142	5	Aau74575 Human mut
20	76	53.5	116	3	Agg02311 Human sec
21	75	52.8	75	7	Adb1824 Human inh
22	75	52.8	142	5	Aau74576 Human sur
23	74	52.1	165	6	Ada09936 Human sur
24	59	41.5	83	7	Adb1823 Human inh
25	41	28.9	140	2	Aaw19749 Mouse inh

99 6 4.2 65 4 AAM43557 Human pol
100 6 4.2 65 4 AAU19925 Novel hum

ALIGNMENTS

RESULT 1

AAW61359
ID AAW61359 standard; protein; 142 AA.
XX
AC AAW61359;
XX
DT 25-SEP-1998 (first entry)
XX
DE Survivin protein.
XX
KW survivin; apoptosis; cellular apoptosis; transplacental;
KW motor neuron degenerative disease; HIV infection; immunosuppression;
KW gastrointestinal perturbations; cardiovascular disorder.
XX
OS Homo sapiens.
XX
PN WO9822589-A2.
XX
PD 28-MAY-1998.
XX
PF 20-NOV-1997; 97WO-US021880.
XX
PR 20-NOV-1996; 96US-0031435P.
XX
PR 20-NOV-1997; 97US-00975080.
XX
PA (UYVA) UNIV YALE.
XX
PI Altieri DC;
XX
DR WPI; 1998-312475/27.
XX
DR N-PSDB; AAV27941.
XX
PT Modulating apoptosis by controlling the Survivin gene - useful for
PT treating transplant rejection, degenerative disorders and tumours.
XX
PS Disclosure; Fig 10; 108pp; English.
XX
CC The survivin gene can be used to control apoptosis through modification
CC of the gene. Survivin peptides can be used to inhibit cellular apoptosis,
CC e.g. for enhancing the viability of organs and tissues prior to their
CC transplantation, for preserving the growth of cells in culture or for
CC treating conditions involving abnormal apoptosis, e.g. degenerative
CC diseases such as motor neuron degenerative diseases, HIV infection,
CC dermatological effects of ageing, disorders and diseases such as
CC immunosuppression, gastrointestinal perturbations, cardiovascular
CC disorders, apoptosis related to reperfusion damage, rejection of tissue
CC transplantation and Alzheimer's disease. Agents which block Survivin
CC activity can be used to treat e.g. tumours

SQ Sequence 142 AA;

Query Match 100.0%; Score 142; DB 2; Length 142;
Best Local Similarity 100.0%; Pred. No. 1e-142;
Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGATLPPAWQFLKDHRISTFKNWPFLGCACTPERMAEAGFIHCPTENEPDLAQCF 60
DB 1 MGATLPPAWQFLKDHRISTFKNWPFLGCACTPERMAEAGFIHCPTENEPDLAQCF 60
QY 61 FKELEGNEPDDPTEEHKHSKSGCAFLSVKKQFPELTGLGFLKDRERAKNKIAKETNNK 120
DB 61 FKELEGNEPDDPTEEHKHSKSGCAFLSVKKQFPELTGLGFLKDRERAKNKIAKETNNK 120
QY 121 KKEFEETAKVRRRAIEQLAAMD 142
DB 121 KKEFEETAKVRRRAIEQLAAMD 142
QY 121 KKEFEETAKVRRRAIEQLAAMD 142
DB 121 KKEFEETAKVRRRAIEQLAAMD 142

RESULT 3
AAG65360

RESULT 2

AA49080
ID AAY49080 standard; protein; 142 AA.
XX
AC AAY49080;
XX
DT 17-JAN-2000 (first entry)
XX
DE Human Survivin amino acid sequence.
XX
KW Survivin; IAP; apoptosis inhibitor; tumour cell; mitotic spindle;
KW effector cell protease receptor-1; EPR-1; embryonic tissue; tubulin;
KW abnormal cell growth; tumorigenesis.
XX
OS Homo sapiens.
XX
PN WO9950440-A2.
XX
PD 07-OCT-1999.
XX
PF 01-APR-1999; 99WO-US007205.
XX
PR 01-APR-1998; 98US-0080288P.
XX
PA (UYVA) UNIV YALE.
XX
PI Altieri DC;
XX
DR WPI; 1999-591329/50.
DR N-PSDB; AAZ31037.
XX
PT Identifying agents that modulate Survivin interactions.
XX
PS Example; Fig 8A; 56pp; English.
XX
CC This is the amino acid sequence of the human survivin protein. Survivin
CC is a 142 amino acid protein of approximately 16.5kD. Survivin is a member
CC of the IAP family of apoptosis inhibitors, and the gene is located on
CC chromosome 17q25. The nucleic acid sequence of Survivin is related to the
CC Effector Cell Protease Receptor-1 (EPR-1). Survivin is expressed in
CC tumour cells and embryonic tissue. The sequence is used in the invention
CC which involves identifying an agent that modulates interactions between
CC Survivin and tubulin. Agents that modulate interaction between Survivin
CC and tubulin or mitotic spindles may be administered to a mammal to
CC modulate biological or pathological processes mediated by Survivin, for
CC example Survivin-mediated inhibition of cellular apoptosis. Thus an
CC inhibiting agent may be used to block abnormal cell growth, for example
CC during tumorigenesis. An agent that increases interaction may be used to
CC extend cell growth in culture

SQ Sequence 142 AA;

Query Match 100.0%; Score 142; DB 2; Length 142;
Best Local Similarity 100.0%; Pred. No. 1e-142;
Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGATLPPAWQFLKDHRISTFKNWPFLGCACTPERMAEAGFIHCPTENEPDLAQCF 60
DB 1 MGATLPPAWQFLKDHRISTFKNWPFLGCACTPERMAEAGFIHCPTENEPDLAQCF 60
QY 61 FKELEGNEPDDPTEEHKHSKSGCAFLSVKKQFPELTGLGFLKDRERAKNKIAKETNNK 120
DB 61 FKELEGNEPDDPTEEHKHSKSGCAFLSVKKQFPELTGLGFLKDRERAKNKIAKETNNK 120
QY 121 KKEFEETAKVRRRAIEQLAAMD 142
DB 121 KKEFEETAKVRRRAIEQLAAMD 142

ID AC AAG65360 standard; protein; 142 AA.
 AC AAG65360;
 DT 30-NOV-2001 (first entry)
 DE Human Her-3 polypeptide sequence.
 DE Her-3; epidermal growth factor; EGF; receptor/tyrosine kinase; human;
 KW antiinflammatory; cytostatic; antibacterial; antisense.
 KW Homo sapiens.
 OS US6277640-B1.
 PN 21-AUG-2001.
 PD 31-JUL-2000; 2000US-00630706.
 PF 31-JUL-2000; 2000US-00630706.
 PR (ISIS-) ISIS PHARM INC.
 XX Bennett CF, Cowser LM;
 PI WPI; 2001-535134/S9.
 DR N-PSDB; AAH47531.
 XX Antisense compounds capable of modulating expression of human Her-3,
 PT member of epidermal growth factor family of receptor/tyrosine kinases,
 PT useful for preventing or delaying infection, inflammation or tumor
 PT formation.
 XX Example 15; Col 57-70; 49pp; English.
 XX The invention provides antisense compounds capable of inhibiting the
 CC expression of human Her-3, a member of epidermal growth factor (EGF)
 CC family of receptor/tyrosine kinases. The antisense oligonucleotides are
 CC useful for inhibiting the expression of Her-3 in cells or tissues. They
 CC are commonly used as research reagents and in diagnostics for example, to
 CC elucidate the function of particular genes. The antisense compounds are
 CC also useful for distinguishing between functions of various members of a
 CC biological pathway and for research use. They are also utilized for
 CC diagnostics, therapeutics, prophylaxis and in kits. They are useful
 CC prophylactically, e.g. to prevent or delay infection, inflammation or
 CC tumor formation. The present sequence represents the human Her-3 sequence
 CC (GenBank Accession No. U75285)
 XX Sequence 142 AA;
 SQ Query Match 100.0%; Score 142; DB 4; Length 142;
 Best Local Similarity 100.0%; Pred. No. 1e-142;
 Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGAPTLPPAQWFLKDHRISTFKWPFLEGGCACTPERMAEAGFIHCPTEPEDLAQCFFC 60
 DB 1 MGAPTLPPAQWFLKDHRISTFKWPFLEGGCACTPERMAEAGFIHCPTEPEDLAQCFFC 60
 QY 61 FKELEGWEPDDPIEBHKHSSGC AFLSVKQFPELTIGEFKLDREAKNKIAKETNNK 120
 DB 61 FKELEGWEPDDPIEBHKHSSGC AFLSVKQFPELTIGEFKLDREAKNKIAKETNNK 120
 QY 121 KKEFEETAKKVRRAIEQLAAMD 142
 DB 121 KKEFEETAKKVRRAIEQLAAMD 142
 RESULT 4
 AAU74571
 ID AAU74571 standard; protein; 142 AA.
 XX AAU74571;
 AC AAU74571;
 XX

DT 08-MAY-2002 (first entry)
 XX Human survivin polypeptide.
 DE Human; survivin; inhibitor of apoptosis protein; IAP; cytostatic; p21;
 KW tubulin interaction; caspase-3; CDK4; zinc chelation activity; apoptosis;
 KW dimerisation; ovary; breast; pancreas; central nervous system; blood;
 KW lung; skin; lymph node; brain; kidney; liver; nasopharyngeal cavity;
 KW thyroid; prostate; colon; rectum; cervix; endometrium; cancer; AIDS;
 KW cell proliferative disorder; acquired immunodeficiency syndrome;
 KW neurodegenerative disease; ischaemic injury; toxin-induced liver disease;
 KW myelodysplastic syndrome; protein coordinate data.
 OS Homo sapiens.
 XX WC200202622-A2.
 PN 10-JAN-2002.
 PD 29-JUN-2001; 2001WO-US020872.
 PF 29-JUN-2000; 2000US-00608352.
 PR (SALK) SALK INST BIOLOGICAL STUDIES.
 XX Noel JP, Verdacia M, Hunter T, Huang H;
 PI WPI; 2002-171638/22.
 DR Novel isolated crystalline survivin polypeptide, useful to screen and
 PT design compounds that bind to or interact with inhibitor of apoptosis
 PT protein and protein family members, and for design of novel therapeutics.
 XX Claim 42; Fig 2; 102pp; English.
 XX The invention relates to an isolated crystalline human survivin
 CC polypeptide, an inhibitor of apoptosis protein (IAP). The polypeptide is
 CC useful for determining the ability of a survivin binding agent to
 CC modulate tubulin interaction, p21 caspase-3 and CDK4 requirement or zinc
 CC chelation activity and for identifying an agent such as a peptide or zinc
 CC peptidomimetic which inhibits dimerisation of survivin. The ability of an
 CC agent to modulate dimerisation can be determined through detection of a
 CC change in apoptosis in a target cell expressing survivin. Binding agents
 CC are useful for increasing apoptosis in a cell derived from a tissue
 CC selected from ovary, breast, pancreas, lymph node, skin, blood, lung,
 CC brain, kidney, liver, nasopharyngeal cavity, thyroid, central nervous
 CC system, prostate, colon, rectum, cervix or endometrium, with a cell
 CC proliferative disorder such as cancer. The molecules can also be used in
 CC treatment or prevention of apoptosis which occurs as a part of AIDS,
 CC neurodegenerative diseases, ischaemic injury, toxin-induced liver disease
 CC and myelodysplastic syndromes. This sequence represents the human
 CC survivin polypeptide
 XX Sequence 142 AA;
 SQ Query Match 100.0%; Score 142; DB 5; Length 142;
 Best Local Similarity 100.0%; Pred. No. 1e-142;
 Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGAPTLPPAQWFLKDHRISTFKWPFLEGGCACTPERMAEAGFIHCPTEPEDLAQCFFC 60
 DB 1 MGAPTLPPAQWFLKDHRISTFKWPFLEGGCACTPERMAEAGFIHCPTEPEDLAQCFFC 60
 QY 61 FKELEGWEPDDPIEBHKHSSGC AFLSVKQFPELTIGEFKLDREAKNKIAKETNNK 120
 DB 61 FKELEGWEPDDPIEBHKHSSGC AFLSVKQFPELTIGEFKLDREAKNKIAKETNNK 120
 QY 121 KKEFEETAKKVRRAIEQLAAMD 142
 DB 121 KKEFEETAKKVRRAIEQLAAMD 142
 RESULT 5

AA014948
 ID AAO14948 standard; protein; 142 AA.
 XX
 AC AAO14948;
 XX
 DT 06-AUG-2002 (first entry)
 XX
 DE Survivin-like protein 6.
 XX
 KW Survivin-like protein; diagnosis; screening; cancer;
 KW apoptosis abnormality; gene therapy.
 XX
 OS Unidentified.
 XX
 PN WO200233071-A1.
 XX
 PD 25-APR-2002.
 XX
 PF 16-OCT-2001; 2001WO-JP009071.
 XX
 PR 17-OCT-2000; 2000JP-00316721.
 PR 20-DEC-2000; 2000JP-00386809.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Tanaka H, Kaieda I;
 XX
 DR WPI; 2002-435536/46.
 DR N-PSDB; AAL42859.
 XX
 PT Baculovirus IAP repeat domain or RING-finger domain-containing survivin-like polypeptides and encoded DNAs, applicable in diagnosis and screening compounds for treating various cancers and apoptosis abnormality.
 XX
 PS Disclosure; Page 122-123; 136pp; Japanese.
 XX
 CC The invention comprises the amino acid and coding sequences of survivin-like proteins. The survivin-like DNA and protein sequences are useful in diagnostics and screening compounds for treating various cancers and apoptosis abnormality, including gene therapy. The present amino acid sequence represents a survivin-like protein of the invention
 XX
 SQ Sequence 142 AA;
 Query Match 100.0%; Score 142; DB 5; Length 142;
 Best Local Similarity 100.0%; Pred. No. 1e-142;
 Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGAPTLPPAQPFKDHRISTFKNWPFLGCACTPERMAEAGFIHCPTENEPDLAQCFPC 60
 Db 1 MGAPTLPPAQPFKDHRISTFKNWPFLGCACTPERMAEAGFIHCPTENEPDLAQCFPC 60
 QY 61 FKELEGWEPDDPIEHHKHSSGCAFLSVKKQFEELTLGFLKLDREAKNKIAKETNNK 120
 Db 61 FKELEGWEPDDPIEHHKHSSGCAFLSVKKQFEELTLGFLKLDREAKNKIAKETNNK 120
 QY 121 KKEFEETAKVRRRAIEQLAAMD 142
 Db 121 KKEFEETAKVRRRAIEQLAAMD 142
 RESULT 6
 ABP72162
 ID ABP72162 standard; protein; 142 AA.
 XX
 AC ABP72162;
 XX
 DT 22-APR-2003 (first entry)
 XX
 DE Human Survivin.
 XX
 KW Human; Survivin; inhibitor of apoptosis; cell death; apoptosis; cancer; cytostatic; cardiant; neuroprotective; gene therapy.

XX Homo sapiens.
 OS WO2003004606-A2.
 PN 16-JAN-2003.
 PD 03-JUL-2002; 2002WO-US021002.
 PF 03-JUL-2001; 2001US-00898158.
 PR (UYCO) UNIV COLUMBIA NEW YORK.
 PA Troy CM, Shelanski ML;
 PI WPI; 2003-210351/20.
 DR N-PSDB; ABZ58106.
 XX
 PT New nucleic acid encoding an inhibitor-of-apoptosis protein, useful for treating cancer, neurodegenerative disorder or cardiomyopathy.
 XX
 PS Disclosure; Fig 20A; 124pp; English.
 XX
 CC The present sequence is the protein sequence of human Survivin protein. The invention provides a nucleic acid, such as an antisense oligonucleotide, which specifically hybridizes to a nucleic acid encoding an inhibitor of apoptosis protein. Survivin is an example of an inhibitor of apoptosis or inducer of cell death protein of the invention. A claimed method for inducing a cell's death comprises contacting the cell with the nucleic acid under conditions permitting the nucleic acid to enter the cell, especially the use of a vector, liposome, or a mechanical or electrical means. The method is used to treat acute lymphocytic leukaemia, acute myelogenous leukaemia, lung cancer, breast cancer, ovarian cancer, prostate cancer, lymphoma, Hodgkin's disease, malignant melanoma, neuroblastoma, renal cell carcinoma and squamous cell carcinoma (all claimed). The invention also provides a second nucleic acid, which specifically hybridizes to a nucleic acid encoding a protein, other than caspase-2, that induces cell death. A claimed method for inhibiting a cell's death comprises contacting the cell with the nucleic acid under conditions permitting the nucleic acid to enter the cell. The method is used to treat a neurodegenerative disorder (especially a brain disorder or central nervous system disorder), or a heart disorder (especially cardiomyopathy) in a human (all claimed)
 XX
 SQ Sequence 142 AA;
 Query Match 100.0%; Score 142; DB 6; Length 142;
 Best Local Similarity 100.0%; Pred. No. 1e-142;
 Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGAPTLPPAQPFKDHRISTFKNWPFLGCACTPERMAEAGFIHCPTENEPDLAQCFPC 60
 Db 1 MGAPTLPPAQPFKDHRISTFKNWPFLGCACTPERMAEAGFIHCPTENEPDLAQCFPC 60
 QY 61 FKELEGWEPDDPIEHHKHSSGCAFLSVKKQFEELTLGFLKLDREAKNKIAKETNNK 120
 Db 61 FKELEGWEPDDPIEHHKHSSGCAFLSVKKQFEELTLGFLKLDREAKNKIAKETNNK 120
 QY 121 KKEFEETAKVRRRAIEQLAAMD 142
 Db 121 KKEFEETAKVRRRAIEQLAAMD 142
 RESULT 7
 ABR61582
 ID ABR61582 standard; protein; 142 AA.
 XX
 AC ABR61582;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Human survivin protein.
 XX

KW RasGAP; Aurora kinase; cytostatic; anti-tumoural; human; survivin.
 XX Homo sapiens.
 OS
 PN W02003087395-A2.
 XX
 XX
 XX
 PD 23-OCT-2003.
 XX
 XX
 PF 15-APR-2003; 2003WO-IB002972.
 XX
 XX
 PR 15-APR-2002; 2002US-0372483P.
 XX
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 XX
 XX Garbay C, Gigoux V, Camonis J, L'hoste S, Samson J;
 PI
 XX WPI; 2003-845340/78.
 DR
 DR N-PSDB; ACF58071.
 XX
 XX Identifying anti-tumoral compounds, comprises determining the capacity of
 PT a compound to inhibit interaction between RasGAP and Drosophila
 PT melanogaster (Dm) aurora kinase, or between RasGAP, Dm aurora kinase and
 PT aurora binding protein.
 XX
 XX Disclosure; Page 67; Opp; English.
 XX
 XX The invention relates to identifying a biologically active compound with
 CC anti-tumoural properties, where the compound is studied for its capacity
 CC to inhibit the interaction between: (a) RasGAP and the Drosophila
 CC melanogaster Aurora kinase or an orthologue of the kinase, or its
 CC fragment able to interact with RasGAP; or (b) RasGAP, an Aurora-binding
 CC protein and the D. melanogaster Aurora kinase or an orthologue of the
 CC kinase, or its fragment. The method is useful for identifying anti-
 CC tumoural agents. The present sequence represents a human survivin
 CC protein, an aurora-binding protein
 XX
 XX Sequence 142 AA;

Query Match 100.0%; Score 142; DB 7; Length 142;
 Best Local Similarity 100.0%; Pred. No. 1e-142;
 Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGAPTLPPAWQPLKDHRISTFKNWPFLGGCACTPERMAEAGFIHCPTENEPDLAQCFPC 60
 Db 1 MGAPTLPPAWQPLKDHRISTFKNWPFLGGCACTPERMAEAGFIHCPTENEPDLAQCFPC 60
 QY 61 FKELEGWEPDDPIBEHKKHSSGCAFLSVKKQFELTLGEFLKDRERAKNKIAKETNNK 120
 Db 61 FKELEGWEPDDPIBEHKKHSSGCAFLSVKKQFELTLGEFLKDRERAKNKIAKETNNK 120
 QY 121 KKEFEETAKKVRRAIEQLAAMD 142
 Db 121 KKEFEETAKKVRRAIEQLAAMD 142

RESULT 8
 AAU29999
 ID AAU29999 standard; protein; 143 AA.
 XX
 AC AAU29999;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Novel human secreted protein #490.
 XX
 KW Human; vaccination; gene therapy; nutritional supplement;
 KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN W0200179449-A2.
 XX

PD 25-OCT-2001.
 XX
 XX 16-APR-2001; 2001WO-US008636.
 XX
 PR 18-APR-2000; 2000US-00552929.
 PR 26-JAN-2001; 2001US-00770160.
 XX
 XX (HYSB-) HYSEQ INC.
 PA
 XX
 XX Tang YT, Liu C, Drmanac RT;
 PI
 XX WPI; 2001-611725/70.
 DR
 XX
 PT Nucleic acids encoding a range of human polypeptides, useful in genetic
 PT vaccination, testing and therapy.
 XX
 XX Claim 20; Page 219; 765pp; English.
 XX
 XX The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising the
 CC nucleic acids encoding the polypeptides and cells genetically engineered
 CC to express them are also useful for producing the proteins. The proteins
 CC are useful in genetic vaccination, testing and therapy, and can be used
 CC as nutritional supplements. They may be used to increase stem cell
 CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon
 CC and/or nerve tissue growth or regeneration; immune suppression and/or
 CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.
 CC AAU2510-AAU3304 represent the amino acid sequences of novel human
 CC secreted proteins of the invention
 XX
 XX Sequence 143 AA;

Query Match 100.0%; Score 142; DB 4; Length 143;
 Best Local Similarity 100.0%; Pred. No. 1e-142;
 Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGAPTLPPAWQPLKDHRISTFKNWPFLGGCACTPERMAEAGFIHCPTENEPDLAQCFPC 60
 Db 1 MGAPTLPPAWQPLKDHRISTFKNWPFLGGCACTPERMAEAGFIHCPTENEPDLAQCFPC 60
 QY 61 FKELEGWEPDDPIBEHKKHSSGCAFLSVKKQFELTLGEFLKDRERAKNKIAKETNNK 120
 Db 61 FKELEGWEPDDPIBEHKKHSSGCAFLSVKKQFELTLGEFLKDRERAKNKIAKETNNK 120
 QY 121 KKEFEETAKKVRRAIEQLAAMD 142
 Db 121 KKEFEETAKKVRRAIEQLAAMD 142

RESULT 9
 AAU74573
 ID AAU74573 standard; protein; 142 AA.
 XX
 AC AAU74573;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE Human mutant W10A survivin polypeptide.
 XX
 KW Human; survivin; inhibitor of apoptosis protein; IAP; cytosolic; p21;
 KW tubulin interaction; caspase-3; CDK4; zinc chelation activity; apoptosis;
 KW dimerization; ovary; breast; pancreas; central nervous system; blood;
 KW lung; skin; lymph node; brain; kidney; liver; nasopharyngeal cavity;
 KW thyroid; prostate; colon; rectum; cervix; endometrium; cancer; AIDS;
 KW cell proliferative disorder; acquired immunodeficiency syndrome;
 KW neurodegenerative disease; ischaemic injury; toxin-induced liver disease;
 KW myelodysplastic syndrome; protein coordinate data; mutant; mutein.
 KW

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XX OS Homo sapiens.
XX OS Synthetic.
XX FT Key Location/Qualifiers
XX FT Misc-difference 10
XX FT /note= "Wild-type Trp substituted by Ala"
XX PN WO200202622-A2.
XX XX
XX PD 10-JAN-2002.
XX XX
XX PF 29-JUN-2001; 2001WO-US020872.
XX XX
XX PR 29-JUN-2000; 2000US-00608352.
XX XX
XX PA (SALK ) SALK INST BIOLOGICAL STUDIES.
XX PI Noel JP, Verdacia M, Hunter T, Huang H;
XX DR WPI; 2002-171638/22.
XX XX
XX PT Novel isolated crystalline survivin polypeptide, useful to screen and
XX PT design compounds that bind to or interact with inhibitor of apoptosis
XX PT protein and protein family members, and for design of novel therapeutics.
XX PS Claim 8; Page; 102pp; English.
XX XX
XX CC The invention relates to an isolated crystalline human survivin
XX CC polypeptide, an inhibitor or apoptosis protein (IAP). The polypeptide is
XX CC useful for determining the ability of a survivin binding agent to
XX CC modulate tubulin interaction, p21, caspase-3 and CDK4 requirement or zinc
XX CC chelation activity and for identifying an agent such as a peptide or
XX CC peptidomimetic which inhibits dimerisation of survivin. The ability of a
XX CC agent to modulate dimerisation can be determined through detection of a
XX CC change in apoptosis in a target cell expressing survivin. Binding agents
XX CC are useful for increasing apoptosis in a cell derived from a tissue
XX CC selected from ovary, breast, pancreas, lymph node, skin, blood, lung,
XX CC brain, kidney, liver, nasopharyngeal cavity, thyroid, central nervous
XX CC system, prostate, colon, rectum, cervix or endometrium, with a cell
XX CC proliferative disorder such as cancer. The molecules can also be used in
XX CC treatment or prevention of apoptosis which occurs as a part of AIDS,
XX CC neurodegenerative diseases, ischaemic injury, toxin-induced liver disease
XX CC and myelodysplastic syndromes. This sequence represents a human mutant
XX CC survivin polypeptide. Note: This sequence is not featured in the printed
XX CC specification but was derived from the wild type protein shown in
XX CC AAU74571
XX SQ Sequence 142 AA;
XX
XX Query Match 93.0%; Score 132; DB 5; Length 142;
XX Best Local Similarity 100.0%; Pred. No. 4.6e-132; Indels 0; Gaps 0;
XX Matches 132; Conservative 0; Mismatches 0;
XX
XX QY 11 QPFLKDHRISTFKNWPFLGCGACTPERMAEAGFIHCPTENEPLAQCFPCFKELEGWEPD 70
XX DB 11 QPFLKDHRISTFKNWPFLGCGACTPERMAEAGFIHCPTENEPLAQCFPCFKELEGWEPD 70
XX
XX QY 71 DDFIEBKHSSGCAFLSVKKQFEELTLGEFLKDRERAKNKIAKETNNKKKEPETAKK 130
XX DB 71 DDFIEBKHSSGCAFLSVKKQFEELTLGEFLKDRERAKNKIAKETNNKKKEPETAKK 130
XX
XX QY 131 VRRAIQLAAMD 142
XX DB 131 VRRAIQLAAMD 142
XX
XX RESULT 10
XX ABUS6477
XX ID ABUS6477 standard; protein; 141 AA.
XX AC
XX ABUS6477;
XX XX

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DT 02-APR-2003 (first entry)
XX Lung cancer-associated polypeptide #70.
XX
XX KW Lung cancer-associated polypeptide; cytostatic; emphysema;
XX KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
XX KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
XX KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
XX KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
XX
XX OS Unidentified.
XX PN WO200286443-A2.
XX PD 31-OCT-2002.
XX
XX PF 18-APR-2002; 2002WO-US012476.
XX PR 18-APR-2001; 2001US-0284770P.
XX PR 10-MAY-2001; 2001US-0290492P.
XX PR 09-NOV-2001; 2001US-0339245P.
XX PR 13-NOV-2001; 2001US-0350666P.
XX PR 29-NOV-2001; 2001US-0334370P.
XX PR 12-APR-2002; 2002US-0372246P.
XX PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
XX PI Aziz N, Murray R;
XX
XX DR WPI; 2003-093161/08.
XX DR N-PSDB; ABX76199.
XX
XX PT Detecting a lung cancer-associated transcript in a cell from a patient
XX PT for treating lung cancer, by contacting a biological sample from the
XX PT patient with a polynucleotide that exhibits increased or decreased
XX PT expression in lung cancer.
XX
XX PS Claim 27; Page 242; 453pp; English.
XX
XX CC The invention relates to a method for detecting a lung cancer-associated
XX CC transcript in a cell from a patient, comprising contacting a biological
XX CC sample from the patient with a polynucleotide that selectively hybridises
XX CC to a sequence that is at least 80 % identical to a gene that exhibits
XX CC increased or decreased expression in lung cancer samples. Lung cancer-
XX CC associated polynucleotides and polypeptides are used for identifying a
XX CC compound that modulates a lung cancer-associated polypeptide, for
XX CC inhibiting proliferation of a lung cancer-associated cell to treat lung
XX CC cancer in a patient and for treating a mammal having lung cancer by
XX CC administering a modulatory compound identified. The methods are useful
XX CC for treating lung cancer, such as small cell lung cancer, non-small cell
XX CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,
XX CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
XX CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
XX CC bronchiectasis. The genes, polynucleotides and polypeptides are useful
XX CC for diagnostic purposes and as targets for screening for therapeutic
XX CC compounds that modulate lung cancer, such as antibodies. Sequences
XX CC ABUS6408-ABUS6745 represent lung cancer-associated polypeptides of the
XX CC invention
XX SQ Sequence 141 AA;
XX
XX Query Match 90.8%; Score 129; DB 6; Length 141;
XX Best Local Similarity 100.0%; Pred. No. 7e-129;
XX Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MGAPTLPPAWQPFLLKDHRISTFKNWPFLGCGACTPERMAEAGFIHCPTENEPLAQCFPC 60
XX DB 1 MGAPTLPPAWQPFLLKDHRISTFKNWPFLGCGACTPERMAEAGFIHCPTENEPLAQCFPC 60
XX
XX QY 61 FKELEGWEPDDPIEBKHSSGCAFLSVKKQFEELTLGEFLKDRERAKNKIAKETNNK 120
XX DB 61 FKELEGWEPDDPIEBKHSSGCAFLSVKKQFEELTLGEFLKDRERAKNKIAKETNNK 120

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QY 121 KKEFEETAK 129
 Db 121 KKEFEETAK 129

RESULT 11
 AAU74582
 ID AAU74582 standard; protein; 125 AA.
 XX
 AC AAU74582;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE Human deletion mutant delta126-142 survivin polypeptide.
 XX
 KW Human; survivin; inhibitor of apoptosis protein; IAP; cytosolic; p21;
 KW tubulin interaction; caspase-3; CDK4; zinc chelation activity; apoptosis;
 KW dimerisation; ovary; breast; pancreas; central nervous system; blood;
 KW lung; skin; lymph node; brain; kidney; liver; nasopharyngeal cavity;
 KW thyroid; prostate; colon; rectum; cervix; endometrium; cancer; AIDS;
 KW cell proliferative disorder; acquired immunodeficiency syndrome;
 KW neurodegenerative disease; ischaemic injury; toxin-induced liver disease;
 KW myelodysplastic syndrome; protein coordinate data; mutant; mutin.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200202622-A2.
 PD 10-JAN-2002.
 XX
 PF 29-JUN-2001; 2001WO-US020872.
 XX
 PR 29-JUN-2000; 2000US-00608352.
 XX
 PA (SALK) SALK INST BIOLOGICAL STUDIES.
 XX
 PI Noel JP, Verdacia M, Hunter T, Huang H;
 XX
 DR WPI; 2002-171638/22.
 XX
 PT Novel isolated crystalline survivin polypeptide, useful to screen and
 PT design compounds that bind to or interact with inhibitor of apoptosis
 PT protein and protein family members, and for design of novel therapeutics.
 XX
 PS Claim 8; Page; 102pp; English.
 XX
 CC The invention relates to an isolated crystalline human survivin
 CC polypeptide, an inhibitor of apoptosis protein (IAP). The polypeptide is
 CC useful for determining the ability of a survivin binding agent to
 CC modulate tubulin interaction, p21, caspase-3 and CDK4 requirement or zinc
 CC chelation activity and for identifying an agent such as a peptide or
 CC peptidomimetic which inhibits dimerisation of survivin. The ability of an
 CC agent to modulate dimerisation can be determined through detection of a
 CC change in apoptosis in a target cell expressing survivin. Binding agents
 CC are useful for increasing apoptosis in a cell derived from a tissue
 CC selected from ovary, breast, pancreas, lymph node, skin, blood, lung,
 CC brain, kidney, liver, nasopharyngeal cavity, thyroid, central nervous
 CC system, prostate, colon, rectum, cervix or endometrium, with a cell
 CC treatment or prevention of apoptosis which occurs as a part of AIDS,
 CC neurodegenerative diseases, ischaemic injury, toxin-induced liver disease
 CC and myelodysplastic syndromes. This sequence represents a human deletion
 CC mutant survivin polypeptide, whereby residues 126-142 of the wild-type
 CC sequence have been deleted. Note: this sequence is not featured in the
 CC printed specification but was derived from the wild type protein shown in
 CC AAU74571

Sequence 125 AA;
 Query Match 88.0%; Score 125; DB 5; Length 125;
 Best Local Similarity 100.0%; Pred. No. 1.1e-124; Indels 0; Gaps 0;
 Matches 125; Conservative 0; Mismatches 0;

RESULT 12
 AAU74574
 ID AAU74574 standard; protein; 142 AA.
 XX
 AC AAU74574;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE Human mutant T34E survivin polypeptide.
 XX
 KW Human; survivin; inhibitor of apoptosis protein; IAP; cytosolic; p21;
 KW tubulin interaction; caspase-3; CDK4; zinc chelation activity; apoptosis;
 KW dimerisation; ovary; breast; pancreas; central nervous system; blood;
 KW lung; skin; lymph node; brain; kidney; liver; nasopharyngeal cavity;
 KW thyroid; prostate; colon; rectum; cervix; endometrium; cancer; AIDS;
 KW cell proliferative disorder; acquired immunodeficiency syndrome;
 KW neurodegenerative disease; ischaemic injury; toxin-induced liver disease;
 KW myelodysplastic syndrome; protein coordinate data; mutant; mutin.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200202622-A2.
 PD 10-JAN-2002.
 XX
 PF 29-JUN-2001; 2001WO-US020872.
 XX
 PR 29-JUN-2000; 2000US-00608352.
 XX
 PA (SALK) SALK INST BIOLOGICAL STUDIES.
 XX
 PI Noel JP, Verdacia M, Hunter T, Huang H;
 XX
 DR WPI; 2002-171638/22.
 XX
 PT Novel isolated crystalline survivin polypeptide, useful to screen and
 PT design compounds that bind to or interact with inhibitor of apoptosis
 PT protein and protein family members, and for design of novel therapeutics.
 XX
 PS Claim 8; Page; 102pp; English.
 XX
 CC The invention relates to an isolated crystalline human survivin
 CC polypeptide, an inhibitor of apoptosis protein (IAP). The polypeptide is
 CC useful for determining the ability of a survivin binding agent to
 CC modulate tubulin interaction, p21, caspase-3 and CDK4 requirement or zinc
 CC chelation activity and for identifying an agent such as a peptide or
 CC peptidomimetic which inhibits dimerisation of survivin. The ability of an
 CC agent to modulate dimerisation can be determined through detection of a
 CC change in apoptosis in a target cell expressing survivin. Binding agents
 CC are useful for increasing apoptosis in a cell derived from a tissue
 CC selected from ovary, breast, pancreas, lymph node, skin, blood, lung,
 CC brain, kidney, liver, nasopharyngeal cavity, thyroid, central nervous
 CC system, prostate, colon, rectum, cervix or endometrium, with a cell
 CC treatment or prevention of apoptosis which occurs as a part of AIDS,
 CC neurodegenerative diseases, ischaemic injury, toxin-induced liver disease
 CC and myelodysplastic syndromes. This sequence represents a human deletion
 CC mutant survivin polypeptide, whereby residues 126-142 of the wild-type
 CC sequence have been deleted. Note: this sequence is not featured in the
 CC printed specification but was derived from the wild type protein shown in
 CC AAU74571

CC treatment or prevention of apoptosis which occurs as a part of AIDS,
 CC neurodegenerative diseases, ischemic injury, toxin-induced liver disease
 CC and myelodysplastic syndromes. This sequence represents a human mutant
 CC survivin polypeptide. Note: This sequence is not featured in the printed
 CC specification but was derived from the wild type protein shown in
 CC AAU74571
 XX
 SQ Sequence 142 AA;
 Query Match 76.1%; Score 108; DB 5; Length 142;
 Best Local Similarity 100.0%; Pred. No. 1.6e-106;
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 35 PERMAEAGFIHCPTEHPDIAQCFKCELEGWEPDDPIEHHKSSGCAFLSVKKQFE 94
 DB 35 PERMAEAGFIHCPTEHPDIAQCFKCELEGWEPDDPIEHHKSSGCAFLSVKKQFE 94
 QY 95 ELTLGEFLKDRERAKNIAKETNNKKKEFEETAKKVRRAIEQLAAMD 142
 DB 95 ELTLGEFLKDRERAKNIAKETNNKKKEFEETAKKVRRAIEQLAAMD 142
 RESULT 13
 AAU74577
 ID AAU74577 standard; protein; 142 AA.
 XX
 AC AAU74577;
 DT 08-MAY-2002 (first entry)
 DE Human mutant T97E survivin polypeptide.
 KW Human; survivin; inhibitor of apoptosis protein; IAP; cytostatic; p21;
 KW tubulin interaction; caspase-3; CDK4; zinc chelation activity; apoptosis;
 KW dimerisation; ovary; breast; pancreas; central nervous system; blood;
 KW lung; skin; lymph node; brain; kidney; liver; nasopharyngeal cavity;
 KW thyroid; prostate; colon; rectum; cervix; endometrium; cancer; AIDS;
 KW cell proliferative disorder; acquired immunodeficiency syndrome;
 KW neurodegenerative disease; ischemic injury; toxin-induced liver disease;
 KW myelodysplastic syndrome; protein coordinate data; mutant; muten.
 XX Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 97 /note= "Wild-type Thr substituted by Glu"
 FT
 XX WO200202622-A2.
 FN
 XX
 PD 10-JAN-2002.
 XX
 PF 29-JUN-2001; 2001WO-US020872.
 XX
 PR 29-JUN-2000; 2000US-00608352.
 XX
 XX (SALK) SALK INST BIOLOGICAL STUDIES.
 PA
 XX Noel JP, Verdacia M, Hunter T, Huang H;
 XX WPI; 2002-171638/22.
 DR
 XX Novel isolated crystalline survivin polypeptide, useful to screen and
 PT design compounds that bind to or interact with inhibitor of apoptosis
 PT protein and protein family members, and for design of novel therapeutics.
 XX
 PS Claim 8; Page; 102pp; English.
 XX
 CC The invention relates to an isolated crystalline human survivin
 CC polypeptide, an inhibitor or apoptosis protein (IAP). The polypeptide is
 CC useful for determining the ability of a survivin binding agent to
 CC modulate tubulin interaction, p21, caspase-3 and CDK4 requirement or zinc
 CC chelation activity and for identifying an agent such as a peptide or

CC peptidomimetic which inhibits dimerisation of survivin. The ability of an
 CC agent to modulate dimerisation can be determined through detection of a
 CC change in apoptosis in a target cell expressing survivin. Binding agents
 CC are useful for increasing apoptosis in a cell derived from a tissue
 CC selected from ovary, breast, pancreas, lymph node, skin, blood, lung,
 CC brain, kidney, liver, nasopharyngeal cavity, thyroid, central nervous
 CC system, prostate, colon, rectum, cervix or endometrium, with a cell
 CC proliferative disorder such as cancer. The molecules can also be used in
 CC treatment or prevention of apoptosis which occurs as a part of AIDS,
 CC neurodegenerative diseases, ischemic injury, toxin-induced liver disease
 CC and myelodysplastic syndromes. This sequence represents a human mutant
 CC survivin polypeptide. Note: This sequence is not featured in the printed
 CC specification but was derived from the wild type protein shown in
 CC AAU74571
 XX
 SQ Sequence 142 AA;
 Query Match 67.6%; Score 96; DB 5; Length 142;
 Best Local Similarity 100.0%; Pred. No. 9.2e-94;
 Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGAPTLPPAWQPFLLKDHRISTFTKQWPFLEGCACTPERMAEAGFIHCPTEHPDIAQCFFC 60
 DB 1 MGAPTLPPAWQPFLLKDHRISTFTKQWPFLEGCACTPERMAEAGFIHCPTEHPDIAQCFFC 60
 QY 61 FKELEGWEPDDPIEHHKSSGCAFLSVKKQFEEL 96
 DB 61 FKELEGWEPDDPIEHHKSSGCAFLSVKKQFEEL 96
 RESULT 14
 AAU74572
 ID AAU74572 standard; protein; 142 AA.
 XX
 AC AAU74572;
 DT 08-MAY-2002 (first entry)
 DE Human mutant L54M survivin polypeptide.
 KW Human; survivin; inhibitor of apoptosis protein; IAP; cytostatic; p21;
 KW tubulin interaction; caspase-3; CDK4; zinc chelation activity; apoptosis;
 KW dimerisation; ovary; breast; pancreas; central nervous system; blood;
 KW lung; skin; lymph node; brain; kidney; liver; nasopharyngeal cavity;
 KW thyroid; prostate; colon; rectum; cervix; endometrium; cancer; AIDS;
 KW cell proliferative disorder; acquired immunodeficiency syndrome;
 KW neurodegenerative disease; ischemic injury; toxin-induced liver disease;
 KW myelodysplastic syndrome; protein coordinate data; mutant; muten.
 XX Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 54 /note= "Wild-type Leu substituted by Met"
 FT
 XX WO200202622-A2.
 FN
 XX
 PD 10-JAN-2002.
 XX
 PF 29-JUN-2001; 2001WO-US020872.
 XX
 PR 29-JUN-2000; 2000US-00608352.
 XX
 XX (SALK) SALK INST BIOLOGICAL STUDIES.
 PA
 XX Noel JP, Verdacia M, Hunter T, Huang H;
 XX WPI; 2002-171638/22.
 DR
 XX Novel isolated crystalline survivin polypeptide, useful to screen and
 PT design compounds that bind to or interact with inhibitor of apoptosis
 PT protein and protein family members, and for design of novel therapeutics.
 XX

XX PS Claim 7; Page; 102pp; English.

XX CC The invention relates to an isolated crystalline human survivin

XX CC polypeptide, an inhibitor of apoptosis protein (IAP). The polypeptide is

XX CC useful for determining the ability of a survivin binding agent to

XX CC modulate tubulin interaction, p21, caspase-3 and CDK4 requirement or zinc

XX CC chelation activity and for identifying an agent such as a peptide or

XX CC peptidomimetic which inhibits dimerisation of survivin. The ability of an

XX CC agent to modulate dimerisation can be determined through detection of a

XX CC change in apoptosis in a target cell expressing survivin. Binding agents

XX CC are useful for increasing apoptosis in a cell derived from a tissue

XX CC selected from ovary, breast, pancreas, lymph node, skin, blood, lung,

XX CC brain, kidney, liver, nasopharyngeal cavity, thyroid, central nervous

XX CC system, prostate, colon, rectum, cervix or endometrium, with a cell

XX CC proliferative disorder such as cancer. The molecules can also be used in

XX CC treatment or prevention of apoptosis which occurs as a part of AIDS,

XX CC neurodegenerative diseases, ischaemic injury, toxin-induced liver disease

XX CC and myelodysplastic syndromes. This sequence represents a human mutant

XX CC survivin polypeptide. Note: This sequence is not featured in the printed

XX CC specification but was derived from the wild type protein shown in

XX CC AAU74571

XX SQ Sequence 142 AA;

Query Match 62.0%; Score 88; DB 5; Length 142;

Best Local Similarity 100.0%; Pred. No. 3e-85;

Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 55 AQCFFCPKELEGWEPDDPIEHHKXSSGCAFLSVKKQFEELTGLGFLKLDRAKNKIA 114

Db 55 AQCFFCPKELEGWEPDDPIEHHKXSSGCAFLSVKKQFEELTGLGFLKLDRAKNKIA 114

Qy 115 KETNNKKKEFEETAKVRRRAIEQLAAMD 142

Db 115 KETNNKKKEFEETAKVRRRAIEQLAAMD 142

RESULT 15

AAU74578

ID AAU74578 standard; protein; 142 AA.

XX AC AAU74578;

XX DT 08-MAY-2002 (first entry)

XX DE Human mutant W10A/L98A/F101R/L102S survivin polypeptide.

XX KW Human; survivin; inhibitor of apoptosis protein; IAP; cytostatic; p21;

XX KW tubulin interaction; caspase-3; CDK4; zinc chelation activity; apoptosis;

XX KW dimerisation; ovary; breast; pancreas; central nervous system; blood;

XX KW lung; skin; lymph node; brain; kidney; liver; nasopharyngeal cavity;

XX KW thyroid; prostate; colon; rectum; cervix; endometrium; cancer; AIDS;

XX KW cell proliferative disorder; acquired immunodeficiency syndrome;

XX KW neurodegenerative disease; ischaemic injury; toxin-induced liver disease;

XX KW myelodysplastic syndrome; protein coordinate data; mutant; mutin.

XX OS Homo sapiens.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Misc-difference 10

FT /note= "Wild-type Trp substituted by Ala"

FT Misc-difference 98

FT /note= "Wild-type Leu substituted by Ala"

FT Misc-difference 101

FT /note= "Wild-type Phe substituted by Arg"

FT Misc-difference 102

FT /note= "Wild-type Leu substituted by Ser"

XX WO200202622-A2.

XX PN 10-JAN-2002.

XX PD

XX PF 29-JUN-2001; 2001WO-US020872.

XX PR 29-JUN-2000; 2000US-00608352.

XX PA (SALK) SALK INST BIOLOGICAL STUDIES.

XX PI Noel JP, Verdacia M, Hunter T, Huang H;

XX DR WPI; 2002-171638/22.

XX PT Novel isolated crystalline survivin polypeptide, useful to screen and

XX PT design compounds that bind to or interact with inhibitor of apoptosis

XX PT protein and protein family members, and for design of novel therapeutics.

XX PS Claim 8; Page; 102pp; English.

XX CC The invention relates to an isolated crystalline human survivin

XX CC polypeptide, an inhibitor of apoptosis protein (IAP). The polypeptide is

XX CC useful for determining the ability of a survivin binding agent to

XX CC modulate tubulin interaction, p21, caspase-3 and CDK4 requirement or zinc

XX CC chelation activity and for identifying an agent such as a peptide or

XX CC peptidomimetic which inhibits dimerisation of survivin. The ability of an

XX CC agent to modulate dimerisation can be determined through detection of a

XX CC change in apoptosis in a target cell expressing survivin. Binding agents

XX CC are useful for increasing apoptosis in a cell derived from a tissue

XX CC selected from ovary, breast, pancreas, lymph node, skin, blood, lung,

XX CC brain, kidney, liver, nasopharyngeal cavity, thyroid, central nervous

XX CC system, prostate, colon, rectum, cervix or endometrium, with a cell

XX CC proliferative disorder such as cancer. The molecules can also be used in

XX CC treatment or prevention of apoptosis which occurs as a part of AIDS,

XX CC neurodegenerative diseases, ischaemic injury, toxin-induced liver disease

XX CC and myelodysplastic syndromes. This sequence represents a human mutant

XX CC survivin polypeptide. Note: This sequence is not featured in the printed

XX CC specification but was derived from the wild type protein shown in

XX CC AAU74571

XX SQ Sequence 142 AA;

Query Match 61.3%; Score 87; DB 5; Length 142;

Best Local Similarity 100.0%; Pred. No. 3.5e-84;

Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 QPFLKHRISTFKWPFLEGGCACTPERVAEAGFIHCPTENEPDLAQCFFCPKELEGWEPD 70

Db 11 QPFLKHRISTFKWPFLEGGCACTPERVAEAGFIHCPTENEPDLAQCFFCPKELEGWEPD 70

Qy 71 DDPIEHHKXSSGCAFLSVKKQFEELT 97

Db 71 DDPIEHHKXSSGCAFLSVKKQFEELT 97

RESULT 16

AAU74579

ID AAU74579 standard; protein; 142 AA.

XX AC AAU74579;

XX DT 08-MAY-2002 (first entry)

XX DE Human mutant L6G/W10A/L98A/F101R/L102S survivin polypeptide.

XX KW Human; survivin; inhibitor of apoptosis protein; IAP; cytostatic; p21;

XX KW tubulin interaction; caspase-3; CDK4; zinc chelation activity; apoptosis;

XX KW dimerisation; ovary; breast; pancreas; central nervous system; blood;

XX KW lung; skin; lymph node; brain; kidney; liver; nasopharyngeal cavity;

XX KW thyroid; prostate; colon; rectum; cervix; endometrium; cancer; AIDS;

XX KW cell proliferative disorder; acquired immunodeficiency syndrome;

XX KW neurodegenerative disease; ischaemic injury; toxin-induced liver disease;

XX KW myelodysplastic syndrome; protein coordinate data; mutant; mutin.

XX OS Homo sapiens.

XX OS Synthetic.

XX PH Key Location/Qualifiers
 FT Misc-difference 6 /note= "Wild-type Leu substituted by Gly"
 FT Misc-difference 10 /note= "Wild-type Trp substituted by Ala"
 FT Misc-difference 98 /note= "Wild-type Leu substituted by Ala"
 FT Misc-difference 101 /note= "Wild-type Phe substituted by Arg"
 FT Misc-difference 102 /note= "Wild-type Leu substituted by Ser"
 XX WO200202622-A2.
 XX 10-JAN-2002.
 XX 29-JUN-2001; 2001WO-US020872.
 XX 29-JUN-2000; 2000US-00608352.
 XX (SALK) SALK INST BIOLOGICAL STUDIES.
 XX Noel JP, Verdacia M, Hunter T, Huang H;
 XX WPI; 2002-171638/22.
 XX Novel isolated crystalline survivin polypeptide, useful to screen and design compounds that bind to or interact with inhibitor of apoptosis protein and protein family members, and for design of novel therapeutics.
 XX Claim 8; Page; 102pp; English.
 XX The invention relates to an isolated crystalline human survivin polypeptide, an inhibitor of apoptosis protein (IAP). The polypeptide is useful for determining the ability of a survivin binding agent to modulate tubulin interaction, p21, caspase-3 and CDK4 requirement or zinc chelation activity and for identifying an agent such as a peptide or peptidomimetic which inhibits dimerisation of survivin. The ability of an agent to modulate dimerisation can be determined through detection of a change in apoptosis in a target cell expressing survivin. Binding agents are useful for increasing apoptosis in a cell derived from a tissue selected from ovary, breast, pancreas, lymph node, skin, blood, lung, brain, kidney, liver, nasopharyngeal cavity, thyroid, central nervous system, prostate, colon, rectum, cervix or endometrium, with a cell proliferative disorder such as cancer. The molecules can also be used in treatment or prevention of apoptosis which occurs as a part of AIDS, neurodegenerative diseases, ischaemic injury, toxin-induced liver disease and myelodysplastic syndromes. This sequence represents a human mutant survivin polypeptide. Note: This sequence is not featured in the printed specification but was derived from the wild type protein shown in AAU74571

XX SQ Sequence 142 AA;
 Query Match 61.3%; Score 87; DB 5; Length 142;
 Best Local Similarity 100.0%; Pred. No. 3.5e-84;
 Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 QPFLKDHRISTFKNWPFLGCACTPERVAEAGFHCTENEPDLAQCFCKLEGWEPD 70
 DB 11 QPFLKDHRISTFKNWPFLGCACTPERVAEAGFHCTENEPDLAQCFCKLEGWEPD 70
 QY 71 DDPTEHKKHSGSCAFSLVKKQFELT 97
 DB 71 DDPTEHKKHSGSCAFSLVKKQFELT 97

RESULT 17
 AAU74580
 ID AAU74580 standard; protein; 142 AA.
 XX
 AC AAU74580;

XX DT 08-MAY-2002 (first entry)
 XX DE Human mutant W10A/F93A/L98R survivin polypeptide.
 XX KW Human; survivin; inhibitor of apoptosis protein; IAP; cytostatic; p21; tubulin interaction; caspase-3; CDK4; zinc chelation activity; apoptosis; dimerization; ovary; breast; pancreas; central nervous system; blood; lung; skin; lymph node; brain; kidney; liver; nasopharyngeal cavity; thyroid; prostate; colon; rectum; cervix; endometrium; cancer; AIDS; cell proliferative disorder; acquired immunodeficiency syndrome; neurodegenerative disease; ischaemic injury; toxin-induced liver disease; myelodysplastic syndrome; protein coordinate data; mutant; mutain.
 XX OS Homo sapiens.
 XX OS Synthetic.
 XX PH Key Location/Qualifiers
 FT Misc-difference 10 /note= "Wild-type Trp substituted by Ala"
 FT Misc-difference 93 /note= "Wild-type Phe substituted by Ala"
 FT Misc-difference 98 /note= "Wild-type Leu substituted by Arg"
 XX WO200202622-A2.
 XX 10-JAN-2002.
 XX 29-JUN-2001; 2001WO-US020872.
 XX 29-JUN-2000; 2000US-00608352.
 XX (SALK) SALK INST BIOLOGICAL STUDIES.
 XX Noel JP, Verdacia M, Hunter T, Huang H;
 XX WPI; 2002-171638/22.
 XX Novel isolated crystalline survivin polypeptide, useful to screen and design compounds that bind to or interact with inhibitor of apoptosis protein and protein family members, and for design of novel therapeutics.
 XX Claim 8; Page; 102pp; English.
 XX The invention relates to an isolated crystalline human survivin polypeptide, an inhibitor of apoptosis protein (IAP). The polypeptide is useful for determining the ability of a survivin binding agent to modulate tubulin interaction, p21, caspase-3 and CDK4 requirement or zinc chelation activity and for identifying an agent such as a peptide or peptidomimetic which inhibits dimerisation of survivin. The ability of an agent to modulate dimerisation can be determined through detection of a change in apoptosis in a target cell expressing survivin. Binding agents are useful for increasing apoptosis in a cell derived from a tissue selected from ovary, breast, pancreas, lymph node, skin, blood, lung, brain, kidney, liver, nasopharyngeal cavity, thyroid, central nervous system, prostate, colon, rectum, cervix or endometrium, with a cell proliferative disorder such as cancer. The molecules can also be used in treatment or prevention of apoptosis which occurs as a part of AIDS, neurodegenerative diseases, ischaemic injury, toxin-induced liver disease and myelodysplastic syndromes. This sequence represents a human mutant survivin polypeptide. Note: This sequence is not featured in the printed specification but was derived from the wild type protein shown in AAU74571

XX SQ Sequence 142 AA;
 Query Match 57.7%; Score 82; DB 5; Length 142;
 Best Local Similarity 100.0%; Pred. No. 7.3e-79;
 Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 QPFLKDHRISTFKNWPFLGCACTPERVAEAGFHCTENEPDLAQCFCKLEGWEPD 70
 QY 11 QPFLKDHRISTFKNWPFLGCACTPERVAEAGFHCTENEPDLAQCFCKLEGWEPD 70
 QY 71 DDPTEHKKHSGSCAFSLVKKQFELT 97
 DB 71 DDPTEHKKHSGSCAFSLVKKQFELT 97

Db 11 QPFLKDHRISTFKNPFLEGGCACTPERMAEAGFIHCPTENEPDLAQCFCKELEGWEPD 70
 Qy 71 DDPFIEHKKHSSGCAFLSVKKQ 92
 Db 71 DDPFIEHKKHSSGCAFLSVKKQ 92

RESULT 18
 AAU74581
 ID AAU74581 standard; protein; 142 AA.
 XX AC AAU74581;
 XX DT 08-MAY-2002 (first entry)
 XX DE Human mutant L6G/W10A/F93A/L98R survivin polypeptide.
 XX KW Human; survivin; inhibitor of apoptosis protein; IAP; cytosolic; p21;
 KW tubulin interaction; caspase-3; CDK4; zinc chelation activity; apoptosis;
 KW dimerisation; ovary; breast; pancreas; central nervous system; blood;
 KW lung; skin; lymph node; brain; kidney; liver; nasopharyngeal cavity;
 KW thyroid; prostate; colon; rectum; cervix; endometrium; cancer; AIDS;
 KW cell proliferative disorder; acquired immunodeficiency syndrome;
 KW neurodegenerative disease; ischaemic injury; toxin-induced liver disease;
 KW myelodysplastic syndrome; protein coordinate data; mutant; muten.
 XX OS Homo sapiens.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Misc-difference 6 /note= "Wild-type Leu substituted by Gly"
 FT FT Misc-difference 10 /note= "Wild-type Trp substituted by Ala"
 FT FT Misc-difference 93 /note= "Wild-type Phe substituted by Ala"
 FT FT Misc-difference 98 /note= "Wild-type Leu substituted by Arg"
 FT XX WO200202622-A2.
 XX 10-JAN-2002.
 XX 29-JUN-2001; 2001WO-US020872.
 XX 29-JUN-2000; 2000US-00608352.
 XX (SALK) SALK INST BIOLOGICAL STUDIES.
 XX Noel JP, Verdacia M, Hunter T, Huang H;
 XX WPI; 2002-171638/22.
 XX Novel isolated crystalline survivin polypeptide, useful to screen and
 PT design compounds that bind to or interact with inhibitor of apoptosis
 PT protein and protein family members, and for design of novel therapeutics.
 XX Claim 8; Page; 102pp; English.
 XX The invention relates to an isolated crystalline human survivin
 CC polypeptide, an inhibitor of apoptosis protein (IAP). The polypeptide is
 CC useful for determining the ability of a survivin binding agent to
 CC modulate tubulin interaction, p21, caspase-3 and CDK4 requirement or zinc
 CC chelation activity and for identifying an agent such as a peptide or
 CC peptidomimetic which inhibits dimerisation of survivin. The ability of an
 CC agent to modulate dimerisation can be determined through detection of a
 CC change in apoptosis in a target cell expressing survivin. Binding agents
 CC are useful for increasing apoptosis in a cell derived from a tissue
 CC selected from ovary, breast, pancreas, lymph node, skin, blood, lung,
 CC brain, kidney, liver, nasopharyngeal cavity, thyroid, central nervous
 CC system, prostate, colon, rectum, cervix or endometrium, with a cell
 CC proliferative disorder such as cancer. The molecules can also be used in
 CC treatment or prevention of apoptosis which occurs as a part of AIDS,

CC neurodegenerative diseases, ischaemic injury, toxin-induced liver disease
 CC and myelodysplastic syndromes. This sequence represents a human mutant
 CC survivin polypeptide. Note: This sequence is not featured in the printed
 CC specification but was derived from the wild type protein shown in
 CC AAU74571
 XX SQ Sequence 142 AA;
 Query Match 57.7%; Score 82; DB 5; Length 142;
 Best Local Similarity 100.0%; Pred. No. 7.3e-79;
 Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 11 QPFLKDHRISTFKNPFLEGGCACTPERMAEAGFIHCPTENEPDLAQCFCKELEGWEPD 70
 Db 11 QPFLKDHRISTFKNPFLEGGCACTPERMAEAGFIHCPTENEPDLAQCFCKELEGWEPD 70
 Qy 71 DDPFIEHKKHSSGCAFLSVKKQ 92
 Db 71 DDPFIEHKKHSSGCAFLSVKKQ 92

RESULT 19
 AAU74575
 ID AAU74575 standard; protein; 142 AA.
 XX AC AAU74575;
 XX DT 08-MAY-2002 (first entry)
 XX DE Human mutant H80A survivin polypeptide.
 XX KW Human; survivin; inhibitor of apoptosis protein; IAP; cytosolic; p21;
 KW tubulin interaction; caspase-3; CDK4; zinc chelation activity; apoptosis;
 KW dimerisation; ovary; breast; pancreas; central nervous system; blood;
 KW lung; skin; lymph node; brain; kidney; liver; nasopharyngeal cavity;
 KW thyroid; prostate; colon; rectum; cervix; endometrium; cancer; AIDS;
 KW cell proliferative disorder; acquired immunodeficiency syndrome;
 KW neurodegenerative disease; ischaemic injury; toxin-induced liver disease;
 KW myelodysplastic syndrome; protein coordinate data; mutant; muten.
 XX OS Homo sapiens.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Misc-difference 80 /note= "Wild-type His substituted by Ala"
 FT FT WO200202622-A2.
 XX 10-JAN-2002.
 XX 29-JUN-2001; 2001WO-US020872.
 XX 29-JUN-2000; 2000US-00608352.
 XX (SALK) SALK INST BIOLOGICAL STUDIES.
 XX Noel JP, Verdacia M, Hunter T, Huang H;
 XX WPI; 2002-171638/22.
 XX Novel isolated crystalline survivin polypeptide, useful to screen and
 PT design compounds that bind to or interact with inhibitor of apoptosis
 PT protein and protein family members, and for design of novel therapeutics.
 XX Claim 8; Page; 102pp; English.
 XX The invention relates to an isolated crystalline human survivin
 CC polypeptide, an inhibitor of apoptosis protein (IAP). The polypeptide is
 CC useful for determining the ability of a survivin binding agent to
 CC modulate tubulin interaction, p21, caspase-3 and CDK4 requirement or zinc
 CC chelation activity and for identifying an agent such as a peptide or
 CC peptidomimetic which inhibits dimerisation of survivin. The ability of an
 CC agent to modulate dimerisation can be determined through detection of a
 CC change in apoptosis in a target cell expressing survivin. Binding agents
 CC are useful for increasing apoptosis in a cell derived from a tissue
 CC selected from ovary, breast, pancreas, lymph node, skin, blood, lung,
 CC brain, kidney, liver, nasopharyngeal cavity, thyroid, central nervous
 CC system, prostate, colon, rectum, cervix or endometrium, with a cell
 CC proliferative disorder such as cancer. The molecules can also be used in
 CC treatment or prevention of apoptosis which occurs as a part of AIDS,

CC agent to modulate dimerisation can be determined through detection of a
 CC change in apoptosis in a target cell expressing survivin. Binding agents
 CC are useful for increasing apoptosis in a cell derived from a tissue
 CC selected from ovary, breast, pancreas, lymph node, skin, blood, lung,
 CC brain, kidney, liver, nasopharyngeal cavity, thyroid, central nervous
 CC system, prostate, colon, rectum, cervix or endometrium, with a cell
 CC proliferative disorder such as cancer. The molecules can also be used in
 CC treatment or prevention of apoptosis which occurs as a part of AIDS,
 CC neurodegenerative diseases, ischaemic injury, toxin-induced liver disease
 CC and myelodysplastic syndromes. This sequence represents a human mutant
 CC survivin polypeptide. Note: This sequence is not featured in the printed
 CC specification but was derived from the wild type protein shown in
 CC AAU74571

XX
 SQ Sequence 142 AA;
 Query Match 55.6%; Score 79; DB 5; Length 142;
 Best Local Similarity 100.0%; Pred. No. 1.1e-75;
 Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGAPTLPPAWQPFLLKDHRISTFKWPFLEGGCACTPERMAEAGFHCPTENEPDLAQCFCC 60
 DB 1 MGAPTLPPAWQPFLLKDHRISTFKWPFLEGGCACTPERMAEAGFHCPTENEPDLAQCFCC 60
 QY 61 FKELEGWEPDDPIEEHKK 79
 DB 61 FKELEGWEPDDPIEEHKK 79

RESULT 20
 AAG02311
 ID AAG02311 standard; protein; 116 AA.
 AC AAG02311;
 DT 06-OCT-2000 (first entry)
 DE Human secreted protein, SEQ ID NO: 6392.
 KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KW gene therapy; chromosome mapping.
 OS Homo sapiens.
 XX EP1033401-A2.
 XX 06-SEP-2000.
 XX 21-FEB-2000; 2000EP-00200610.
 XX 26-FEB-1999; 99US-0122487P.
 XX (GEST) GENSET.
 XX Dumas Milne Edwards J, Duclert A, Giordano J;
 DR WPI; 2000-500381/45.
 DR N-PSDB; AAC02317.

XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
 XX
 PS Claim 13; SEQ ID NO 6392; 71pp + Sequence Listing; English.
 XX
 CC The present sequence is a polypeptide encoded by one of a large number of
 CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
 CC prepared from total human RNAs or polyA+ RNAs derived from 30 different
 CC tissues. EST sequences usually correspond mainly to the 3' untranslated
 CC region (UTR) of the mRNA because they are often obtained from oligo-dT
 CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
 CC sequences derived from the 5' ends of mRNAs and even in those cases where
 CC longer cDNA sequences have been obtained, the full 5' UTR is rarely

CC included, 5' ESTs are derived from mRNAs with intact 5' ends and can
 CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
 CC are also used in diagnostic, forensic, gene therapy and chromosome
 CC mapping procedures. They are used to obtain upstream regulatory sequences
 CC and to design expression and secretion vectors
 XX
 SQ Sequence 116 AA;

Query Match 53.5%; Score 76; DB 3; Length 116;
 Best Local Similarity 100.0%; Pred. No. 1.5e-72;
 Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGAPTLPPAWQPFLLKDHRISTFKWPFLEGGCACTPERMAEAGFHCPTENEPDLAQCFCC 60
 DB 1 MGAPTLPPAWQPFLLKDHRISTFKWPFLEGGCACTPERMAEAGFHCPTENEPDLAQCFCC 60
 QY 61 FKELEGWEPDDPIEE 76
 DB 61 FKELEGWEPDDPIEE 76

RESULT 21
 ADB61824
 ID ADB61824 standard; protein; 75 AA.
 AC ADB61824;
 DT 04-DEC-2003 (first entry)
 DE Human inhibitor of apoptosis (IAP) protein Survivin BIR3 domain.
 KW baculovirus inhibitor of apoptosis repeat domain; BIR domain;
 KW apoptosis pathway; embryonic development; viral pathogenesis; cancer;
 KW autoimmune disorder; neurodegenerative disease; apoptotic response;
 KW systemic lupus erythematosus; multiple sclerosis; viral infection;
 KW herpes virus; poxvirus; adenovirus; inhibitor of apoptosis; IAP; XIAP;
 KW HIAP1; CIAP2; HIAP2; CIAP1; RING zinc finger; caspase-3; caspase-7;
 KW caspase-9; cytostatic; neoplasm; leukaemia; colon carcinoma;
 KW cervical cancer; uterine cancer; testicular cancer;
 KW small cell lung carcinoma; uterine cancer; renal cell carcinoma;
 KW Wilm's tumour; human; BIR 3 domain.
 XX Homo sapiens.
 XX WO2003040172-A2.
 XX 15-MAY-2003.
 XX 12-NOV-2002; 2002WO-CA001738.
 XX 09-NOV-2001; 2001US-032300P.
 XX 08-APR-2002; 2002US-0370934P.
 XX (AEGE-) AEGERA THERAPEUTICS INC.
 XX Boudreaux A, Korneluk RG, La Casse E, Liston P;
 XX WPI; 2003-513532/48.

XX Polypeptide capable of forming a complex with a polypeptide comprising a
 PT baculovirus inhibitor of apoptosis repeat domain useful for treating
 PT cancer and other neoplasms.
 XX
 PS Disclosure; Fig 1A; 53pp; English.
 XX
 CC This invention relates to a substantially pure polypeptide having a
 CC length of less than 100 amino acids and capable of forming a complex with
 CC a polypeptide that includes a baculovirus inhibitor of apoptosis repeat
 CC (BIR) domain. The apoptosis pathway is known to play a critical role in
 CC embryonic development, viral pathogenesis, cancer, autoimmune disorders
 CC and neurodegenerative diseases. The failure of the apoptotic response has
 CC been implicated in the development of cancer, autoimmune disorders (for
 CC example systemic lupus erythematosus and multiple sclerosis) and viral

XX PF 23-MAR-2001; 2001JP-00084438.
 XX PF 23-MAR-2001; 2001JP-00084438.
 XX PA (HOKK-) HOKKAIDO TLO KK.
 XX DR WPI; 2003-397157/38.
 XX PT A novel nonapeptide survivin 2B80 capable of inducing cytotoxic T-cells,
 PT useful in vaccines for the treatment of cancer.
 XX PS Example 3; Page 4-5; 10pp; Japanese.
 XX CC The invention relates to a human survivin-derived cancer antigen,
 CC designated survivin 2B80. Survivin 2B80 is a HLA-A24 antigen, and is
 CC capable of inducing cytotoxic T-cells (CTLs) which target cancer cells
 CC having HLA-A24 expression. Survivin 2B80 can be used in the treatment of
 CC cancer, specifically in a cancer vaccine or as an anticancer agent. The
 CC present sequence represents full-length human survivin which was used in
 CC an example from the invention.
 XX SQ Sequence 165 AA;
 Query Match 52.1%; Score 74; DB 6; Length 165;
 Best Local Similarity 100.0%; Pred. No. 2.7e-70;
 Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGAPTLPPAWQFLKDHRISTFKWPFLEGGCACTPERMAEAGFIHCPTENEPDLAQCFFC 60
 DB 1 MGAPTLPPAWQFLKDHRISTFKWPFLEGGCACTPERMAEAGFIHCPTENEPDLAQCFFC 60
 QY 61 FKELEGWEPDDPI 74
 DB 61 FKELEGWEPDDPI 74
 RESULT 24
 ADB61823
 ID ADB61823 standard; protein; 83 AA.
 AC ADB61823;
 DT 04-DEC-2003 (first entry)
 DE Human inhibitor of apoptosis (IAP) protein BC000784 BIR3 domain.
 KW baculovirus inhibitor of apoptosis repeat domain; BIR domain;
 KW apoptosis pathway; embryonic development; viral pathogenesis; cancer;
 KW autoimmune disorder; neurodegenerative disease; apoptotic response;
 KW systemic lupus erythematosus; multiple sclerosis; viral infection;
 KW herpes virus; poxvirus; adenovirus; inhibitor of apoptosis; IAP; XIAP;
 KW HIAP1; CIAP2; HIAP2; CIAP1; RING zinc finger; caspase-3; caspase-7;
 KW caspase-9; cytoskeletal; neoplasm; leukaemia; colon carcinoma;
 KW cervical cancer; uterine cancer; testicular cancer;
 KW small cell lung carcinoma; uterine cancer; renal cell carcinoma;
 KW Wilm's tumour; human; BIR 3 domain.
 XX Homo sapiens.
 XX WO2003040172-A2.
 XX 15-MAY-2003.
 XX 12-NOV-2002; 2002WO-CA001738.
 XX 09-NOV-2001; 2001US-0322300P.
 XX 08-APR-2002; 2002US-0370934P.
 XX (ABGE-) AEGERA THERAPEUTICS INC.
 XX Boudreault A, Korneluk RG, La Casse E, Liston P;
 XX

DR WPI; 2003-513532/48.
 XX Polypeptide capable of forming a complex with a polypeptide comprising a
 PT baculovirus inhibitor of apoptosis repeat domain useful for treating
 PT cancer and other neoplasms.
 XX Disclosure; Fig 1A; 53pp; English.
 XX This invention relates to a substantially pure polypeptide having a
 CC length of less than 100 amino acids and capable of forming a complex with
 CC a polypeptide that includes a baculovirus inhibitor of apoptosis repeat
 CC (BIR) domain. The apoptosis pathway is known to play a critical role in
 CC embryonic development, viral pathogenesis, cancer, autoimmune disorders
 CC and neurodegenerative diseases. The failure of the apoptotic response has
 CC been implicated in the development of cancer, autoimmune disorders (for
 CC example systemic lupus erythematosus and multiple sclerosis) and viral
 CC infections (including herpes virus, poxvirus and adenovirus). The
 CC inhibitors of apoptosis (IAPs) are a family of proteins possessing one or
 CC more baculovirus IAP repeat (BIR) domains. Human IAPs, XIAP, HIAP1
 CC (CIAP2) and HIAP2 (GIAP1) all possess three BIR domains and carboxy
 CC terminal RING zinc fingers. The IAPs bind and inhibit caspases -3, -7 and
 CC -9 which are proteases involved in the initiation of apoptosis. Compounds
 CC which inhibit the activity of IAPs may therefore have cytostatic activity
 CC through the enhancement of apoptosis. The polypeptides of the invention
 CC are candidate peptide ligands for binding to the BIR domain of IAPs. They
 CC may be useful for the treatment of cancer and other neoplasms, such as
 CC leukaemias, colon carcinoma, cervical cancer, uterine cancer, testicular
 CC cancer, small cell lung carcinoma, uterine cancer, renal cell carcinoma
 CC and Wilm's tumour, and for enhancing apoptosis. The present sequence is
 CC that of the human inhibitor of apoptosis (IAP) protein BC000784 BIR3
 CC domain which was used to demonstrate homology to other human IAP protein
 CC BIR domains to which the peptides of the invention are targeted to bind.
 XX SQ Sequence 83 AA;
 Query Match 41.5%; Score 59; DB 7; Length 83;
 Best Local Similarity 100.0%; Pred. No. 1.3e-54;
 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 15 KDHRISTFKWPFLEGGCACTPERMAEAGFIHCPTENEPDLAQCFFCFKELGWEPPDDDP 73
 DB 1 KDHRISTFKWPFLEGGCACTPERMAEAGFIHCPTENEPDLAQCFFCFKELGWEPPDDDP 59
 RESULT 25
 AAW19749
 ID AAW19749 standard; protein; 140 AA.
 AC AAW19749;
 DT 16-SEP-1997 (first entry)
 DE Mouse inhibitor of apoptosis protein homologue MIHE.
 DE Inhibitor of apoptosis protein; IAP; mammalian IAP homologue; MIHE;
 KW degenerative disease; infectious disease; autoimmune disease; cancer;
 KW therapy; diagnosis.
 XX Mus musculus.
 XX WO9723501-A1.
 XX 03-JUL-1997.
 XX 20-DEC-1996; 96WO-AU000827.
 XX 22-DEC-1995; 95AU-00007275.
 XX (AMRA-) AMRAD OPERATIONS PTY LTD.
 XX Vaux DL;
 XX WPI; 1997-350966/32.
 DR

DR N-PSDB; AAT72714.
 XX Isolated protein homologues of viral inhibitors of apoptosis - used to
 PT modulate apoptosis for treatment of degenerative, infectious or
 PT auto-immune diseases and cancer.
 XX
 PS Claim 11; Page 71-72; 136pp; English.
 XX
 CC MIHE (AAW19749) is a murine homologue of baculovirus inhibitor of
 CC apoptosis protein (IAP). Its amino acid sequence was deduced from an
 CC isolated nucleic acid (see also AAT72714) obtd. by a database search for
 CC sequences homologous to a baculovirus IAP repeat (BIR) consensus sequence
 CC (see also AAW19744). Unlike IAP, MIHE does not contain a RING finger
 CC domain. IAP homologues (see also AAW19745-48 and AAW19750-52) and their
 CC derivatives and chemical analogues can be used in methods for modulating
 CC apoptosis in animal cells, specifically for treatment, by inhibition, of
 CC degenerative and infectious disease or, by promotion, of cancer and
 CC autoimmune disease
 XX
 SQ Sequence 140 AA;
 Query Match 28.9%; Score 41; DB 2; Length 140;
 Best Local Similarity 100.0%; Pred. No. 3e-35;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 31 CACTPERMAEAGTHCPTENEPLAQCFFCFKLEGWEPDD 71
 DB 31 CACTPERMAEAGTHCPTENEPLAQCFFCFKLEGWEPDD 71
 RESULT 26
 AAU74583
 ID AAU74583 standard; protein; 140 AA.
 AC AAU74583;
 XX
 DT 08-MAY-2002 (first entry)
 DE Mouse survivin polypeptide.
 XX
 KW Human; survivin; inhibitor of apoptosis protein; IAP; cytostatic; p21;
 KW tubulin interaction; caspase-3; CDK4; zinc chelation activity; apoptosis;
 KW dimerisation; ovary; pancreas; central nervous system; blood;
 KW lung; skin; lymph node; brain; kidney; liver; nasopharyngeal cavity;
 KW thyroid; prostate; colon; rectum; cervix; endometrium; cancer; AIDS;
 KW cell proliferative disorder; acquired immunodeficiency syndrome; mouse;
 KW neurodegenerative disease; ischaemic injury; toxin-induced liver disease;
 KW myelodysplastic syndrome; protein coordinate data.
 XX
 OS Mus sp.
 XX
 PN WO200202622-A2.
 PD 10-JAN-2002.
 XX
 XX 29-JUN-2001; 2001WO-US020872.
 PF
 XX 29-JUN-2000; 2000US-00608352.
 PR
 XX (SALK) SALK INST BIOLOGICAL STUDIES.
 PA
 XX Noel JP, Verdacia M, Hunter T, Huang H;
 PI WPI; 2002-171638/22.
 DR
 XX Novel isolated crystalline survivin polypeptide, useful to screen and
 PT design compounds that bind to or interact with inhibitor of apoptosis
 PT protein and protein family members, and for design of novel therapeutics.
 XX
 PS Disclosure; fig 2; 102pp; English.
 XX
 CC The invention relates to an isolated crystalline human survivin
 CC polypeptide, an inhibitor or apoptosis protein (IAP). The polypeptide is

CC useful for determining the ability of a survivin binding agent to
 CC modulate tubulin interaction, p21, caspase-3 and CDK4 requirement or zinc
 CC chelation activity and for identifying an agent such as a peptide or
 CC peptidomimetic which inhibits dimerisation of survivin. The ability of an
 CC agent to modulate dimerisation can be determined through detection of a
 CC change in apoptosis in a target cell expressing survivin. Binding agents
 CC are useful for increasing apoptosis in a cell derived from a tissue
 CC selected from ovary, breast, pancreas, lymph node, skin, blood, lung,
 CC brain, kidney, liver, nasopharyngeal cavity, thyroid, central nervous
 CC system, prostate, colon, rectum, cervix or endometrium, with a cell
 CC proliferative disorder such as cancer. The molecules can also be used in
 CC treatment or prevention of apoptosis which occurs as a part of AIDS,
 CC neurodegenerative diseases, ischaemic injury, toxin-induced liver disease
 CC and myelodysplastic syndromes. This sequence represents the mouse
 CC survivin polypeptide
 XX
 SQ Sequence 140 AA;
 Query Match 28.9%; Score 41; DB 5; Length 140;
 Best Local Similarity 100.0%; Pred. No. 3e-35;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 31 CACTPERMAEAGTHCPTENEPLAQCFFCFKLEGWEPDD 71
 DB 31 CACTPERMAEAGTHCPTENEPLAQCFFCFKLEGWEPDD 71
 RESULT 27
 AAU30231
 ID AAU30231 standard; protein; 155 AA.
 AC AAU30231;
 XX
 DT 18-DEC-2001 (first entry)
 DE Novel human secreted protein #722.
 DE
 XX Human; vaccination; gene therapy; nutritional supplement;
 KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200179449-A2.
 PD 25-OCT-2001.
 XX
 PF 16-APR-2001; 2001WO-US008656.
 XX
 PR 18-APR-2000; 2000US-00552929.
 PR 26-JAN-2001; 2001US-00770160.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT;
 XX WPI; 2001-611725/70.
 DR
 XX Nucleic acids encoding a range of human polypeptides, useful in genetic
 PT vaccination, testing and therapy.
 PT
 XX Claim 20; Page 263; 765pp; English.
 PS
 XX The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising the
 CC nucleic acids encoding the polypeptides and cells genetically engineered
 CC to express them are also useful for producing the proteins. The proteins

CC are useful in genetic vaccination, testing and therapy, and can be used
 CC as nutritional supplements. They may be used to increase stem cell
 CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon
 CC and/or nerve tissue growth or regeneration; immune suppression and/or
 CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.
 CC AAU29510-AAU3304 represent the amino acid sequences of novel human
 CC secreted proteins of the invention
 XX
 SQ Sequence 155 AA;

Query Match 25.4%; Score 36; DB 4; Length 155;
 Best Local Similarity 100.0%; Pred. No. 7e-30;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 38 MAEAGFIHCPTNEPDLAQCFCFKELEGWEPDDDP 73
 DB 1 MAEAGFIHCPTNEPDLAQCFCFKELEGWEPDDDP 36

RESULT 28
 ABP70506
 ID ABP70506 standard; peptide; 24 AA.
 XX
 AC ABP70506;
 XX
 DT 22-APR-2003 (first entry)
 XX
 DE Peptide comprising translocating motif, derived from survivin.
 XX
 KW Translocating factor; translocation; cell membrane; disease; tumour;
 KW infection.
 XX
 OS Synthetic.

Key Location/Qualifiers
 Modified-site 1 /note= "biotin attached"

WO2003002598-A2.
 09-JAN-2003.

01-JUL-2002; 2002WO-GB003027.

29-JUN-2001; 2001GB-00016047.

(IMPL-) IMPLIX LTD.

Crisanti A;

WPI; 2003-201490/19.

Use of a protein or its fragment for the manufacture of a composition for
 treating a disease characterized by a deficiency in the production or
 function of the endogenous protein, or to regulate biochemical pathway.

Example 2; Page 30; 44pp; English.

The present sequence represents a peptide comprising a translocating
 factor motif. The peptide motif enables translocation across the cell
 membrane. The conjugate was tested for translocation, which was observed.
 The peptide motif is derived from a formula given in the specification.
 The peptide motifs and proteins and conjugates comprising that motif are
 useful for the manufacture of a medicament for treating or diagnosing a
 disease, e.g. tumour, or viral and bacterial infections. The conjugate is
 useful in therapy or diagnosis

Sequence 24 AA;

Query Match 16.9%; Score 24; DB 6; Length 24;
 Best Local Similarity 100.0%; Pred. No. 7.2e-18;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 111 NKIAKETNNKKKEFEETAKKVRRA 134
 DB 1 NKIAKETNNKKKEFEETAKKVRRA 24

RESULT 29

ABP70505
 ID ABP70505 standard; peptide; 21 AA.

XX
 AC ABP70505;

DT 22-APR-2003 (first entry)

XX Peptide comprising translocating motif, derived from baculoviral protein.
 XX Translocating factor; translocation; cell membrane; disease; tumour;
 XX infection.
 XX Synthetic.

Key Location/Qualifiers
 Modified-site 1 /note= "biotin attached"

WO2003002598-A2.

09-JAN-2003.

01-JUL-2002; 2002WO-GB003027.

29-JUN-2001; 2001GB-00016047.

(IMPL-) IMPLIX LTD.

Crisanti A;

WPI; 2003-201490/19.

Use of a protein or its fragment for the manufacture of a composition for
 treating a disease characterized by a deficiency in the production or
 function of the endogenous protein, or to regulate biochemical pathway.

Example 2; Page 30; 44pp; English.

The present sequence represents a peptide comprising a translocating
 factor motif. The peptide motif enables translocation across the cell
 membrane. The conjugate was tested for translocation, which was observed.
 The peptide motif is derived from a formula given in the specification.
 The peptide motifs and proteins and conjugates comprising that motif are
 useful for the manufacture of a medicament for treating or diagnosing a
 disease, e.g. tumour, or viral and bacterial infections. The conjugate is
 useful in therapy or diagnosis

Sequence 21 AA;

Query Match 14.8%; Score 21; DB 6; Length 21;
 Best Local Similarity 100.0%; Pred. No. 9.9e-15;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 114 AKETNNKKKEFEETAKKVRRA 134
 DB 1 AKETNNKKKEFEETAKKVRRA 21

RESULT 30
 AAW61358
 ID AAW61358 standard; peptide; 20 AA.

XX
 AC AAW61358;

DT 25-SEP-1998 (first entry)

DE Survivin functionally relevant peptide.

XX survivin; apoptosis; cellular apoptosis; transplantation;
 KW motor neuron degenerative disease; HIV infection; immunosuppression;
 KW gastrointestinal perturbations; cardiovascular disorder.
 XX Homo sapiens.
 XX WO9822589-A2.
 XX 28-MAY-1998.
 XX 20-NOV-1997; 97WO-US021880.
 XX 20-NOV-1996; 96US-0031435P.
 XX 20-NOV-1997; 97US-00975080.
 XX (UYUA) UNIV YALE.
 XX Altieri DC;
 XX WPI; 1998-312475/27.
 XX Modulating apoptosis by controlling the Survivin gene - useful for
 PT treating transplant rejection, degenerative disorders and tumours.
 XX Claim 7; Page 75; 108pp; English.
 XX The survivin peptide is a functionally relevant area of the protein. A
 CC mutation resulting in the substitutions of amino acids at sites 3, 9 and
 CC 20 with Alanine results in a complete loss of function of survivin in
 CC transfected cells. The survivin gene can be used to control apoptosis
 CC through modification of the gene. Survivin peptides can be used to
 CC inhibit cellular apoptosis, e.g. for enhancing the viability of organs
 CC and tissues prior to their transplantation, for preserving the growth of
 CC cells in culture or for treating conditions involving abnormal apoptosis,
 CC e.g. degenerative diseases such as motor neuron degenerative diseases,
 CC HIV infection, dermatological effects of ageing, disorders and diseases
 CC such as immunosuppression, gastrointestinal perturbations, cardiovascular
 CC disorders, apoptosis related to reperfusion damage, rejection of tissue
 CC transplantation and Alzheimer's disease. Agents which block Survivin
 CC activity can be used to treat e.g. tumours
 XX Sequence 20 AA;
 Query Match 14.1%; Score 20; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.1e-13;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 65 EGVPEDDPPIEHHKHSKC 84
 Db 1 EGVPEDDPPIEHHKHSKC 20
 RESULT 31
 ID AAW61360 standard; peptide; 17 AA.
 AC AAW61360;
 XX 25-SEP-1998 (first entry)
 DE Survivin seventeenmer peptide.
 XX survivin; apoptosis; cellular apoptosis; transplantation;
 KW motor neuron degenerative disease; HIV infection; immunosuppression;
 KW gastrointestinal perturbations; cardiovascular disorder.
 XX Homo sapiens.
 XX WO9822589-A2.
 XX 28-MAY-1998.
 XX (UYUA) UNIV YALE.

PF 20-NOV-1997; 97WO-US021880.
 XX 20-NOV-1996; 96US-0031435P.
 XX 20-NOV-1997; 97US-00975080.
 XX (UYUA) UNIV YALE.
 XX Altieri DC;
 XX WPI; 1998-312475/27.
 XX Modulating apoptosis by controlling the Survivin gene - useful for
 PT treating transplant rejection, degenerative disorders and tumours.
 XX Example 2; Page 51; 108pp; English.
 XX The seventeenmer peptide was used to produce a survivin sequence-specific
 CC antibody. The survivin gene can be used to control apoptosis through
 CC modification of the gene. Survivin peptides can be used to inhibit
 CC cellular apoptosis, e.g. for enhancing the viability of organs and
 CC tissues prior to their transplantation, for preserving the growth of
 CC cells in culture or for treating conditions involving abnormal apoptosis,
 CC e.g. degenerative diseases such as motor neuron degenerative diseases,
 CC HIV infection, dermatological effects of ageing, disorders and diseases
 CC such as immunosuppression, gastrointestinal perturbations, cardiovascular
 CC disorders, apoptosis related to reperfusion damage, rejection of tissue
 CC transplantation and Alzheimer's disease. Agents which block Survivin
 CC activity can be used to treat e.g. tumours
 XX Sequence 17 AA;
 Query Match 12.0%; Score 17; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.5e-10;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 APTLPPAWQPFLLKHRI 19
 Db 1 APTLPPAWQPFLLKHRI 17
 RESULT 32
 ID AAE11066 standard; peptide; 17 AA.
 AC AAE11066;
 XX 18-DEC-2001 (first entry)
 DE Human survivin peptide.
 XX Survivin dependent apoptosis; p34(cdc2)-cyclin B1 kinase complex;
 KW caspase-9; tumour suppressor; antisense therapy; cytostatic;
 KW human. inhibitor of apoptosis; IAP.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FT Modified-site 7.10
 FT /note= "Phosphorylation site for p34(cdc2)-cyclin B1
 FT kinase complex"
 FT Modified-site 7
 FT /note= "Phosphorylated Thr"
 XX WO200164741-A2.
 XX 07-SEP-2001.
 XX 28-FEB-2001; 2001WO-US006341.
 XX 29-FEB-2000; 2000US-00515514.
 XX (UYUA) UNIV YALE.

PI Altieri DC;
 XX WPI; 2001-589861/66.
 XX Modulating survivin apoptosis pathways by using an agent that modulates
 PT phosphorylation of survivin, interaction between survivin and p34-cyclin
 PT B1 kinase complex and interaction between survivin and caspase-9.
 XX
 PS Claim 7; Page 45; 97pp; English.
 XX
 CC The invention relates to a method for modulating apoptosis, in particular
 CC survivin dependent apoptosis in a cell. The method involves administering
 CC to the cell an agent which modulates the interaction between survivin and
 CC p34(cdc2)-cyclin B1 kinase complex, phosphorylation of survivin by the
 CC p34(cdc2)-cyclin B1 kinase complex and interaction between survivin and
 CC caspase-9. Survivin antagonist is useful for inhibiting tumour growth in
 CC a mammal. Agents that modulate, preferably dephosphorylate survivin at
 CC Thr34, act as potential tumour suppressors and prevent the formation of
 CC anti-apoptotic complex with caspase. The method is also useful in
 CC anticancer therapy. The present sequence is human survivin peptide. This
 CC peptide functions as a novel inhibitor of apoptosis (IAP)
 XX
 XX Sequence 17 AA;
 SQ
 Query Match 12.0%; Score 17; DB 4; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.5e-10;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 28 LEGCACTPERMABAGFI 44
 DB 1 LEGCACTPERMABAGFI 17
 RESULT 33
 ADA09938
 ID ADA09938 standard; peptide; 10 AA.
 AC ADA09938;
 XX
 DT 06-NOV-2003 (first entry)
 DE Human HLA-A24 antigen survivin 92, SEQ ID NO:3.
 XX Human; survivin; survivin 2B80; survivin 92; HLA-A24 antigen;
 XX human leukocyte antigen; cytotoxic T-cell; CTL; induction; cancer;
 XX vaccine; anticancer agent; cytostatic.
 XX Homo sapiens.
 OS
 XX JF2002284797-A.
 XX
 XX 03-OCT-2002.
 XX
 XX 23-MAR-2001; 2001JP-00084438.
 XX
 XX 23-MAR-2001; 2001JP-00084438.
 XX (HOKK-) HOKKAIDO TLO KK.
 XX
 XX WPI; 2003-397157/38.
 XX
 XX A novel nonapeptide survivin 2B80 capable of inducing cytotoxic T-cells,
 PT useful in vaccines for the treatment of cancer.
 XX
 PS Example 3; Page 5; 10pp; Japanese.
 XX
 CC The invention relates to a human survivin-derived cancer antigen,
 CC designated survivin 2B80. Survivin 2B80 is a HLA-A24 antigen, and is
 CC capable of inducing cytotoxic T-cells (CTLs) which target cancer cells
 CC having HLA-A24 expression. Survivin 2B80 can be used in the treatment of
 CC cancer, specifically in a cancer vaccine or as an anticancer agent. The
 CC present sequence represents a different survivin-derived HLA-A24 antigen,
 CC survivin 92, which corresponds to residues 115-124 of full-length human

CC survivin (ADA09936) and which was used in an example from the invention.
 XX
 SQ Sequence 10 AA;
 Query Match 7.0%; Score 10; DB 6; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0025;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 92 QFEELTLGEF 101
 DB 1 QFEELTLGEF 10
 RESULT 34
 AAEL1070
 ID AAEL1070 standard; peptide; 17 AA.
 XX
 AC AAEL1070;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Human survivin peptide mutant.
 XX
 KW Survivin dependent apoptosis; p34(cdc2)-cyclin B1 kinase complex;
 KW caspase-9; tumour suppressor; antisense therapy; cytostatic; human;
 KW mutant; mutelin.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 7..10
 FT /note= "Phosphorylation site for p34(cdc2)-cyclin B1
 FT kinase complex"
 FT Misc-difference 7
 FT /note= "Wild type Thr substituted with Ala; Corresponds
 FT to position 34 of wild type survivin peptide"
 XX
 PN WC200164741-A2.
 XX
 XX 07-SEP-2001.
 XX
 XX 28-FEB-2001; 2001WO-US006341.
 XX
 XX 29-FEB-2000; 2000US-00515514.
 XX
 XX (UYFA) UNIV YALE.
 XX
 XX Altieri DC;
 XX
 XX WPI; 2001-589861/66.
 XX
 XX Modulating survivin apoptosis pathways by using an agent that modulates
 PT phosphorylation of survivin, interaction between survivin and p34-cyclin
 PT B1 kinase complex and interaction between survivin and caspase-9.
 XX
 PS Example 2; Page; 97pp; English.
 XX
 CC The invention relates to a method for modulating apoptosis, in particular
 CC survivin dependent apoptosis in a cell. The method involves administering
 CC to the cell an agent which modulates the interaction between survivin and
 CC p34(cdc2)-cyclin B1 kinase complex, phosphorylation of survivin by the
 CC p34(cdc2)-cyclin B1 kinase complex and interaction between survivin and
 CC caspase-9. Survivin antagonist is useful for inhibiting tumour growth in
 CC a mammal. Agents that modulate, preferably dephosphorylate survivin at
 CC Thr34, act as potential tumour suppressors and prevent the formation of
 CC anti-apoptotic complex with caspase. The method is also useful in
 CC anticancer therapy. The present sequence is human survivin peptide mutant
 CC (T34A). Note: This sequence is not found in the specification but is
 CC derived from the human survivin peptide sequence (AAEL1066) shown in page
 CC 45 of the specification
 XX
 XX Sequence 17 AA;

```

Query Match          7.0%; Score 10; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 PERMAEAGFI 44
DB 8 PERMAEAGFI 17
|||||

RESULT 35
AAE11069
ID AAE11069 standard; peptide; 9 AA.
XX AC
XX AC AAE11069;
XX DT
XX DT 18-DEC-2001 (first entry)
XX DE Human survivin phosphorylation motif.
XX KW Survivin dependent apoptosis; p34(cdc2)-cyclin B1 kinase complex;
XX KW caspase-9; tumour suppressor; antisense therapy; cytostatic.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Modified-site 4..7
XX FT /note= "phosphorylation site for p34(cdc2)-cyclin B1
XX FT kinase complex"
XX FN WO200164741-A2.
XX XX
XX PD 07-SEP-2001.
XX PF 28-FEB-2001; 2001WO-US006341.
XX XX
XX PR 29-FEB-2000; 2000US-00515514.
XX XX
XX PA (UYVA) UNIV YALE.
XX PI Altieri DC;
XX DR WPI; 2001-589861/66.
XX XX
XX PT Modulating survivin apoptosis pathways by using an agent that modulates
XX PT phosphorylation of survivin, interaction between survivin and p34-cyclin
XX PT B1 kinase complex and interaction between survivin and caspase-9.
XX PS Example 1; Fig 1A; 97pp; English.
XX CC The invention relates to a method for modulating apoptosis, in particular
XX CC survivin dependent apoptosis in a cell. The method involves administering
XX CC to the cell an agent which modulates the interaction between survivin and
XX CC p34(cdc2)-cyclin B1 kinase complex, phosphorylation of survivin by the
XX CC p34(cdc2)-cyclin B1 kinase complex and interaction between survivin and
XX CC caspase-9. Survivin antagonist is useful for inhibiting tumour growth in
XX CC a mammal. Agents that modulate, preferably dephosphorylate survivin at
XX CC Thr34, act as potential tumour suppressors and prevent the formation of
XX CC anti-apoptotic complex with caspase. The method is also useful in
XX CC antisense therapy. The present sequence is human survivin phosphorylation
XX CC motif
XX SQ Sequence 9 AA;

Query Match          6.3%; Score 9; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 CACTPERMA 39
DB 1 CACTPERMA 9
|||||

Query Match          6.3%; Score 9; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 AFLSVKQF 93
DB 1 AFLSVKQF 9
|||||

RESULT 37
AAR27745
ID AAR27745 standard; protein; 1822 AA.
XX AC AAR27745;
XX XX
XX DT 24-OCT-2003 (revised)
XX DT 25-MAR-2003 (revised)
XX DT 04-MAR-1993 (first entry)
XX DE Extracellular factor related protein.
XX KW EF*; detection; prevention; screening; diagnostic.
XX OS Streptococcus suis; type II (non-pathogenic).
XX FH Key Location/Qualifiers
XX FT Peptide 1..46
XX FT /note= "signal peptide"
XX FT Peptide 47..1822

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```

RESULT 36
ADA09937
ID ADA09937 standard; peptide; 9 AA.
XX AC
XX AC ADA09937;
XX DT
XX DT 06-NOV-2003 (first entry)
XX DE Human HLA-A24 antigen survivin 85, SEQ ID NO:2.
XX KW Human; survivin; survivin 2B80; survivin 85; HLA-A24 antigen;
XX KW human leukocyte antigen; cytotoxic T-cell; CTL; induction; cancer;
XX KW vaccine; anticancer agent; cytostatic.
XX OS Homo sapiens.
XX FN JP2002284797-A.
XX PD 03-OCT-2002.
XX PF 23-MAR-2001; 2001JP-00084438.
XX XX
XX PR 23-MAR-2001; 2001JP-00084438.
XX PA (HOKK-) HOKKAIDO TLO KK.
XX DR WPI; 2003-397157/38.
XX XX
XX FT A novel nonapeptide survivin 2B80 capable of inducing cytotoxic T-cells,
XX FT useful in vaccines for the treatment of cancer.
XX PS Example 3; Page 5; 10pp; Japanese.
XX CC The invention relates to a human survivin-derived cancer antigen,
XX CC designated survivin 2B80. Survivin 2B80 is a HLA-A24 antigen, and is
XX CC capable of inducing cytotoxic T-cells (CTLs) which target cancer cells
XX CC having HLA-A24 expression. Survivin 2B80 can be used in the treatment of
XX CC cancer, specifically in a cancer vaccine or as an anticancer agent. The
XX CC present sequence represents a different survivin-derived HLA-A24 antigen,
XX CC survivin 85, which corresponds to residues 108-116 of full-length human
XX CC survivin (ADA09936) and which was used in an example from the invention.
XX SQ Sequence 9 AA;

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```

Query Match          6.3%; Score 9; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 85 AFLSVKQF 93
DB 1 AFLSVKQF 9
|||||

```

```

RESULT 37
AAR27745
ID AAR27745 standard; protein; 1822 AA.
XX AC AAR27745;
XX XX
XX DT 24-OCT-2003 (revised)
XX DT 25-MAR-2003 (revised)
XX DT 04-MAR-1993 (first entry)
XX DE Extracellular factor related protein.
XX KW EF*; detection; prevention; screening; diagnostic.
XX OS Streptococcus suis; type II (non-pathogenic).
XX FH Key Location/Qualifiers
XX FT Peptide 1..46
XX FT /note= "signal peptide"
XX FT Peptide 47..1822

```

```

FT Region /note= "mature peptide"
FT 858..861
FT /note= "repetitive Asn-Pro-Asn-Leu sequence"
FT 934..937
FT /note= "repetitive Asn-Pro-Asn-Leu sequence"
FT 999..1002
FT /note= "repetitive Asn-Pro-Asn-Leu sequence"
FT 1075..1078
FT /note= "repetitive Asn-Pro-Asn-Leu sequence"
FT 1264..1267
FT /note= "repetitive Asn-Pro-Asn-Leu sequence"
FT 1362..1365
FT /note= "repetitive Asn-Pro-Asn-Leu sequence"
FT 1438..1441
FT /note= "repetitive Asn-Pro-Asn-Leu sequence"
FT 1514..1517
FT /note= "repetitive Asn-Pro-Asn-Leu sequence"
FT 1590..1593
FT /note= "repetitive Asn-Pro-Asn-Leu sequence"
FT 1666..1669
FT /note= "repetitive Asn-Pro-Asn-Leu sequence"
FT 1741..1744
FT /note= "repetitive Asn-Pro-Asn-Leu sequence"
XX WO9216630-A1.
XX 01-OCT-1992.
XX 19-MAR-1992; 92WO-NL0000054.
XX 21-MAR-1991; 91NL-00000510.
XX (DIER-) CENT DIERGENESKUNDIG INST.
XX Smith HE, Vecht U;
XX WPI; 1992-349215/42.
XX N-PSDB; AAQ29471.
XX Deoxyribonucleic acid encoding virulence characteristic of Streptococcus
XX suis - useful for antibody and polypeptide for diagnosing and preventing
XX infections in pigs and humans.
XX Claim 9; Fig 1b; 86pp; English.
XX The sequence is that of the extracellular factor related protein from
XX Streptococcus suis type II (non-pathogenic) which allows the detection
XX and the prevention of infections by S. suis in a more effective manner
XX than was previously possible. It facilitates screening of e.g. pigs and
XX elimination of infected and carrier pigs can then be carried out. The new
XX diagnostic tests can distinguish between avirulent and virulent strains.
XX It may be used in the prodn. of a vaccine. See also AAQ27744 and
XX AAQ27746. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 24-
XX OCT-2003 to standardise OS field)
XX SQ Sequence 1822 AA;
XX Query Match 5.6%; Score 8; DB 2; Length 1822;
XX Best Local Similarity 100.0%; Pred. No. 43;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 109 AKNKIAKE 116
Db 1057 AKNKIAKE 1064
RESULT 38
ABU57366
ID ABU57366 standard; peptide; 9 AA.
XX
AC ABU57366;
XX
DT 08-APR-2003 (first entry)

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XX DE
XX KW MHC; major histocompatibility complex; human; cytostatic; anti-HIV;
XX anti-inflammatory; dermatological; antiasthmatic; antidiabetic; virucide;
XX antiarteriosclerotic; antitumor; antirheumatic; antiarthritic; AIDS;
XX antipsoriatic; immunosuppressive; inflammatory bowel disease; measles;
XX Crohn's disease; ulcerative colitis; sclerosis; type I diabetes; pox;
XX rheumatoid arthritis; psoriasis; atopic dermatitis; asthma; chicken pox;
XX malignant melanoma; carcinoma; cancer; leukaemia; lymphoma; hepatitis;
XX rubella; herpes; human immunodeficiency virus.
XX OS Synthetic.
XX FN WO200272631-A2.
XX PD 19-SEP-2002.
XX PF 13-MAR-2002; 2002WO-DK000169.
XX PR 14-MAR-2001; 2001DK-00000435.
XX PR 14-MAR-2001; 2001DK-00000436.
XX PR 14-MAR-2001; 2001DK-00000441.
XX PR 14-MAR-2001; 2001US-0275447B.
XX PR 14-MAR-2001; 2001US-0275448P.
XX PR 14-MAR-2001; 2001US-0275470P.
XX (DAKO-) DAKOCYTOMATION DENMARK AS.
XX PA (DYNA-) DYNAL BIOTECH ASA.
XX PI Winther L, Petersen LO, Buus S, Schoeller J, Ruub E, Amellem O;
XX WPI; 2002-759837/82.
XX PT New Major Histocompatibility Complex (MHC) molecule construct, useful for
XX treating, preventing, stabilizing or alleviating a disease involving MHC
XX recognizing cells e.g., cancer.
XX Example 1; Page 159; 304pp; English.
XX This invention relates to a new Major Histocompatibility Complex (MHC)
XX molecule construct comprising a carrier molecule to which one or more MHC
XX molecules are attached either directly or via one or more entities. The
XX construct of the invention may have cytostatic, antiinflammatory,
XX dermatological, antiasthmatic, antidiabetic, anti-HIV, virucide,
XX antiarteriosclerotic, antitumor, antirheumatic, antiarthritic,
XX antipsoriatic and immunosuppressive activities and may be used in gene
XX therapy. The MHC molecule construct is useful as a therapeutic
XX composition in vivo or ex vivo therapy, for treating, preventing,
XX stabilising or alleviating a disease involving MHC recognising cells, for
XX monitoring MHC recognising cells or establishing a prognosis of a disease
XX or diagnosing a disease, or determining the status of a disease or the
XX effectiveness of a medication against a disease, involving MHC
XX recognising cells, e.g., chronic inflammatory bowel disease such as
XX Crohn's disease or ulcerative colitis, sclerosis, type I diabetes,
XX rheumatoid arthritis, psoriasis, atopic dermatitis, asthma, malignant
XX melanoma, renal carcinoma, breast cancer, lung cancer, cancer of the
XX uterus, cervical cancer, prostate cancer, brain cancer, head and neck
XX cancer, leukaemia, cutaneous lymphoma, hepatic carcinoma, colorectal
XX cancer, bladder cancer, rejection-related disease, Graft-versus-host-
XX related disease, or a viral disease associated with hepatitis. Acquired
XX Immunodeficiency Syndrome (AIDS), measles, pox, chicken pox, rubella or
XX herpes. The MHC molecule construct is also useful for flow cytometry,
XX histology or cytology. The present sequence represents a peptide used to
XX create the MHC molecule construct of the invention
XX Sequence 9 AA;
XX Query Match 4.9%; Score 7; DB 5; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 1.4e-06;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 98 LGFFLKL 104

```

Db 3 LGFFLKL 9

RESULT 39
AAM19295
ID AAM19295 strand: protein; 73 AA.

AC AAM19295;

DT 12-OCT-2001 (first entry)

DE Peptide #5729 encoded by probe for measuring cervical gene expression.

XX KW Probe; human; microarray; gene expression; cervical epithelial cell;

XX OS Homo sapiens.

XX PN WO200157278-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US000670.

XX PR 04-FEB-2000; 2000US-0180312P.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 30-JUN-2000; 2000US-00608408.

XX PR 03-AUG-2000; 2000US-00632366.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX DR MPI; 2001-488901/53.

XX PT Human genome-derived single exon nucleic acid probes useful for analyzing

XX PT gene expression in human cervical epithelial cells.

XX PS Claim 27; SEQ ID NO 24121; 487bp; English.

XX CC The present invention relates to human single exon nucleic acid probes

XX CC (SEN1; see AAM10068-AAM28459). The present sequence is a peptide encoded

XX CC by one such probe. The SENs are derived from human Hela cells. The SENs

XX CC can be used to produce a single exon microarray, which can be used for

XX CC measuring human gene expression in a sample derived from human cervical

XX CC epithelial cells. By measuring gene expression, the probes are therefore

XX CC useful in grading and/or staging of diseases of the cervix, notably

XX CC cervical cancer. Note: The sequence data for this patent did not form

XX CC part of the printed specification, but was obtained in electronic format

XX CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 73 AA;

Query Match 4.9%; Score 7; DB 4; Length 73;

Best Local Similarity 100.0%; Pred. No. 25;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 NKIAKET 117

Db 1 NKIAKET 7

RESULT 40

ABB38577

DT 04-FEB-2002 (first entry)

XX DE Peptide #6083 encoded by human foetal liver single exon probe.

XX KW Human; foetal liver; gene expression; single exon nucleic acid probe.

XX OS Homo sapiens.

XX PN WO200157277-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US000669.

XX PR 04-FEB-2000; 2000US-0180312P.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 30-JUN-2000; 2000US-00608408.

XX PR 03-AUG-2000; 2000US-00632366.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX DR MPI; 2001-483447/52.

XX PT Human genome-derived single exon nucleic acid probes useful for analyzing

XX PT gene expression in human foetal liver.

XX PS Claim 27; SEQ ID NO 31212; 639bp + Sequence listing; English.

XX CC The invention relates to a single exon nucleic acid probe for measuring

XX CC human gene expression in a sample derived from human foetal liver. The

XX CC single exon nucleic acid probes may be used for predicting, measuring and

XX CC displaying gene expression in samples derived from human foetal liver. The

XX CC present sequence is a peptide encoded by a single exon nucleic acid probe

XX CC of the invention. Note: The sequence data for this patent did not form

XX CC part of the printed specification, but was obtained in electronic format

XX CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 73 AA;

Query Match 4.9%; Score 7; DB 4; Length 73;

Best Local Similarity 100.0%; Pred. No. 25;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 NKIAKET 117

Db 1 NKIAKET 7

RESULT 41

AAM32028

DT 04-FEB-2002 (first entry)

XX DE Peptide #6065 encoded by probe for measuring placental gene expression.

XX KW Probe; microarray; human; placenta; antenatal diagnosis;

XX OS genetic disorder.

XX PN WO200157272-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US000663.

XX PR 04-FEB-2000; 2000US-0180312P.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 30-JUN-2000; 2000US-00608408.

XX PR 03-AUG-2000; 2000US-00632366.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX DR MPI; 2001-483447/52.

XX PT Human genome-derived single exon nucleic acid probes useful for analyzing

XX PT gene expression in human foetal liver.

XX PS Claim 27; SEQ ID NO 31212; 639bp + Sequence listing; English.

XX CC The invention relates to a single exon nucleic acid probe for measuring

XX CC human gene expression in a sample derived from human foetal liver. The

XX CC single exon nucleic acid probes may be used for predicting, measuring and

XX CC displaying gene expression in samples derived from human foetal liver. The

XX CC present sequence is a peptide encoded by a single exon nucleic acid probe

XX CC of the invention. Note: The sequence data for this patent did not form

XX CC part of the printed specification, but was obtained in electronic format

XX CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 73 AA;

Query Match 4.9%; Score 7; DB 4; Length 73;

Best Local Similarity 100.0%; Pred. No. 25;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 NKIAKET 117

Db 1 NKIAKET 7

RESULT 42

ABB38577

DT 04-FEB-2002 (first entry)

PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00609408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 DR WPI; 2001-488897/53.
 XX
 PT Human genome-derived single exon nucleic acid probes useful for analyzing
 XX gene expression in human placenta.
 PS Claim 27; SEQ ID NO 32297; 654bp; English.
 XX
 CC The present invention relates to single exon nucleic acid probes (SENPs;
 CC see A13315-A157546). The present sequence is a peptide encoded by one
 CC such probe. The probes are useful for producing a microarray for
 CC predicting, measuring and displaying gene expression in samples derived
 CC from human placenta. The probes are useful for antenatal diagnosis of
 CC human genetic disorders
 CC
 SQ Sequence 73 AA;
 Query Match 4.9%; Score 7; DB 4; Length 73;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 111 NRIAKET 117
 Db 1 NRIAKET 7
 RESULT 42
 ID ABB23701 standard; protein; 73 AA.
 AC ABB23701;
 XX
 DT 23-JAN-2002 (first entry)
 DE Protein #5700 encoded by probe for measuring heart cell gene expression.
 XX
 KW Human; gene expression; heart; microarray; vascular system;
 KW cardiovascular disease; hypertension; cardiac arrhythmia;
 KW congenital heart disease.
 XX
 OS Homo sapiens.
 XX
 FN W0200157274-A2.
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US000666.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00609408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 DR WPI; 2001-488897/53.
 XX

PT Single exon nucleic acid probes for analyzing gene expression in human
 PT hearts.
 XX
 PS Claim 15; SEQ ID NO 25471; 530bp; English.
 XX
 CC The present invention relates to single exon nucleic acid probes for
 CC measuring human gene expression in a sample derived from human heart (see
 CC ABA21535-ABA41305). The present sequence is a protein encoded by one such
 CC probe. The probes may be used for predicting, measuring and displaying
 CC gene expression in samples derived from the human heart via microarrays.
 CC By measuring gene expression, the probes are useful for predicting,
 CC diagnosing, grading, staging, monitoring and prognosing diseases of the
 CC human heart and vascular system e.g. cardiovascular disease,
 CC hypertension, cardiac arrhythmias and congenital heart disease. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 73 AA;
 Query Match 4.9%; Score 7; DB 4; Length 73;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 111 NRIAKET 117
 Db 1 NRIAKET 7
 RESULT 43
 ID AAM71736 standard; protein; 73 AA.
 AC AAM71736;
 XX
 DT 06-NOV-2001 (first entry)
 DE Human bone marrow expressed probe encoded protein SEQ ID NO: 32042.
 XX
 KW Human; bone marrow expressed exon; gene expression analysis; probe;
 KW microarray; cancer; leukaemia; lymphoma; myeloma.
 XX
 OS Homo sapiens.
 XX
 FN W0200157276-A2.
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US000668.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00609408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 DR WPI; 2001-488897/53.
 XX
 PT Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human bone marrow.
 PS Example 4; SEQ ID NO 32042; 658bp + Sequence Listing; English.
 XX
 CC The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC bone marrow. They can be used to measure gene expression in bone marrow
 CC samples, which may enable the improved diagnosis and treatment of cancers

CC such as lymphoma, leukaemia and myeloma. The present sequence is a
CC protein encoded by one of the probes of the invention

CC Sequence 73 AA:

Query Match 4.9%; Score 7; DB 4; Length 73;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 NKIAKET 117
DB 1 NKIAKET 7

RESULT 44
AAM59201
ID AAM59201 standard; protein; 73 AA.

AC AAM59201;

DT 05-NOV-2001 (first entry)

XX Human brain expressed single exon probe encoded protein SEQ ID NO: 31306.

XX Human; brain expressed exon; gene expression analysis; probe; microarray;

XX Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.

XX Homo sapiens.

XX WO200157275-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000667.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

PA (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

DR WPI; 2001-483446/52.

PT Single exon nucleic acid probes for analyzing gene expression in human
PT brains.

PS Example 4; SEQ ID NO 31306; 650bp + Sequence Listing; English.

XX The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is a protein encoded by one of
CC the probes of the invention

CC Sequence 73 AA:

Query Match 4.9%; Score 7; DB 4; Length 73;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 NKIAKET 117
DB 1 NKIAKET 7

RESULT 45
ABG53421
ID ABG53421 standard; peptide; 73 AA.

AC ABG53421;

DT 25-FEB-2003 (first entry)

XX Human liver peptide, SEQ ID No 32069.

XX Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;

XX hypercholesterolaemia; coronary heart disease.

XX Homo sapiens.

XX WO200157273-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000664.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

PA (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

DR WPI; 2001-488898/53.

PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human adult liver.

PS Claim 27; SEQ ID NO 32069; 658bp; English.

XX The invention relates to a single exon nucleic acid probe (SENP) (i) for
CC measuring human gene expression in a sample derived from human adult
CC liver, comprising one of 13109 defined nucleotide sequences given in the
CC specification (or complements/ fragments). The probe hybridises at high
CC stringency to a nucleic acid molecule expressed in the human adult liver.
CC (i) may be used for predicting, measuring and displaying gene expression
CC in samples derived from human adult liver. The genes identified may be
CC involved in genetic liver diseases such as cirrhosis,
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
CC associated with coronary heart disease. ABG47348-ABG59930 represent human
CC liver single exon encoded peptides of the invention. Note: The sequence
CC information for this patent does not appear in the printed specification
CC but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

CC Sequence 73 AA:

Query Match 4.9%; Score 7; DB 4; Length 73;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 NKIAKET 117
DB 1 NKIAKET 7

RESULT 46
ABG41550
ID ABG41550 standard; peptide; 73 AA.

AC ABG41550;

DT 19-AUG-2002 (first entry)

XX DE Human peptide encoded by genome-derived single exon probe SEQ ID 31215.
 XX XX Human; single exon probe; asthma; lung cancer; COPD; ILD;
 XX XX Chronic obstructive pulmonary disease; interstitial lung disease;
 XX XX familial idiopathic pulmonary fibrosis; neurofibromatosis;
 XX XX tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
 XX XX Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
 XX XX pulmonary histiocytosis; lymphangioleiomyomatosis; Karagazer syndrome;
 XX XX primary alveolar proteinosis; fibrocystic pulmonary dysplasia;
 XX XX hyaline membrane disease.
 XX OS Homo sapiens.
 XX PN WO200186003-A2.
 XX PD 15-NOV-2001.
 XX PF 30-JUN-2001; 2001WO-US000665.
 XX PR 04-FEB-2000; 2000US-0180312P.
 XX PR 26-MAY-2000; 2000US-0207456P.
 XX PR 30-JUN-2000; 2000US-00608408.
 XX PR 03-AUG-2000; 2000US-00632366.
 XX PR 21-SEP-2000; 2000US-0234687P.
 XX PR 27-SEP-2000; 2000US-0236359P.
 XX PR 04-OCT-2000; 2000US-00024263.
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX DR WPI; 2002-114183/15.
 XX PT Spatially-addressable set of single exon nucleic acid probes, used to
 XX PT measure gene expression in human lung samples.
 XX PS Claim 27; SEQ ID NO 31215; 634pp; English.
 CC The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human lung comprising single exon nucleic acid probes having one of
 CC 12614 nucleic acid sequences mentioned in the specification, or their
 CC complements or the 12387 open reading frames derived from the 12614
 CC probes. Also included are a microarray comprising the novel set of probes
 CC; the novel set of probes which hybridise at high stringency to a nucleic
 CC acid expressed in the human lung; measuring gene expression in a sample
 CC derived from human lung; comprising (a) contacting the array with a
 CC collection of detectably labeled nucleic acids derived from human lung
 CC mRNA; and (b) measuring the label detectably bound to each probe of the
 CC array; identifying exons in a eukaryotic genome, comprising (a)
 CC algorithmically predicting at least one exon from genomic sequences of
 CC the eukaryote; and (b) detecting specific hybridisation of detectably
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
 CC having a fragment identical to the predicted exon, the probe is included
 CC in the above mentioned microarray; assigning exons to a single gene,
 CC comprising (a) identifying exons from genomic sequence by the method
 CC above and (b) measuring the expression of each of the exons in several
 CC tissues and/or cell types using hybridisation to a single exon
 CC microarrays having a probe with the exon, where a common pattern of
 CC expression of the exons in the tissues and/or cell types indicates that
 CC the exons should be assigned to a single gene; a peptide comprising one
 CC of 12011 sequences, mentioned in the specification, or encoded by the
 CC probes/open reading frames (ORF). The probes are used for gene expression
 CC analysis, and for identifying exons in a gene, particularly using human
 CC lung derived mRNA and for the study of lung diseases such as asthma, lung
 CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
 CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
 CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
 CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
 CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
 CC Karagazer syndrome, fibrocystic pulmonary dysplasia, primary ciliary

CC dykinesis, pulmonary hypertension and hyaline membrane disease. The
 CC present sequence is a peptide/protein encoded by a single exon probe of
 CC the invention. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 CC XX
 CC SQ Sequence 73 AA;
 CC
 CC Query Match 4.9%; Score 7; DB 5; Length 73;
 CC Best Local Similarity 100.0%; Pred. No. 25;
 CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 111 NRIKET 117
 CC Db 1 NRIKET 7
 CC
 CC RESULT 47
 CC AAM8735
 CC ID AAM8735 standard; protein; 101 AA.
 CC AC
 CC XX AAM8735;
 CC XX
 CC DT 01-MAR-1999 (first entry)
 CC XX
 CC DE Secreted protein encoded by gene 202 clone HNGBR45.
 CC XX
 CC XX Human; secreted protein; fusion protein; gene therapy; protein therapy;
 CC XX diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
 CC XX developmental abnormality; foetal deficiency; blood; allergy; renal;
 CC XX immune system; asthma; lymphocytic disease; brain; hepatitis; lymphoma;
 CC XX inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
 CC XX cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
 CC XX osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
 CC XX endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
 CC OS Homo sapiens.
 CC XX
 CC PN WO9854963-A2.
 CC PD 10-DEC-1998.
 CC XX
 CC PF 04-JUN-1998; 98WO-US011422.
 CC XX
 CC PR 06-JUN-1997; 97US-0048875P.
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 CC PR 06-JUN-1997; 97US-0048881P.
 CC PR 06-JUN-1997; 97US-0048882P.
 CC PR 06-JUN-1997; 97US-0048883P.
 CC PR 06-JUN-1997; 97US-0048884P.
 CC PR 06-JUN-1997; 97US-0048885P.
 CC PR 06-JUN-1997; 97US-0048892P.
 CC PR 06-JUN-1997; 97US-0048893P.
 CC PR 06-JUN-1997; 97US-0048894P.
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 CC PR 06-JUN-1997; 97US-0048898P.
 CC PR 06-JUN-1997; 97US-0048899P.
 CC PR 06-JUN-1997; 97US-0048900P.
 CC PR 06-JUN-1997; 97US-0048901P.
 CC PR 06-JUN-1997; 97US-0048915P.
 CC PR 06-JUN-1997; 97US-0048916P.
 CC PR 06-JUN-1997; 97US-0048917P.
 CC PR 06-JUN-1997; 97US-0048949P.
 CC PR 06-JUN-1997; 97US-0048962P.
 CC PR 06-JUN-1997; 97US-0048963P.
 CC PR 06-JUN-1997; 97US-0048964P.
 CC PR 06-JUN-1997; 97US-0048970P.
 CC PR 06-JUN-1997; 97US-0048971P.

CC	06-JUN-1997;	97US-0048972P.
PR	06-JUN-1997;	97US-0048974P.
PR	06-JUN-1997;	97US-0049019P.
PR	06-JUN-1997;	97US-0049020P.
PR	06-JUN-1997;	97US-0049373P.
PR	06-JUN-1997;	97US-0049374P.
PR	06-JUN-1997;	97US-0049375P.
PR	05-SEP-1997;	97US-0057584P.
PR	05-SEP-1997;	97US-0057627P.
PR	05-SEP-1997;	97US-0057628P.
PR	05-SEP-1997;	97US-0057629P.
PR	05-SEP-1997;	97US-0057634P.
PR	05-SEP-1997;	97US-0057635P.
PR	05-SEP-1997;	97US-0057642P.
PR	05-SEP-1997;	97US-0057643P.
PR	05-SEP-1997;	97US-0057644P.
PR	05-SEP-1997;	97US-0057645P.
PR	05-SEP-1997;	97US-0057646P.
PR	05-SEP-1997;	97US-0057647P.
PR	05-SEP-1997;	97US-0057648P.
PR	05-SEP-1997;	97US-0057649P.
PR	05-SEP-1997;	97US-0057650P.
PR	05-SEP-1997;	97US-0057651P.
PR	05-SEP-1997;	97US-0057654P.
PR	05-SEP-1997;	97US-0057661P.
PR	05-SEP-1997;	97US-0057662P.
PR	05-SEP-1997;	97US-0057663P.
PR	05-SEP-1997;	97US-0057664P.
PR	05-SEP-1997;	97US-0057665P.
PR	05-SEP-1997;	97US-0057666P.
PR	05-SEP-1997;	97US-0057667P.
PR	05-SEP-1997;	97US-0057668P.
PR	05-SEP-1997;	97US-0057760P.
PR	05-SEP-1997;	97US-0057771P.
PR	05-SEP-1997;	97US-0057774P.
PR	05-SEP-1997;	97US-0057775P.
PR	05-SEP-1997;	97US-0057776P.
PR	05-SEP-1997;	97US-0057777P.
PR	05-SEP-1997;	97US-0057778P.
PR	18-DEC-1997;	97US-0070923P.
PA	(HUMA-) HUMAN GENOME SCI INC.	
XX	Young P, Greene JM, Ferrie AM, Ruben SM, Rosen CA, Hu J,	
PI	Olsen HS, Ehner R, Brewer LA, Moore PA, Shi Y, Florence C,	
PI	Florence K, Lathier DM, Ni J, Fan P, Wei Y, Fischer CL, Soggett DR,	
PI	Li Y, Zeng Z, Kyaw H, Yu G, Feng P, Dillon PJ, Endress G,	
PI	Carter KC.	
DR	WPI, 1999-059865/05.	
DR	N-PSDB: AAW84612.	
XX		
PT	New isolated human genes and the secreted polypeptides they encode -	
PT	useful for diagnosis and treatment of e.g. cancers, neurological	
PT	disorders, immune diseases, inflammation or blood disorders.	
XX		
PS	Claim 11; Page 584; 772pp; English.	
XX		
CC	The invention relates to nucleic acid sequences (AAW84411 to AAW84633)	
CC	encoding human secreted proteins (AAW88534 to AAW88736). The secreted	
CC	protein gene sequences are deposited with the ATCC under deposit numbers	
CC	ATCC 97973, 97974, 97975, 97976, 97977, 209007, 209008, 209009, 209010,	
CC	209011, 209080, 209081, 209082, 209083, 209084, 209085, 209511. Host	
CC	cells comprising recombinant vectors containing the nucleic acid	
CC	sequences are used for the recombinant production of the secreted	
CC	proteins. The polynucleotide and amino acid sequences are useful for are	
CC	useful for preventing, treating or ameliorating medical conditions e.g.	
CC	by protein or gene therapy. Pathological conditions can be also diagnosed	
CC	by determining the amount of the new polypeptides in a sample or by	

CC	determining the presence of mutations in the new polypeptides.
CC	Specific uses are described for each of the polynucleotides, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, neurodegenerative disorders, developmental abnormalities and foetal deficiencies, blood disorders, tumours, leukaemias, diseases of the immune system, autoimmune diseases, hepatic and renal disease, lymphomas, inflammation, allergies, ischemic shock, Alzheimer's and cognitive disorders, schizophrenia, osteoarthritis, prostate diseases, obesity, disorders involving osteoclasts such as osteoporosis, arthritis or malfunctions, diseases of testes, lung or thymus, digestive/endocrine disorders, infections and AIDS. The polypeptides are also useful for identifying their binding partners. The present sequence represents human secreted protein (see descriptor line for gene number and clone identification)
XX	Sequence 101 AA;
SQ	
Query Match	4.9%; Score 7; DB 2; Length 101;
Best Local Similarity	100.0%; Pred. No. 34;
Matches	7; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Dd	
13 FLKDRI 19	
22 FLKDRI 28	
RESULT 48	
ID	ABBS0502
ID	ABBS0502 standard; protein; 101 AA.
AC	
XX	ABBS0502;
DT	
DE	07-FEB-2002 (first entry)
XX	
XX	Human secreted protein encoded by gene 202 SEQ ID NO:450.
KM	Human; secreted protein; immunomodulatory; antisclerotic; anti-HIV; dermatological; immunosuppressive; anti-inflammatory; immunostimulant; cytotoxic; cardiac; vascular; anti-angiogenic; ophthalmological; neuroprotective; nootropic; anticoagulant; antialzheimers; vulnery; antiParkinsonian; antimicrobial; gene therapy; vaccine; immune disorder; multiple sclerosis; systemic lupus erythematosus; HIV infection; cancer; human immunodeficiency virus; hyperproliferative disorder; wound healing; Gaucher's disease; cardiovascular disease; Schmitz syndrome; chemotaxis; Chagas's cardiomyopathy; coronary arteriosclerosis; angiocenic disorder; corneal graft neovascularisation; diabetic retinopathy; regeneration; neurological disorder; Huntington's chorea; Alzheimer's disease; Parkinson's disease; infectious disease.
KW	Homo sapiens.
OS	
XX	
FN	WC000162891-A2.
XX	
ED	30-AUG-2001.
XX	
PF	21-FEB-2001; 2001WC-US005614.
XX	
PR	24-FEB-2000; 2000US-0184836F.
FR	29-MAR-2000; 2000US-0193170P.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.
PI	Nà J., Epper R., Lafleur DW., Moore PA., Olsen HS., Rosen CA.; Ruben SM., Soppet DR., Young PE., Shi Y., Florence KA., Wei Y., Florence C., Hu J., Li Y., Kyaw H., Fischer CL., Ferrie AM., Fan P., Feng P., Endress GA., Dillon PJ., Carter KC., Brewer LA., Yu G., Zeng Z., Greene JM.;
XX	WP1: 2001-625724/72.
DR	RN-PSDB; ABA83395.
XX	
LT	Nucleic acids encoding 207 human secreted polypeptides, useful for preventing, diagnosing and/or treating, e.g. cancers, Parkinson's disease

PT and diabetic retinopathy.
XX
PS Claim 11; Page 1196; 1533pp; English.
XX
CC ABB50301 to ABB51287 and ABA83194 to ABA83441 represent human secreted
CC proteins (I) and polynucleotide (II) sequences. (I) and (II) have various
CC activities based on the tissues and cells the genes are expressed in.
CC Example of these activities include: immunomodulatory; antisclerotic;
CC dermatological; immunosuppressive; antiinflammatory; immunostimulant;
CC anti-HIV; cytostatic; cardiant; anti-angiogenic; ophthalmological;
CC neuroprotective; nootropic; anticonvulsant; antialzheimer's; vascular;
CC antiparkinsonian; antimicrobial; and vulnerary. (I) and (II) can be used
CC in gene therapy and vaccine production. (I) and (II) can be used in the
CC prevention, diagnosis and treatment of immune disorders (e.g. multiple
CC sclerosis, systemic lupus erythematosus and human immunodeficiency virus
CC (HIV) infections), hyperproliferative disorders (e.g. cancers and
CC Gaucher's disease), cardiovascular diseases (e.g. Scimitar syndrome,
CC disorders (e.g. corneal graft neovascularization) and diabetic
CC retinopathy), neurological disorders (e.g. Huntington's chorea,
CC Alzheimer's disease and Parkinson's disease), infectious diseases and/or
CC for promoting wound healing, regeneration and/or chemotaxis. ABA83195 to
CC ABA83193 and ABB50300 represent sequences used in the exemplification of
CC the present invention
XX
SQ Sequence 101 AA;

Query Match 4.9%; Score 7; DB 4; Length 101;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 FLKDHR 19
Db 22 FLKDHR 28

RESULT 49
ABO44759
ID ABO44759 standard; protein; 101 AA.
XX
XX ABO44759;
AC
XX
DT 02-OCT-2003 (first entry)
XX
XX
DE Novel human secreted protein #202.
XX
XX
KW Human; gene therapy; autoimmune disorder; multiple sclerosis; cancer;
KW systemic lupus erythematosus; haematopoietic cell disorder; allergy;
KW agammaglobulinemia; ataxia telangiectasia; blood coagulation disorder;
KW aplastic anaemia; thrombocytopenia; graft-versus-host disease; arthritis;
KW inflammatory condition; ischaemia-reperfusion injury; infectious disease;
KW hyperproliferative disorder; purpura; viral infection; regeneration;
KW bacterial infection; ulcer; Alzheimer's disease.
XX
OS Homo sapiens.
XX
XX US2003065160-A1.
XX
XX
PD 03-APR-2003.
XX
XX
PF 07-DEC-2001; 2001US-00004860.
XX
XX
PR 06-JUN-1997; 97US-0048875P.
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PR 06-JUN-1997; 97US-0048893P.
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PR 06-JUN-1997; 97US-0049056P.
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PI Carter KC;
XX WPI, 2003-540804/51.
DR N-PSDB; ACH04896.
XX
PT New isolated protein, useful for preparing a composition for diagnosing
PT or treating cancer, inflammatory, immune or infectious diseases.
XX
PS Disclosure; SEQ ID NO 450; 1722pp; English.
XX
XX The invention relates to an isolated HEMA580 protein. The protein is
CC useful for preparing a composition for diagnosing or treating autoimmune
CC disorders e.g. multiple sclerosis and systemic lupus erythematosus;
CC haematopoietic cell disorders e.g. agammaglobulinaemia and ataxia
CC telangiectasia; blood coagulation disorders e.g. fibrinogenemia and
CC thrombocytopenia; allergy; graft-versus-host disease; inflammatory
CC conditions e.g. ischaemia-reperfusion injury and arthritis;
CC hyperproliferative disorders e.g. cancer and psoriasis; infectious disease
CC e.g. viral infection and bacterial infection. The polynucleotide or
CC protein can be used to regenerate damaged tissue e.g. ulcers and
CC Alzheimer's disease. The present sequence represents the amino acid
CC sequence of a novel human secreted protein. Note: The sequence data for
CC this patent did not form part of the printed specification but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?docid=20030065160
XX
SQ Sequence 101 AA;
XX
Query Match 4.9%; Score 7; DB 6; Length 101;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX 13 FLKDHR1 19
CY |||||
Db 22 FLKDHR1 28
XX
RESULT 50.
ABO26239
ID ABO26239 standard; protein; 101 AA.
XX
AC ABO26239;
XX
DT 10-SEP-2003 (first entry)
XX
DE Human protein from novel secreted protein gene 202.
XX
KW Human; secreted protein; precerebellin-like protein;
KW neurodegenerative disorder; behavioural disorder; Alzheimer's disease;
KW Parkinson's disease; Huntington's disease; schizophrenia; mania;
KW dementia; paranoa; psychosis; autism; immune disorder; infection;
KW inflammation; allergy; liver disorder; hepatoblastoma; jaundice;
KW hepatitis; immunological disorder; AIDS; leukaemia; rheumatoid arthritis;
KW sepsis; acne; psoriasis; cancer.
XX
XX Homo sapiens.
OS
XX US6525174-B1.
XX
PD 25-FEB-2003.
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XX 04-DEC-1998; 98US-00205258.
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PR 05-SEP-1997;

PI Carter KC;
 XX WPI; 2003-511926/48.
 DR N-FSD3; AC044706.
 XX
 PT New precerebellin-like protein, useful for diagnosing or treating
 PT neurodegenerative and behavioral disorders, immune disorders, liver
 PT disorders, and cancer.
 XX
 PS Disclosure; SEQ ID NO 450; 156pp; English.
 XX
 CC The invention relates to an isolated protein comprising amino acid
 CC residues 33-205 or 1-205 of a novel human secreted protein appearing as
 CC ABO26252. The protein is encoded by one of 238 disclosed cDNA sequences
 CC encoding 238 secreted proteins. ABO26252 is a precerebellin-like protein.
 CC Also included are a composition comprising the protein and a carrier and
 CC an isolated protein produced by expressing the protein cited above by a
 CC cell, and recovering the protein. The proteins are useful for diagnosing
 CC or treating neurodegenerative and behavioral disorders (e.g. Alzheimer's
 CC disease, Parkinson's disease, Huntington's disease, schizophrenia, mania,
 CC dementia, paranoia, psychoses or autism), immune disorders (e.g. AIDS,
 CC infection, inflammation, allergy), liver disorders (e.g. hepatoblastoma,
 CC jaundice, hepatitis), immunological disorders (e.g. AIDS, leukaemia,
 CC rheumatoid arthritis, sepsis, acne, psoriasis) and cancer. The present
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from USPTO
 CC at: seqdata.uspto.gov/sequence.html?docid=6525174B1
 CC
 SQ Sequence 101 AA;
 XX
 QY
 DB 13 FLKDHRI 19
 22 FLKDHRI 28
 XX
 RESULT 51
 AD088028
 ID AD088028 standard; protein; 130 AA.
 AC
 XX
 AD088028;
 DT 01-JAN-2004 (first entry)
 XX
 DS Ribosomal protein similar to FCWPI #244.
 XX
 XX Antifungal protein; ribosomal protein; FCWPI; ALYAF;
 KM plant fungal infection; Alternaria; Ascochyta; Botrytis; Cercospora;
 KM Colletotrichum; Diplodia; Fusarium; Gaeanomyces; Helminthosporium;
 KM Macrophomina; Mycosphaerella; Nectria; Peronospora; Phoma;
 KM Phymatotrichum; Phytophthora; Plasmopara; Podospheera; Puccinia; Puthium;
 KM Pseudoperonospora; Pyricularia; Pythium; Rhizoctonia; Sclerotium; Sclerotinia;
 KM Septoria; Thielaviopsis; Venturia; Verticillium.
 XX
 OS Unidentified.
 XX
 US6573361-B1.
 PN 03-JUN-2003.
 XX
 PD 07-DEC-2000; 2000US-00732210.
 XX
 PF 07-DEC-1999; 99US-0169340P.
 PR 07-DEC-1999; 99US-0169513P.
 XX
 (MONS) MONSANTO TECHNOLOGY LLC.
 PA
 XX
 Bunkers GU, Liang J, Miltanck CA, Seale JW, Wu YS;

DR WPI; 2003-754558/71.
 XX
 PT Novel antifungal protein FCWPI, isolated from *Fusarium culmorum*, useful
 PT for controlling fungal infections in plants.
 XX
 PS Example 21; SEQ ID NO 281; 27pp; English.
 XX
 CC The invention relates to an isolated antifungal ribosomal protein from
 CC *Fusarium culmorum*, FCWPI. Also included is a fusion protein between the
 CC signal peptide of the antifungal protein ALYAF from *Alysiaceae* and FCWPI,
 CC encoded by the nucleic acid appearing as AD087758. The FCWPI proteins are
 CC useful for controlling fungal infections in plants, such as those caused
 CC by *Alternaria* (e.g. *Alternaria brassicae*, *Alternaria solani*),
 CC *Ascochyta* (e.g. *Ascochyta blight*), *Botrytis* (e.g. *Botrytis cinerea*),
 CC *Cercospora* (e.g. *Cercospora kikuchii*, *Cercospora zea-maydis*),
 CC *Colletotrichum* (e.g. *Colletotrichum lindemuthianum*), *Diplodia* (e.g.
 CC *Diplodia maydis*), *Fusarium* (e.g. *Fusarium nivale*, *Fusarium oxysporum*,
 CC *Fusarium graminearum*, *Fusarium culmorum*, *Fusarium solani*, *Fusarium*
 CC *moniliforme*, *Fusarium roseum*), *Gaeumannomyces* (e.g. *Gaeumannomyces*
 CC *graminis* f.sp. *tritici*), *Helminthosporium* (e.g. *Helminthosporium turcicum*
 CC), *Helminthosporium carbonum*, *Helminthosporium maydis*, *Macrophomina*
 CC (e.g. *Macrophomina phaseolina*, *Magnaporthe grisea*), *Mycosphaerella*
 CC (e.g. *Mycosphaerella figiensis*), *Nectria* (e.g. *Nectria haematococca*),
 CC *Peronospora* (e.g. *Peronospora manshurica*, *Peronospora tabacina*), *Phoma*
 CC (e.g. *Phoma betae*), *Phymatotrichum* (e.g. *Phymatotrichum omnivorum*),
 CC *Phytophthora* (e.g. *Phytophthora cinnamomi*, *Phytophthora cactorum*,
 CC *Phytophthora phaseoli*, *Phytophthora parasitica*, *Phytophthora*
 CC *citrophthora*, *Phytophthora megasperma* f.sp. *sojae*, *Phytophthora*
 CC *infestans*), *Plasmopara* (e.g. *Plasmopara viticola*), *Podospheera* (e.g.
 CC *Podospheera leucotricha*), *Puccinia* (e.g. *Puccinia sorghi*, *Puccinia*
 CC *scrifformis*, *Puccinia graminis* f.sp. *tritici*, *Puccinia asparagi*,
 CC *Puccinia recondita*, *Puccinia arachidis*), *Puthium* (e.g. *Puthium*
 CC *aphanidermatum*), *Pyrenophora* (e.g. *Pyrenophora tritici-repentens*), (e.g.
 CC *Pyricularia* (e.g. *Pyricularia oryzae*), *Pythium* (e.g. *Pythium ultimum*),
 CC *Rhizoctonia* (e.g. *Rhizoctonia solani*, *Rhizoctonia cerealis*), *Sclerotium*
 CC (e.g. *Sclerotium rolfsii*), *Sclerotinia* (e.g. *Sclerotinia sclerotiorum*),
 CC *Septoria* (e.g. *Septoria lycopersici*, *Septoria glycines*, *Stagonospora*
 CC *nodorum* / *Phaeosphaeria nodorum*, *Septoria tritici*), *Thielaviopsis* (e.g.
 CC *Thielaviopsis basicola*), *Uncinula* (e.g. *Uncinula necator*), *Venturia*
 CC (e.g. *Venturia inaequalis*) or *Verticillium* (e.g. *Verticillium dahliae*,
 CC *Verticillium albo-atrum*). Mutations in the proteolytic consensus
 CC sequences contained within FCWPI provides improved stability of its
 CC antifungal activity. Also disclosed are ribosomal proteins with similar
 CC PI (>71) and molecular weight (<20kDa) to FCWPI, which may act as
 CC antifungal proteins. The present sequence represents one of the ribosomal
 CC proteins similar to FCWPI. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?docid=6573361B1.
 CC
 SQ Sequence 130 AA;
 XX
 QY
 DB 94 EELTIGE 100
 47 EELTIGE 53
 XX
 RESULT 52
 AD095705
 ID AD095705 standard; protein; 167 AA.
 AC
 XX
 AD095705;
 DT 01-JAN-2004 (first entry)
 XX
 DS E. faecium protein sequence SEQ ID 5332.
 XX
 DE Vaccine; urinary tract infection; bacteraemia; endocarditis; wound;
 XX abdominal-pelvic infection.
 KM

XX	18-OCT-2001.
PF	11-APR-2001; 2001WQ-FRC001118.
XX	
PR	11-APR-2000; 2000CR-00004629.
XX	
PA	(INSP) INST PASTEUR.
PI	Buchrieser C, Frangoul L, Couve E, Rusniok C, Finkl H, Dhoux P,
PI	Dussunger O, Chechuani F, Nedati H, Glaser P, Kunst F, Cossart P;
PI	Daniels J, Gobel W, Krefz U, Xahn M, Ng E, Vazquez-Boland JA;
PI	Domínguez-Bernal G, Garrido-García P, Tlerréz-Martínez A, Amend A;
PI	Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L;
PI	Pérez-Díaz J, Baquero F, García Del Portillo P, Gómez-López N;
PI	Meduerto E, De Pablo B, Wehlend J, Kaerst U, Entian K, Hauf J;
PI	Rose M, Voss H;
XX	
DR	WPI; 2002-010914/01.
XX	
PT	Genomic sequence for <i>Listeria monocytogenes</i> , useful e.g. for treatment
PT	and prevention of <i>Listeria</i> and related bacterial infections, and related
PT	polypeptides.
PS	
PS	Claim 6; SEQ ID NO 1488; 192pp; French.
XX	
CC	The present invention relates to the genome sequence of <i>Listeria</i>
CC	<i>monocytogenes</i> EGD-e (see AB03041). The genome sequence and fragments of
CC	it are useful for selecting probes and primers for detecting genes in <i>L.</i>
CC	<i>monocytogenes</i> and related organisms, and for studying genetic
CC	polymorphisms and other genomes. The present sequence is a protein
CC	encoded by the genome sequence of the present invention. Proteins
CC	expressed from the genome sequence are useful for raising specific
CC	antibodies, identification of <i>L. monocytogenes</i> and related organisms, and
CC	for biosynthesis and biodegradation, especially biosynthesis of Vitamin
CC	B12. The genome sequence and proteins encoded by it are also useful for
CC	selecting compounds that regulate gene expression and cell replication
CC	and modulate <i>L. monocytogenes</i> -related diseases. In addition, the genome
CC	sequence and proteins encoded by it are useful in pharmaceutical and
CC	vaccine compositions for the treatment or prevention of infections by <i>L.</i>
CC	<i>monocytogenes</i> and related organisms. Note: The sequence data for this
CC	patent did not form part of the printed specification, but was obtained
CC	in electronic format directly from WIPO at
CC	ftp.wipo.int/pub/published_pcl_sequences
XX	
SQ	Sequence 179 AA:
XX	
Query Match	4.9%; Score 7; DB 5; Length 179;
Best Local Similarity	100.0%; Pred. No. 57;
Matches 7; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	127 TAKKVR 133
DB	36 TAKKVR 42
XX	
RESULT 54	
ABU33017	
ID	ABU33017 standard; protein; 179 AA.
XX	
AC	ABU33017;
XX	
DT	19-JUN-2003 (first entry)
XX	
DE	Protein encoded by Prokaryotic essential gene #18544.
XX	
XX	Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX	
OS	<i>Listeria monocytogenes</i> .
XX	
PN	WO20027183-A2.
PD	03-OCT-2002.
XX	

PF 21-MAR-2002; 2002WO-US009107.
 XX
 PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX WPI; 2003-029926/02.
 DR N-PSDB; ACA36887.
 XX
 PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX
 PS Claim 25; SEQ ID NO 60941; 1766bp; English.
 CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a gene in an operon required for
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-regulated gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 SQ Sequence 179 AA;
 CC
 Query Match 4.9%; Score 7; DB 6; Length 179;
 Best Local Similarity 100.0%; Pred. No. 57;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 127 TAKKVR 133
 |||||
 Db 36 TAKKVR 42
 |||||
 RESULT 55
 ABU29201
 ID ABU29201 standard; protein; 182 AA.
 XX
 AC ABU29201;
 XX
 DT 19-JUN-2003 (first entry)
 XX

DE Protein encoded by Prokaryotic essential gene #14728.
 XX
 KM Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX
 OS *Enterococcus faecalis*.
 XX
 FN WO200277183-A2.
 XX
 PD 03-OCT-2002.
 XX
 PF 21-MAR-2002; 2002WO-US009107.
 XX
 PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX WPI; 2003-029926/02.
 DR N-PSDB; ACA33071.
 XX
 PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX
 PS Claim 25; SEQ ID NO 57125; 1766bp; English.
 CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a gene in an operon required for
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-regulated gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 SQ Sequence 182 AA;
 CC
 Query Match 4.9%; Score 7; DB 6; Length 182;
 Best Local Similarity 100.0%; Pred. No. 58;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 127 TAKKVR 133
 |||||
 Db 39 TAKKVR 45
 |||||

RESULT 56
 ABU29837
 ID ABU29837 standard; protein; 182 AA.
 XX
 AC ABU29837;
 XX
 DT 19-JUN-2003 (first entry)
 XX
 DE Protein encoded by prokaryotic essential gene #15364.
 XX
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX
 OS Enterococcus faecium.
 XX
 PN MO200277183-A2.
 XX
 PD 03-OCT-2002.
 XX
 PF 21-MAR-2002; 2002MO-US009107.
 XX
 PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 XX (ELIT-) ELITRA PHARM INC.
 PA Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind UW,
 PI Wall D, Twick J, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 DR N-PSDB; ACA33707.
 XX
 XX WPI; 2003-029926/02.
 PT
 PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 PS
 PS Claim 25; SEQ ID NO 57761; 1766bp; English.
 XX
 XX The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway; (8)
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs; or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX
 SQ Sequence 182 AA;
 XX
 XX Query Match 4.9%; Score 7; DB 6; Length 182;
 XX Best Local Similarity 100.0%; Pred. No. 58;
 XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 127 TAKYRR 133
 DB 39 TAKYRR 45
 RESULT 57
 ID ADC95400
 ID ADC95400 standard; protein; 186 AA.
 XX
 AC ADC95400;
 XX
 DT 01-JAN-2004 (first entry)
 XX
 DE E. faecium protein sequence SEQ ID 5027.
 XX
 XX Vaccine; urinary tract infection; bacteraemia; endocarditis; wound;
 XX abdominal/pelvic infection.
 KW
 KW Enterococcus faecium.
 OS
 OS US6583275-B1.
 PN
 XX
 XX 24-JUN-2003.
 PD
 XX
 PF 30-JUN-1998; 98US-00107532.
 PR
 PR 02-JUL-1997; 97US-0051571P.
 PR 14-MAY-1998; 98US-0085598P.
 XX
 XX (GENO-) GENOME THERAPEUTICS CORP.
 PA
 PI Doucette-Stamm LA, Bush D;
 DR N-PSDB; ADC91746.
 XX
 XX WPI; 2003-799836/75.
 PT
 PT New isolated nucleic acid derived from *Enterococcus faecium* encoding an
 PT *Enterococcus faecium* polypeptide useful for detection, prevention and
 PT treatment of a pathological condition resulting from a bacterial
 PT infection.
 PS
 PS Example 1; SEQ ID NO 5027; 243bp; English.
 XX
 XX The invention relates to an isolated nucleic acid derived from
 CC *Enterococcus faecium* encoding an *Enterococcus faecium* polypeptide having
 CC one of 10 fully defined sequences given in the (or comprising 40
 CC sequential nucleotides chosen from any of the nucleic acids, its
 CC complement or sequences hybridising to it). Also included are a
 CC recombinant vector comprising the nucleic acid operably linked to
 CC transcription regulatory element, a cell comprising the vector and a
 CC single-stranded probe comprising the nucleic acid. The nucleic acids are
 CC chosen from 3654 disclosed sequences encoding 3654 disclosed proteins.
 CC The nucleic acids is useful for diagnosing pathological conditions
 CC resulting from *E. faecium* bacterial infection (e.g. urinary tract
 CC infection, bacteraemia, endocarditis, wounds and abdominal/pelvic
 CC infection), and for screening drugs such as agonists and antagonists. The
 CC nucleic acid is useful for recombinant production of *Candida albicans* -
 CC derived peptides or antisense polypeptides. Pharmaceutical compositions
 CC and vaccines containing the nucleic acid are useful for preventing or
 CC treating *Enterococcus faecium* infections. The present sequence represents
 CC one if the disclosed *E. faecium* proteins.
 XX
 SQ Sequence 186 AA;
 XX
 XX Query Match 4.9%; Score 7; DB 7; Length 186;
 XX Best Local Similarity 100.0%; Pred. No. 60;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 TAKVRR 133
 |||||
 DB 43 TAKVRR 49

RESULT 58
 AAU5105
 ID AAU5105 standard; protein; 194 AA.

AC AAU5105;
 XX
 XX
 DT 13-FEB-2002 (first entry)
 DE Enterococcus faecalis proliferation protein #392.
 XX
 XX Antisense; prokaryotic cellular proliferation protein; antibiotic;
 KM antibacterial; drug design.
 XX
 OS Enterococcus faecalis.
 XX
 PN WO200170955-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 21-MAR-2001; 2001WO-US009180.
 XX
 PR 21-MAR-2000; 2000US-0191078P.
 PR 23-MAY-2000; 2000US-0206848P.
 PR 26-MAY-2000; 2000US-0207727P.
 PR 23-OCT-2000; 2000US-0242578P.
 PR 27-NOV-2000; 2000US-0253625P.
 PR 22-DEC-2000; 2000US-0257931P.
 PR 16-FEB-2001; 2001US-0269308P.
 XX
 XX (ELIT-) ELITRA PHARM INC.
 XX
 PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GU;
 PI Yamamoto RT, Xu HH;
 XX
 DR WPI; 2001-611495/70.
 DR N-PSDB; AAS52964.

PT New polynucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids.
 XX
 PS Example 3; SEQ ID NO 10698; 511pp; English.

CC The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the genes,
 CC themselves and the encoded proteins. The prokaryotes used are Escherichia
 CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
 CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
 CC useful for the identification of potential new targets for antibiotic
 CC development. The antisense nucleic acids can also be used to identify
 CC proteins used in proliferation, to express these proteins, and to obtain
 CC antibodies capable of binding to the expressed proteins. The proteins can
 CC be used to screen compounds in rational drug discovery programmes. The
 CC antisense nucleic acid sequence is also useful to screen for homologous
 CC nucleic acids which are required for cell proliferation in a wide variety
 CC of organisms. The present sequence represents an essential prokaryotic
 CC cellular proliferation protein. Note: The sequence data for this patent
 CC did not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_ptc_sequences
 XX
 XX Sequence 194 AA;

Query Match 4.9%; Score 7; DB 4; Length 194;
 Best Local Similarity 100.0%; Pred. No. 62;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 TAKVRR 133
 |||||
 DB 51 TAKVRR 57

RESULT 59
 ABG12973
 ID ABG12973 standard; protein; 220 AA.

AC ABG12973;
 XX
 XX
 DT 13-FEB-2002 (first entry)
 DE Novel human diagnostic protein #12964.
 XX
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US008631.
 XX
 PR 31-MAR-2000; 2000US-00540217.
 PR 23-AUG-2000; 2000US-00649167.
 XX
 PA (HYSE-) HISEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR N-PSDB; AAS77160.

PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX
 PS Claim 20; SEQ ID NO 43332; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_ptc_sequences
 XX
 XX Sequence 220 AA;

Query Match 4.9%; Score 7; DB 4; Length 220;
 Best Local Similarity 100.0%; Pred. No. 70;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 186 APTLPPA 192

RESULT 60

AAW65048 standard; protein; 307 AA.

AAW65048;

28-SEP-1998 (first entry)

Tsuga pinoresinol-lariciresinol reductase PLR-Th1.

pinoresinol-lariciresinol reductase; dirigent protein; lignan;
transgenic plant; anticancer; cytostatic; antiviral; virucide;
antibiotic; antioxidant; antifedant.

Tsuga heterophylla.

MO9820113-A1.

14-MAY-1998.

07-NOV-1997; 97WO-US020391.

08-NOV-1996; 96US-0030523P.

31-JUL-1997; 97US-0054380P.

(UNITV) UNIV WASHINGTON STATE RES FOUND.

Lewis NG, Davin LB, Dinkovakostova AT, Fujita M, Gang DR;

Sarkonen S;

WPI: 1998-286929/25.

N-PSDB; AAW35186.

New plant-derived dirigent proteins and pinoresinol-lariciresinol
reductases - and related nucleic acid, vectors and transformants, used
for stereospecific production of lignans, useful e.g. as anticancer or
antiviral agents.

Claim 17; Page 134-135; 148pp; English.

PLR-Th1 comprises a (+)-pinoresinol/(+)-lariciresinol reductase (P/LR) of
Tsuga heterophylla. P/LR enzymes catalyse the conversion of pinoresinol
to lariciresinol and then to secoisolariciresinol. 2 isoforms (see
AAW65048-49) of T. heterophylla P/LR have been identified. Further P/LR
enzymes have been obtained from Forsythia intermedia (see AAW65038-43)
and Thuja plicata (see AAW65044-47). The isolation of cDNAs encoding P/LR
(see AAW35175-80 and AAW35182-87) and dirigent proteins (see AAW35160-71)
permits the development of an efficient expression system for these
enzymes, provides useful tools for examining the developmental regulation
of lignan biosynthesis and permits the isolation of related sequences. It
also allows the transformation of a wide range of organisms, including
plants, in order to modify lignan biosynthesis. Optically pure lignans
may have e.g. anticancer, antiviral, antioxidant, antibiotic or
antifeedant activity

Sequence 307 AA;

Query Match 4.9%; Score 7; DB 2; Length 307;

Best Local Similarity 100.0%; Pred. No. 95;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 KVRRAIE 136

Db 135 KVRRAIE 141

RESULT 61

AAW65561 standard; protein; 307 AA.

XX AAW65561;

XX 25-SEP-2001 (first entry)

XX Tsuga heterophylla pinoresinol/lariciresinol reductase, p1r-Tp3 #2.

XX Dirigent protein; pinoresinol/lariciresinol reductase; stereospecificity;
lignan biosynthetic pathway; secoisolariciresinol.

XX Tsuga heterophylla.

XX MO20019833-A2.

XX 12-JUL-2001.

XX 22-DEC-2000; 2000WO-US035265.

XX 30-DEC-1999; 99US-00475316.

XX (UNITV) UNIV WASHINGTON STATE RES FOUND.

XX (UNITV) UNIV MINNESOTA.

XX Lewis NG, Davin LB, Dinkova-Kostova AT, Fujita M, Gang DR;

XX Ford JD, Sarkonen S;

XX WPI: 2001-465260/50.

XX N-PSDB; AAD12522.

XX Dirigent and/or pinoresinol/lariciresinol reductase proteins useful for
producing optically-pure lignans.

XX Claim 24; Page 151-152; 183pp; English.

The present invention relates to an isolated dirigent and/or pinoresinol
/lariciresinol reductase protein from a lignan biosynthetic pathway.
Dirigent and/or pinoresinol/lariciresinol reductase protein and the
nucleic acids that encode it may be expressed either in vivo or in vitro
to produce enzymes involved in the biosynthesis of lignans. The 78-kD
dirigent protein confers stereospecificity in 8',8'-linked lignan
formation and binds to and orients coniferyl alcohol-derived free
radicals, which then under go stereospecific coupling to form (+)-
pinoresinol. Pinoresinol/lariciresinol reductase catalyses the conversion
of pinoresinol to lariciresinol and then to secoisolariciresinol. The
present sequence is Tsuga heterophylla pinoresinol/lariciresinol
reductase, p1r-Tp3 #2

Sequence 307 AA;

Query Match 4.9%; Score 7; DB 4; Length 307;

Best Local Similarity 100.0%; Pred. No. 95;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 KVRRAIE 136

Db 135 KVRRAIE 141

RESULT 62

AAW44811 standard; protein; 308 AA.

AAW44811;

19-MAY-2000 (first entry)

P. taeda dehydrodiconiferyl alcohol benzylic ether reductase.

dehydrodiconiferyl alcohol benzylic ether reductase; lignan content;

lignan biosynthesis; pulp and paper production; loblolly pine;

recombinant expression vector; dehydrodiconiferyl alcohol; DDC.

Pinus taeda.

XX W0200005350-A1.
 XX 03-FEB-2000.
 XX 23-JUL-1999; 99WO-US016746.
 XX 24-JUL-1998; 98US-0094012P.
 XX (UNIW) UNIV WASHINGTON STATE RES FOUND.
 XX Lewis NG, Kasahara H, Gang DR, Davin LB;
 XX WPI; 2000-182684/16.
 XX N-PSDB; AA250238.
 XX
 PT New nucleic acid sequence encoding an enzyme which converts
 PT dehydrodiconiferyl alcohol to 7-O-4'-isodihydrodiconiferyl alcohol
 PT useful for producing transgenic plants with modified lignan biosynthesis.
 XX
 PS Claim 6; Page 45-46; 55pp; English.
 CC The present sequence is Pinus taeda dehydrodiconiferyl alcohol (DDC)
 CC benzylic ether reductase. The corresponding cDNA was cloned into the
 CC expression plasmid pSBETA, expressed in E. coli resulting in this protein
 CC which lacks a beta-galactosidase domain. This was purified from a crude
 CC E. coli extract and resulting protein was assayed for pinoresinol-
 CC lacticresinol activity and its ability to reduce DDC. The purified P.
 CC reductase effected the reduction of the benzylic ether bond of DDC
 CC to convert it to 7-O-4'-(iso) DDC. DDC gene when introduced in a host
 CC cell permits the development of an efficient expression system for the
 CC enzyme, provides useful tools for examining the developmental regulation
 CC of lignan biosynthesis and for isolation of similar proteins. This is
 CC used to modify lignan levels in plants and food items, altering colour,
 CC texture, durability and pest-resistance of wood tissue, altering the
 CC lignan/lignan content of plant species utilised in pulp and paper
 CC production, and enhancing production of defensive lignans/lignans
 XX
 SQ Sequence 308 AA;
 Query Match 4.9%; Score 7; DB 3; Length 308;
 Best Local Similarity 100.0%; Pred. No. 95;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 130 KVRRAIE 136
 Db 136 KVRRAIE 142
 RESULT 63
 AA65049
 ID AA65049 standard; protein, 309 AA.
 XX
 AC AA65049;
 XX
 DT 28-SEP-1998 (first entry)
 XX
 DE Tsuga pinoresinol-lariciresinol reductase pLR-Th2.
 XX
 KW Pinoresinol-lariciresinol reductase; dirigent protein; lignan;
 KW transgenic plant; anticancer; cyostatic; antiviral; virucide;
 KW antibiotic; antioxidant; antifedant.
 XX
 OS Tsuga heterophylla.
 XX
 OS W09820113-A1.
 XX
 PD 14-MAY-1998.
 XX
 PF 07-NOV-1997; 97WO-US020391.
 XX
 PF 08-NOV-1996; 96US-0030522P.
 XX
 PR 31-JUL-1997; 97US-0054380P.
 PR

XX (UNIW) UNIV WASHINGTON STATE RES FOUND.
 XX Lewis NG, Davin LB, Dinkovakostova AT, Fujita M, Gang DR;
 XX Sarkanen S;
 XX WPI; 1998-286928/25.
 XX N-PSDB; AAV35187.
 XX
 PT New plant-derived dirigent proteins and pinoresinol-lariciresinol
 PT reductases - and related nucleic acid, vectors and transformants, used
 PT for stereospecific production of lignans, useful e.g. as anticancer or
 PT antiviral agents.
 XX
 PS Claim 17; Page 138-139; 148pp; English.
 CC PLR-Th2 comprises a (+)-pinoresinol/(+)-lariciresinol reductase (P/LR) of
 CC Tsuga heterophylla. P/LR enzymes catalyse the conversion of pinoresinol
 CC to lariciresinol and then to secoisolariciresinol. 2 isoflome (see
 CC AA65048-49) of T. heterophylla P/LR have been identified. Further P/LR
 CC enzymes have been obtained from Forsythia intermedia (see AA65038-43)
 CC and Thuja plicata (see AA65044-47). The isolation of cDNAs encoding P/LR
 CC (see AAV35175-80 and AAV35182-87) and dirigent proteins (see AAV35160-71)
 CC permits the development of an efficient expression system for these
 CC enzymes, provides useful tools for examining the developmental regulation
 CC of lignan biosynthesis and permits the isolation of related sequences. It
 CC also allows the transformation of a wide range of organisms, including
 CC plants, in order to modify lignan biosynthesis. Optically pure lignans
 CC may have e.g. anticancer, antiviral, antioxidant, antibiotic or
 CC antifedant activity
 XX
 SQ Sequence 309 AA;
 Query Match 4.9%; Score 7; DB 2; Length 309;
 Best Local Similarity 100.0%; Pred. No. 95;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 130 KVRRAIE 136
 Db 137 KVRRAIE 143
 RESULT 64
 AA60562
 ID AA60562 standard; protein, 309 AA.
 XX
 AC AA60562;
 XX
 DT 25-SEP-2001 (first entry)
 XX
 DE Tsuga heterophylla pinoresinol/lariciresinol reductase, pLR-Tp4 #2.
 XX
 KW Dirigent protein; pinoresinol/lariciresinol reductase; stereospecificity;
 KW lignan biosynthetic pathway; secoisolariciresinol.
 XX
 OS Tsuga heterophylla.
 XX
 PN W0200149833-A2.
 XX
 PD 12-JUL-2001.
 XX
 PF 22-DEC-2000; 2000WO-US035265.
 XX
 PF 30-DEC-1999; 99US-00475316.
 XX
 PR (UNIW) UNIV WASHINGTON STATE RES FOUND.
 XX
 PA (MINU) UNIV MINNESOTA.
 XX
 PI Lewis NG, Davin LB, Dinkova-Kostova AT, Fujita M, Gang DR;
 PI Ford JD, Sarkanen S;
 XX
 DR WPI; 2001-465260/50.
 DR N-PSDB; AAD12523.

XX Dirigent and/or pinoreosinol/lariciresinol reductase proteins useful for
 PT producing optically-pure ligands.
 XX
 PS Claim 24; Page 154-155; 183pp; English.
 XX
 CC The present invention relates to an isolated dirigent and/or pinoreosinol
 CC /lariciresinol reductase protein from a ligman biosynthetic pathway.
 CC Dirigent and/or pinoreosinol/lariciresinol reductase protein and the
 CC nucleic acids that encode it may be expressed either in vivo or in vitro
 CC to produce enzymes involved in the biosynthesis of ligmans. The 78-KD
 CC dirigent protein confers stereospecificity in 8,8'-linked ligman
 CC formation and binds to and orients confiteryl alcohol-derived free
 CC radicals, which then under go stereospecific coupling to form (+)-
 CC pinoreosinol. Pinoreosinol/lariciresinol reductase catalyses the conversion
 CC of pinoreosinol to lariciresinol and then to secoisolariciresinol. The
 CC present sequence is Tsuga heterophylla pinoreosinol/lariciresinol
 CC reductase, p1r-Tp1 #2
 CC
 SQ Sequence 309 AA;
 XX
 SQ
 Query Match 4.9%; Score 7; DB 4; Length 309;
 Best Local Similarity 100.0%; Pred. No. 95;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 130 KVRRAIE 136
 DB 137 KVRRAIE 143
 XX
 RESULT 65
 ID AAM65044 standard; protein; 313 AA.
 XX
 AC AAM65044;
 XX
 DT 28-SEP-1998 (first entry)
 XX
 DE Thuja pinoreosinol-lariciresinol reductase p1r-Tp1.
 XX
 KM pinoreosinol-lariciresinol reductase; dirigent protein; ligman;
 KM transgenic plant; anticancer; cytotoxic; antiviral; virucide;
 KM antidiabetic; antioxidant; antileadant.
 OS Thuja plicata.
 OS
 PN WO9820113-A1.
 XX
 PD 14-MAY-1998.
 XX
 PF 07-NOV-1997; 97WO-US020391.
 XX
 PR 08-NOV-1996; 96US-0030522P.
 PR 31-JUL-1997; 97US-0054380P.
 XX
 PA (UNITV) UNIV WASHINGTON STATE RES FOUND.
 XX
 PI Lewis NG, Davin LB, Dinkovakostova AT, Fujita M, Gang DR;
 PI Sarkanen S;
 XX
 DR WPI; 1998-286929/25.
 DR N-PSDB; AAV35182.
 XX
 PT New plant-derived dirigent proteins and pinoreosinol-lariciresinol
 PT reductases - and related nucleic acid, vectors and transformants, used
 PT for stereospecific production of ligmans, useful e.g. as anticancer or
 PT antiviral agents.
 XX
 PS Claim 17; Page 122-123; 148pp; English.
 XX
 CC p1r-Tp1 comprises a (-)-pinoreosinol/(-)-lariciresinol reductase (P/LR) of
 CC Thuja plicata. P/LR enzymes catalyse the conversion of pinoreosinol to
 CC lariciresinol and then to secoisolariciresinol. 4 isoforms (see AAM65044-

CC 47) of T. plicata P/LR have been identified; the other 3 isoforms are
 CC (+)/(+)-P/LR. Further P/LR enzymes have been obtained from Forsythia
 CC intermedia (see AAM65038-43) and Tsuga heterophylla (see AAM65048-49).
 CC The isolation of cDNAs encoding P/LR (see AAV35175-80 and AAV35182-87)
 CC and dirigent proteins (see AAV35160-71) permits the development of an
 CC efficient expression system for these enzymes, provides useful tools for
 CC examining the developmental regulation of ligman biosynthesis and permits
 CC the isolation of related sequences. It also allows the transformation of
 CC a wide range of organisms, including plants, in order to modify ligman
 CC biosynthesis. Optically pure ligmans may have e.g. anticancer, antiviral,
 CC antioxidant, antibiotic or antileadant activity
 CC
 SQ Sequence 313 AA;
 XX
 SQ
 Query Match 4.9%; Score 7; DB 2; Length 313;
 Best Local Similarity 100.0%; Pred. No. 97;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 130 KVRRAIE 136
 DB 140 KVRRAIE 146
 XX
 RESULT 66
 ID AAB06557 standard; protein; 313 AA.
 XX
 AC AAB06557;
 XX
 DT 25-SEP-2001 (first entry)
 XX
 DE Thuja plicata pinoreosinol/lariciresinol reductase, p1r-Tp1.
 XX
 KM Dirigent protein; pinoreosinol/lariciresinol reductase; stereospecificity;
 KM ligman biosynthetic pathway; secoisolariciresinol; western red cedar.
 XX
 OS Thuja plicata.
 OS
 PN WO200149833-A2.
 XX
 PD 12-JUL-2001.
 XX
 PF 22-DEC-2000; 2000WO-US035265.
 XX
 PR 30-DEC-1999; 99US-00475316.
 XX
 PA (UNITV) UNIV WASHINGTON STATE RES FOUND.
 PA (MINU) UNIV MINNESOTA.
 XX
 PI Lewis NG, Davin LB, Dinkova-Kostova AT, Fujita M, Gang DR;
 PI Ford JD, Sarkanen S;
 XX
 DR WPI; 2001-465260/50.
 DR N-PSDB; AAD12518.
 XX
 PT Dirigent and/or pinoreosinol/lariciresinol reductase proteins useful for
 PT producing optically-pure ligmans.
 XX
 PS Claim 27; Page 139-140; 183pp; English.
 XX
 CC The present invention relates to an isolated dirigent and/or pinoreosinol
 CC /lariciresinol reductase protein from a ligman biosynthetic pathway.
 CC Dirigent and/or pinoreosinol/lariciresinol reductase protein and the
 CC nucleic acids that encode it may be expressed either in vivo or in vitro
 CC to produce enzymes involved in the biosynthesis of ligmans. The 78-KD
 CC dirigent protein confers stereospecificity in 8,8'-linked ligman
 CC formation and binds to and orients confiteryl alcohol-derived free
 CC radicals, which then under go stereospecific coupling to form (+)-
 CC pinoreosinol. Pinoreosinol/lariciresinol reductase catalyses the conversion
 CC of pinoreosinol to lariciresinol and then to secoisolariciresinol. The
 CC present sequence is Thuja plicata pinoreosinol/lariciresinol reductase,
 CC p1r-Tp1

SQ Sequence 313 AA;
 Query Match 4.9%; Score 7; DB 4; Length 313;
 Best Local Similarity 100.0%; Pred. No. 97;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 130 KVRRAIE 136
 140 KVRRAIE 146
 Db 140 KVRRAIE 146
 RESULT 67
 AA065046
 -TD AA065046 standard; protein; 314 AA.
 AC AA065046;
 XX
 XX 28-SEP-1998 (first entry)
 DT
 XX
 DE Thuja pinoresinol-lariciresinol reductase pLR-Tp3.
 XX
 KW pinoresinol-lariciresinol reductase; dirigent protein; lignan;
 KM transgenic plant; anticancer; cytostatic; antiviral; virucide;
 KM antibiotic; antioxidant; antifeedant.
 XX
 OS Thuja plicata.
 XX
 EN WO9820113-A1.
 XX
 PD 14-MAY-1998.
 PF 07-NOV-1997; 97WO-US020391.
 XX
 XX 08-NOV-1996; 96US-0030522P.
 PR 31-JUL-1997; 97US-0054380P.
 XX
 PA (UNIW) UNIV WASHINGTON STATE RES FOUND.
 XX
 PI Lewis NG, Davin LB, Dinkovakostova AT, Fujita M, Gang DR;
 PI Sarkanen S;
 DR WPI; 1998-286929/25.
 DR N-PSDB; AAV35184.
 XX
 PT New plant-derived dirigent proteins and pinoresinol-lariciresinol
 PT reductases and related nucleic acid, vectors and transformants, used
 PT for stereospecific production of lignans, useful e.g. as anticancer or
 PT antiviral agents.
 XX
 PS Claim 17; Page 128-129; 148bp; English.
 CC pLR-Tp3 comprises a (+)-pinoresinol/(+)-lariciresinol reductase (P/LR) of
 CC Thuja plicata. P/LR enzymes catalyse the conversion of pinoresinol to
 CC lariciresinol and then to secoisolariciresinol. 4 Isoforms (see AA065044-
 CC 47) of T. plicata P/LR have been identified; the pLR-Tp1 isoform is (-)/(-)
 CC (-)-P/LR. Further P/LR enzymes have been obtained from Forsythia
 CC intermedia (see AA065038-43) and Tsuga heterophylla (see AA065048-49).
 CC The isolation of cDNAs encoding P/LR (see AAV35175-80 and AAV35182-87)
 CC and dirigent proteins (see AAV35160-71) permits the development of an
 CC efficient expression system for these enzymes, provides useful tools for
 CC examining the developmental regulation of lignan biosynthesis and permits
 CC the isolation of related sequences. It also allows the transformation of
 CC a wide range of organisms, including plants, in order to modify lignan
 CC biosynthesis. Optically pure lignans may have e.g. anticancer, antiviral,
 CC antioxidant, antibiotic or antifeedant activity
 CC
 XX Sequence 314 AA;
 SQ
 Query Match 4.9%; Score 7; DB 2; Length 314;
 Best Local Similarity 100.0%; Pred. No. 97;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 130 KVRRAIE 136
 140 KVRRAIE 136
 Db 130 KVRRAIE 136

Db 140 KVRRAIE 146
 RESULT 68
 AA065559
 ID AA065559 standard; protein; 314 AA.
 AC AA065559;
 XX
 XX 25-SEP-2001 (first entry)
 DT
 XX
 DE Thuja plicata pinoresinol/lariciresinol reductase, pLR-Tp3 #1.
 XX
 KW Dirigent protein; pinoresinol/lariciresinol reductase; stereospecificity;
 KM lignan biosynthetic pathway; secoisolariciresinol; western red cedar.
 XX
 OS Thuja plicata.
 XX
 EN WO200149833-A2.
 XX
 PD 12-JUL-2001.
 PF 22-DEC-2000; 2000WO-US035265.
 XX
 PR 30-DEC-1999; 99US-00475316.
 XX
 PA (UNTM) UNIV WASHINGTON STATE RES FOUND.
 PA (MINU) UNIV MINNESOTA.
 XX
 PI Lewis NG, Davin LB, Dinkova-Kostova AT, Fujita M, Gang DR;
 PI Ford JD, Sarkanen S;
 DR WPI; 2001-465260/50.
 DR N-PSDB; AAD12520.
 XX
 PT Dirigent and/or pinoresinol/lariciresinol reductase proteins useful for
 PT producing optically-pure lignans.
 XX
 PS Claim 27; Page 145-146; 183bp; English.
 CC The present invention relates to an isolated dirigent and/or pinoresinol
 CC /lariciresinol reductase protein from a lignan biosynthetic pathway.
 CC Dirigent and/or pinoresinol/lariciresinol reductase protein and the
 CC nucleic acids that encode it may be expressed either in vivo or in vitro
 CC to produce enzymes involved in the biosynthesis of lignans. The 78-kD
 CC dirigent protein confers stereospecificity in 8,8'-linked lignan
 CC formation and binds to and orients coniferyl alcohol-derived free
 CC radicals, which then under go stereospecific coupling to form (+)-
 CC pinoresinol. Pinoresinol/lariciresinol reductase catalyses the conversion
 CC of pinoresinol to lariciresinol and then to secoisolariciresinol. The
 CC present sequence is Thuja plicata pinoresinol/lariciresinol reductase,
 CC pLR-Tp3 #1
 CC
 XX Sequence 314 AA;
 SQ
 Query Match 4.9%; Score 7; DB 4; Length 314;
 Best Local Similarity 100.0%; Pred. No. 97;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 130 KVRRAIE 136
 140 KVRRAIE 146
 Db 140 KVRRAIE 146
 RESULT 69
 AA06570
 ID AA06570 standard; protein; 314 AA.
 AC AA06570;
 XX
 XX 25-SEP-2001 (first entry)
 DT
 XX

DE Schiandra chinensis pinorestinol/lariciresinol reductase protein #7.
 XX
 XX Dirigent protein; pinorestinol/lariciresinol reductase; stereospecificity;
 KW lignan biosynthetic pathway; secoisolariciresinol.
 XX
 XX Schiandra chinensis.
 XX
 XX MO200149833-A2.
 XX
 XX 12-UTL-2001.
 XX
 XX 22-DEC-2000; 2000WO-US035265.
 XX
 XX 30-DEC-1999; 99US-00475316.
 XX
 XX (UNIV) UNIV WASHINGTON STATE RES FOUND.
 PA (MINU) UNIV MINNESOTA.
 XX
 XX Lewis NG, Davin LB, Dinkova-Kostova AT, Fujita M, Gang DR;
 PI Ford JD, Sarfman S;
 XX
 XX WPI; 2001-465260/50.
 DR N-PSDB; AAD12561.
 XX
 XX
 PT Dirigent and/or pinorestinol/lariciresinol reductase proteins useful for
 PT producing optically-pure lignans.
 XX
 XX Claim 33; Page 180-181; 183pp; English.
 XX
 XX The present invention relates to an isolated dirigent and/or pinorestinol
 CC /lariciresinol reductase protein from a lignan biosynthetic pathway.
 CC Dirigent and/or pinorestinol/lariciresinol reductase protein and the
 CC nucleic acids that encode it may be expressed either in vivo or in vitro
 CC to produce enzymes involved in the biosynthesis of lignans. The 78-kD
 CC dirigent protein confers stereospecificity in 8,8'-linked lignan
 CC formation and binds to and orients coiteryl alcohol-derived free
 CC radicals, which then under go stereospecific coupling to form (+)-
 CC pinorestinol. Pinorestinol/lariciresinol reductase catalyses the conversion
 CC of pinorestinol to lariciresinol and then to secoisolariciresinol. The
 CC present sequence is Schiandra chinensis pinorestinol/lariciresinol
 CC reductase
 XX
 XX
 SQ Sequence 314 AA;
 Query Match 4.9%; Score 7; DB 4; Length 314;
 Best Local Similarity 100.0%; Pred. No. 97;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 130 KVRRAE 136
 |||||
 Db 142 KVRRAE 148
 |||||
 RESULT 70
 AAY32075
 ID AAY32075 standard; protein; 572 AA.
 XX
 XX AAY32075;
 AC
 XX
 XX 17-JUN-2000 (first entry)
 DT
 XX
 XX Rapeseed raffinose synthase.
 DE
 XX
 XX Raffinose synthase; rapeseed; transgenic plant.
 KW
 XX
 XX Brassica napus.
 OS
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 129
 FT Misc-difference 132 /note= "encoded by GGY"
 FT Misc-difference 132 /note= "encoded by GGY"
 FT Misc-difference 143

FT
 FT Misc-difference 144 /note= "encoded by CCS"
 FT Misc-difference 148 /note= "encoded by TCR"
 FT Misc-difference 148 /note= "encoded by CGR"
 XX
 XX
 XX EP953643-A2.
 XX
 XX 03-NOV-1999.
 XX
 XX 27-APR-1999; 99EP-00107430.
 XX
 XX 30-APR-1998; 98JP-00120550.
 XX
 XX 30-APR-1998; 98JP-00120551.
 PR 04-DEC-1998; 98JP-00345590.
 PR 10-DEC-1998; 98JP-00351246.
 XX
 XX (SUMO) SUMITOMO CHEM CO LTD.
 XX
 XX Watanabe E, Oeda K;
 PI
 XX
 XX WPI; 1999-593144/51.
 DR N-PSDB; AAZ20210.
 XX
 XX
 PT New sense and antisense genes, useful for altering the level of raffinose
 PT in food plants.
 XX
 XX Claim 27; Page 36-38; 55pp; English.
 XX
 XX This sequence represents rapeseed raffinose synthase, a protein that can
 CC bind a D-galactosyl group through an alpha(1-6) bond to the hydroxy group
 CC attached to the carbon atom at the 6-position of the D-glucose residue in
 CC a sucrose molecule to form raffinose. cDNA (see AAZ20210) encoding the
 CC enzyme was isolated from rapeseed cv. Westar leaf cDNA by PCR. Probes or
 CC primers generated from plant raffinose synthase genes (see AAZ20207-10)
 CC may be used to obtain other raffinose synthase genes by labeled detection
 CC or amplification (claimed). These genes may be used to control the levels
 CC of raffinose produced in plants. Antisense genes can be used to knock out
 CC existing gene activity, and sense genes to increase the level of gene
 CC activity. The resulting transgenic plants may be used as a food source to
 CC alter the growing conditions for gut enterobacteria, providing general
 CC health advantages
 XX
 XX
 SQ Sequence 572 AA;
 Query Match 4.9%; Score 7; DB 2; Length 572;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GAPTLP 8
 |||||
 Db 137 GAPTLP 143
 |||||
 RESULT 71
 ADC96107
 ID ADC96107 standard; protein; 580 AA.
 XX
 XX ADC96107;
 AC
 XX
 XX 01-JAN-2004 (first entry)
 DT
 XX
 XX E. faecium protein sequence SEQ ID 5734.
 DE
 XX
 XX Vaccine; urinary tract infection; bacteraemia; endocarditis; wound;
 KW abdominal-pelvic infection.
 XX
 XX Enterococcus faecium.
 OS
 XX
 XX US6583275-B1.
 PN
 XX
 XX 24-JUN-2003.
 PD

PF 30-JUN-1998; 98US-00107532.
 XX
 PR 02-JUL-1997; 97US-0051571P.
 PR 14-MAY-1998; 98US-0085598P.
 XX
 PA (GENO-) GENOME THERAPEUTICS CORP.
 XX
 PI Doucette-Stamm LA, Bush D;
 XX
 DR WPI: 2003-799836/75.
 XX N-PSDB; ADC92453.
 PT New isolated nucleic acid derived from *Enterococcus faecium* encoding an
 PT *Enterococcus faecium* polypeptide useful for detection, prevention and
 PT treatment of a pathological condition resulting from a bacterial
 PT infection.
 XX
 PS Example 1; SEQ ID NO 5734; 243pp; English.
 CC The invention relates to an isolated nucleic acid derived from
 CC *Enterococcus faecium* encoding an *Enterococcus faecium* polypeptide having
 CC one of 10 fully defined sequences given in the (or comprising 40
 CC sequential nucleotides chosen from any of the nucleic acids, its
 CC complement or sequences hybridizing to it). Also included are a
 CC recombinant vector comprising the nucleic acid operably linked to a
 CC transcription regulatory element, a cell comprising the vector and a
 CC single-stranded probe comprising the nucleic acid. The nucleic acids are
 CC chosen from 3654 disclosed sequences encoding 3654 disclosed proteins.
 CC The nucleic acids is useful for diagnosing pathological conditions
 CC resulting from *E. faecium* bacterial infection (e.g. urinary tract
 CC infection, bacteraemia, endocarditis, wounds and abdominal-pelvic
 CC infection) and for screening drugs such as agonists and antagonists. The
 CC nucleic acid is useful for recombinant production of *Candida albicans* -
 CC derived peptides or antisense polypeptides. Pharmaceutical compositions
 CC and vaccines containing the nucleic acid are useful for preventing or
 CC treating *Enterococcus faecium* infections. The present sequence represents
 CC one if the disclosed *E. faecium* proteins.
 XX
 SQ Sequence 580 AA;
 XX
 QY
 DB 111 NRIKKT 117
 227 NRIKKT 233
 Query Match 4.9%; Score 7; DB 7; Length 580;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 72
 ID AAY32074 standard; protein; 777 AA.
 AC AAY32074;
 XX
 DT 17-JAN-2000 (first entry)
 XX
 DE Mustard raffinose synthase.
 XX
 KM Raffinose synthase; mustard; transgenic plant.
 KM
 OS Brassica juncea.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 210 /note= "encoded by ACR"
 FT
 XX
 PN BP953643-A2.
 XX
 PD 03-NOV-1999.
 XX
 PF 27-APR-1999; 99EP-00107430.
 XX

PR 30-APR-1998; 98EP-00120550.
 PR 30-APR-1998; 98JP-00120551.
 PR 04-DEC-1998; 98JP-00345580.
 PR 10-DEC-1998; 98JP-00351246.
 XX
 PA (SUMO) SUMITOMO CHEM CO LTD.
 XX
 PI Watanabe E, Oeda K;
 XX
 DR WPI: 1999-593144/51.
 DR N-PSDB; AA220209.
 XX
 PT New sense and antisense genes, useful for altering the level of raffinose
 PT in food plants.
 XX
 PS Claim 26; Page 29-31; 55pp; English.
 CC This sequence represents mustard raffinose synthase, a protein that can
 CC bind a D-galactosyl group through an alpha(1-6) bond to the hydroxy group
 CC attached to the carbon atom at the 6-position of the D-glucose residue in
 CC a sucrose molecule to form raffinose. cDNA (see AA220209) encoding the
 CC enzyme was isolated from mustard (*Brassica juncea*) leaf cDNA by PCR.
 CC Probes or primers generated from plant raffinose synthase genes (see
 CC AA220207-10) may be used to obtain other raffinose synthase genes by
 CC labeled detection or amplification (claimed). These genes may be used to
 CC control the levels of raffinose produced in plants. Antisense genes can
 CC be used to knock out existing gene activity and sense genes to increase
 CC the level of gene activity. The resulting transgenic plants may be used
 CC as a food source to alter the growing conditions for gut enterobacteria,
 CC providing general health advantages
 XX
 SQ Sequence 777 AA;
 XX
 QY
 DB 2 GAPLPP 8
 342 GAPLPP 348
 Query Match 4.9%; Score 7; DB 2; Length 777;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 73
 ID AB014746 standard; protein; 823 AA.
 AC AB014746;
 XX
 DT 25-AUG-2003 (first entry)
 XX
 DE Novel human protein #119.
 XX
 KM Human; NOV; gene therapy; endocrine related disease; diabetes;
 KM metabolism-related disease; obesity; central nervous system disorder;
 KM Alzheimer's disease; Parkinson's disease; epilepsy; multiple sclerosis;
 KM schizophrenia; depression; autoimmune disorder; inflammatory disorder;
 KM psoriasis; allergy; lupus erythematosus; asthma; cancer;
 KM inflammatory bowel disease; rheumatoid arthritis; osteoarthritis;
 KM colon cancer; lung cancer; liver cancer; breast cancer; ovarian cancer;
 KM prostate cancer; brain cancer; melanoma; liver disease; liver cirrhosis;
 KM lung disease; emphysema; obstructive pulmonary disease; haemophilia;
 KM stroke; infection.
 KM
 OS Homo sapiens.
 XX
 PN WO2003023002-A2.
 XX
 PD 20-MAR-2003.
 XX
 PF 09-SEP-2002; 2002WO-US028539.
 XX
 PR 07-SEP-2001; 2001US-0318120P.
 PR 07-SEP-2001; 2001US-0318130P.
 PR

PR 10-SEP-2001; 2001US-0318430P.
 PR 17-SEP-2001; 2001US-0322636P.
 PR 17-SEP-2001; 2001US-0322781P.
 PR 17-SEP-2001; 2001US-0322816P.
 PR 17-SEP-2001; 2001US-0322817P.
 PR 19-SEP-2001; 2001US-0323315P.
 PR 20-SEP-2001; 2001US-0323631P.
 PR 20-SEP-2001; 2001US-0323636P.
 PR 25-SEP-2001; 2001US-0324969P.
 PR 25-SEP-2001; 2001US-0325031P.
 PR 26-SEP-2001; 2001US-0324990P.
 PR 17-APR-2002; 2002US-0373212P.
 PR 06-SEP-2002; 2002US-00236177.

(CUBA-) CUBAGEN CORP.

XX Spytek KA, Patnajan M, Gorman L, Li L, Anderson DW, Zhong M;
 PI Gerlach VL, Vernet CM, Ellerman K, Berghs C, Rothenberg ME, Guo X;
 PI Shinkens RA, Leach MD, Catterton E, Kekuda R, Ji W, Miller CE;
 PI Rieger DK, Taupier RJ, Shenoy SG, Liu X, Padigara M, Alsobrook JP;
 PI Lepley DM, Eisinger SR, Burgess CB, Liu X, Padigara M, Alsobrook JP;
 XX WPI: 2003-313242/30.
 DR N-PSDB; ACD19439.

PT New cytoplasmic, nuclear membrane bound or secreted polypeptides (NOVX)
 PT and polynucleotides, useful in gene therapy, e.g. for treating or
 PT preventing obesity, multiple sclerosis, allergy, cancers, hemophilia,
 PT stroke or infections.

PS Claim 1; Page 334; 586pp; English.

XX The invention describes a new isolated polypeptide (NOVX). The NOVX
 CC polypeptide, nucleic acid and antibody are useful as therapeutics.
 CC particularly in the manufacture of a medicament for treating a syndrome
 CC associated with a human disease, which includes a pathology associated
 CC with NOVX polypeptide. The DNA encoding the protein is useful in gene
 CC therapy for treating the disease or condition. In particular, the NOVX
 CC polypeptide or polynucleotide is useful for treating endocrine/
 CC metabolism-related diseases (e.g. obesity or diabetes), central nervous
 CC system disorders (e.g. Alzheimer's disease, Parkinson's disease,
 CC epilepsy, multiple sclerosis, schizophrenia or depression), autoimmune
 CC and inflammatory disorders (e.g. psoriasis, allergy, lupus erythematosus,
 CC asthma, inflammatory bowel disease, rheumatoid arthritis or
 CC osteoarthritis), cancers (e.g. colon, lung, liver, breast, ovarian,
 CC prostate or brain cancers, or melanoma), liver diseases (e.g. liver
 CC cirrhosis), lung diseases (emphysema or obstructive pulmonary disease),
 CC haemophilia, stroke, or infections (e.g. viral, bacterial or parasitic).
 CC These are also useful in developing powerful assay system for functional
 CC analysis of various human disorders, as well as in diagnostic
 CC applications, and for monitoring the effects of drugs during clinical
 CC trials. This is the amino acid sequence of a novel human NOV protein
 XX

SO Sequence 823 AA;

Query Match 4.9%; Score 7; DB 6; Length 823;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 112 KIRAKEN 118
 DB 547 KIRAKEN 553

RESULT 74
 ID ABJ25599 standard; protein; 838 AA.
 XX ABJ25599;
 AC
 XX 16-APR-2003 (first entry)
 DT
 XX Aspergillus fumigatus essential gene protein #257.
 DE

XX Fungicide; cytostatic; essential gene; Aspergillus fumigatus; infection;
 KW cancer; contamination; biofilm; antibody; immune response.
 XX

OS Aspergillus fumigatus.

FN WO200286090-A2.

PD 31-OCT-2002.

PF 23-APR-2002; 2002WO-US013142.

PR 23-APR-2001; 2001US-0285697P.

PR 27-APR-2001; 2001US-0287066P.

PR 05-JUN-2001; 2001US-0295890P.

PR 09-JUL-2001; 2001US-0303899P.

PR 31-AUG-2001; 2001US-0316362P.

(ELIT-) ELITRA PHARM INC.

PI Jiang B, Tishkoff D, Zamudio C, Eroshkin AM, Hu W, Lemieux SM;
 XX WPI: 2003-093124/08.

PT New purified or isolated nucleic acids of essential genes of Aspergillus
 PT fumigatus, useful for treating or preventing infections by A. fumigatus,
 PT or for treating a non-infectious disease in a subject e.g. cancer.

PS Disclosure; Page: 175pp; English.

XX The invention relates to novel purified or isolated nucleic acids of
 CC essential genes of Aspergillus fumigatus. The isolated nucleic acids of
 CC the invention are used to treat or prevent infections by a pathogenic
 CC organism such as A. fumigatus, to treat a non-infectious disease in a
 CC subject (e.g. cancer), to prevent or contain contamination of an object
 CC by A. fumigatus, or to prevent or inhibit formation on a surface of a
 CC biofilm comprising A. fumigatus. The polynucleotides are useful for
 CC expressing recombinant protein for characterization, screening or
 CC therapeutic use, as markers for host tissues in which the pathogenic
 CC organisms invade or reside, for comparing with the DNA sequence of A.
 CC fumigatus to identify duplicated genes or paralogues having the same or
 CC similar biochemical activity and/or function, for comparing with DNA
 CC sequences of other related or distant pathogenic organisms to identify
 CC potential orthologous essential or virulence genes, for selecting and
 CC making oligomers for attachment to a nucleic acid array for examination
 CC of expression patterns, for raising anti-protein antibodies, as an
 CC antigen to raise anti-DNA antibodies or to elicit another immune
 CC response, and for identifying polynucleotides encoding the other protein
 CC with which binding occurs or to identify inhibitors of the binding
 CC interaction. The polypeptides may be used to raise antibodies or to
 CC elicit immune response, as a reagent in assays designed to quantitatively
 CC determine levels of the protein in biological fluids, as a marker for
 CC host tissues in which pathogenic organism invade or reside, and to
 CC isolate correlative receptors or ligands in the case of virulence
 CC factors. This sequence represents a protein of one of the essential genes
 CC of Aspergillus fumigatus of the invention
 XX

SO Sequence 838 AA;

Query Match 4.9%; Score 7; DB 6; Length 838;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 94 BELTIGE 100
 DB 11 BELTIGE 17

RESULT 75
 ID ABB61778 standard; protein; 1205 AA.
 XX ABB61778;
 AC
 XX ABB61778;
 AC

```

XX 26-MAR-2002 (first entry)
XX
XX Drosophila melanogaster polypeptide SEQ ID NO 12126.
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical.
XX
XX Drosophila melanogaster.
XX
XX W0200171042-A2.
XX
XX 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US009231.
XX
XX 23-MAR-2000; 2000US-0191637P.
XX 11-JUL-2000; 2000US-00614150.
XX
XX (BEKE ) PE CORP NY.
XX
XX Venter JC, Adams M, Li FWD, Myers EW;
XX
XX WPI; 2001-656860/75.
XX
XX N-PDB; ABL05881.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signalling and cell-cell
XX interactions.
XX
XX Disclosure; SEQ ID NO 12126; 21pp + Sequence listing; English.
XX
XX
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX sequences (ABL01840-ABL16175) and the encoded proteins (AB857737-
XX AB872072). The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at tcp.wipo.int/pub/published_pct_sequences
XX
XX
XX Sequence 1205 AA;
XX
XX Query Match 4.9%; Score 7; DB 4; Length 1205;
XX Best Local Similarity 100.0%; Pred. No. 3.4e+02;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 3 APTLPPA 9
XX
XX 418 APTLPPA 424

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Search completed: August 11, 2004, 14:23:52
 Job time : 57 secs

Tue Aug 17 05:54:49 2004

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Page 1

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OM protein - protein search, using sw model

Run on: August 11, 2004, 14:25:13 : Search time 46 Seconds
(without alignments)
969.079 Million cell updates/sec

Title: US-09-690-825-34
Perfect score: 142
Sequence: 1 MGAPLTPAMQPLKDHRI...EFETAKVRAIEQIAMD 142

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Gapop 60.0, Gapext 60.0

Searched: 1292805 seqs, 313927144 residues

Word size: 0
Total number of hits satisfying chosen parameters: 1292805

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database:

Published Applications AA:
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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	142	100.0	142	US-10-138-618-34	Sequence 34, Appl
2	142	100.0	142	US-10-665-975-2	Sequence 2, Appl
3	128	90.1	142	US-10-408-765A-2210	Sequence 2210, Ap
4	98	69.0	98	US-09-965-967-23	Sequence 23, Appl
5	20	14.1	20	US-10-138-618-4	Sequence 4, Appl
6	17	12.0	17	US-10-138-618-3	Sequence 3, Appl
7	17	12.0	17	US-10-291-607-12	Sequence 1, Appl
8	9	6.3	9	US-10-291-607-12	Sequence 12, Appl
9	9	6.3	9	US-10-291-607-12	Sequence 11, Appl
10	7	4.9	68	US-10-424-599-148276	Sequence 148276,
11	7	4.9	73	US-09-864-761-38999	Sequence 38999, A
12	7	4.9	99	US-10-424-599-178983	Sequence 178983,
13	7	4.9	101	US-09-933-767-450	Sequence 450, App
14	7	4.9	101	US-10-004-860-450	Sequence 450, App
15	7	4.9	101	US-10-023-282-450	Sequence 450, App

16	7	4.9	126	US-10-424-599-209010	Sequence 209010,
17	7	4.9	176	US-10-437-963-116190	Sequence 116190,
18	7	4.9	179	US-10-282-122A-60941	Sequence 60941, A
19	7	4.9	182	US-10-282-122A-57125	Sequence 57125, A
20	7	4.9	182	US-10-282-122A-57161	Sequence 57161, A
21	7	4.9	185	US-10-424-599-245457	Sequence 245457,
22	7	4.9	194	US-09-815-242-10698	Sequence 10698, A
23	7	4.9	199	US-10-335-977-7963	Sequence 7963, Ap
24	7	4.9	203	US-10-335-977-7964	Sequence 7964, Ap
25	7	4.9	259	US-10-424-599-243648	Sequence 243648,
26	7	4.9	311	US-10-424-599-147883	Sequence 147883,
27	7	4.9	382	US-10-425-114-50128	Sequence 50128, A
28	7	4.9	382	US-10-369-493-13992	Sequence 13992, A
29	7	4.9	388	US-10-424-599-154013	Sequence 154013,
30	7	4.9	415	US-10-424-599-248527	Sequence 248527,
31	7	4.9	428	US-10-421-654-28	Sequence 28,
32	7	4.9	428	US-10-421-654-44	Sequence 44, Appl
33	7	4.9	475	US-10-369-493-10000	Sequence 10000, A
34	7	4.9	610	US-10-437-963-192686	Sequence 192686,
35	7	4.9	744	US-10-369-493-21957	Sequence 21957, A
36	7	4.9	751	US-10-437-963-201149	Sequence 201149,
37	7	4.9	802	US-10-437-963-180519	Sequence 180519,
38	7	4.9	838	US-10-128-714-3257	Sequence 3257, Ap
39	7	4.9	2285	US-09-932-183A-2	Sequence 2,
40	7	4.2	12	US-10-083-768-130	Sequence 130, App
41	6	4.2	30	US-09-939-960-380	Sequence 380, App
42	6	4.2	36	US-09-989-919-109	Sequence 109, App
43	6	4.2	42	US-10-424-599-162708	Sequence 162708,
44	6	4.2	52	US-10-424-599-276718	Sequence 276718,
45	6	4.2	52	US-10-425-114-68762	Sequence 68762, A
46	6	4.2	55	US-09-860-352A-11	Sequence 11, Appl
47	6	4.2	55	US-10-424-599-152902	Sequence 152902,
48	6	4.2	55	US-10-410-764-98	Sequence 98, Appl
49	6	4.2	57	US-10-424-599-158384	Sequence 158384,
50	6	4.2	57	US-10-424-599-352199	Sequence 251199,
51	6	4.2	57	US-10-125-258-62	Sequence 62, Appl
52	6	4.2	58	US-10-424-599-167067	Sequence 167067,
53	6	4.2	58	US-10-424-599-171511	Sequence 171511,
54	6	4.2	58	US-10-437-963-183020	Sequence 183020,
55	6	4.2	62	US-10-424-599-194266	Sequence 194266,
56	6	4.2	63	US-10-424-599-237412	Sequence 237412,
57	6	4.2	63	US-10-125-258-61	Sequence 61, Appl
58	6	4.2	64	US-10-425-114-54599	Sequence 54599, A
59	6	4.2	65	US-09-764-881-122	Sequence 122, App
60	6	4.2	65	US-09-764-875-1113	Sequence 1113, Ap
61	6	4.2	65	US-10-424-599-281627	Sequence 281627,
62	6	4.2	65	US-09-764-881-122	Sequence 122, App
63	6	4.2	65	US-10-242-747-122	Sequence 122, App
64	6	4.2	65	US-10-138-057-235	Sequence 235, App
65	6	4.2	66	US-10-424-599-199019	Sequence 199019,
66	6	4.2	67	US-10-424-599-167358	Sequence 167358,
67	6	4.2	69	US-10-424-599-153000	Sequence 153000,
68	6	4.2	74	US-10-437-963-141151	Sequence 141151,
69	6	4.2	75	US-10-282-122A-45175	Sequence 45175, A
70	6	4.2	76	US-10-437-963-182219	Sequence 182219,
71	6	4.2	77	US-10-424-599-144105	Sequence 144105,
72	6	4.2	77	US-10-424-599-192922	Sequence 192922,
73	6	4.2	82	US-10-424-599-152919	Sequence 152919,
74	6	4.2	84	US-10-424-599-151600	Sequence 234015,
75	6	4.2	85	US-10-424-599-212605	Sequence 216095,
76	6	4.2	86	US-10-424-599-216092	Sequence 146092,
77	6	4.2	86	US-10-425-114-61055	Sequence 61055, A
78	6	4.2	87	US-10-424-599-283512	Sequence 283512,
79	6	4.2	88	US-10-424-599-275337	Sequence 275337,
80	6	4.2	90	US-09-764-881-3322	Sequence 3322, Ap
81	6	4.2	92	US-10-424-599-151600	Sequence 151600,
82	6	4.2	95	US-09-864-408A-1358	Sequence 1358, Ap
83	6	4.2	99	US-10-437-963-17395	Sequence 17395,
84	6	4.2	100	US-09-841-132-563	Sequence 563, App
85	6	4.2	102	US-10-424-599-199829	Sequence 199829,
86	6	4.2	103	US-10-437-963-162484	Sequence 162484,
87	6	4.2	104	US-10-437-963-16812	Sequence 16812,
88	6	4.2	105	US-10-437-963-174606	Sequence 174606,

89 6 4.2 106 14 US-10-083-357-986 Sequence 986, App
90 6 4.2 107 12 US-10-424-559-253306 Sequence 253306,
91 6 4.2 108 12 US-10-282-122A-76441, A Sequence 76441,
92 6 4.2 111 16 US-10-437-963-119889 Sequence 119889,
93 6 4.2 114 12 US-10-424-559-249704 Sequence 249704,
94 6 4.2 116 16 US-10-437-963-155767 Sequence 155767,
95 6 4.2 118 16 US-10-437-963-121763 Sequence 121763,
96 6 4.2 120 16 US-10-437-963-124901 Sequence 124901,
97 6 4.2 121 12 US-10-424-559-163067 Sequence 163067,
98 6 4.2 123 12 US-10-424-559-186413 Sequence 186413,
99 6 4.2 124 16 US-10-437-963-181095 Sequence 181095,
100 6 4.2 127 12 US-10-335-977-7217 Sequence 7217, Ap

ALIGNMENTS

RESULT 1
US-10-138-618-34
; Sequence 34, Application US/10138618
; Publication No. US20030100525A1
; GENERAL INFORMATION:
; APPLICANT: Altieri, Dario C.
; TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
; CELLULAR APOPTOSIS, AND ITS MODULATION
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: MORGAN, LEWIS & BOCKRUS LLP
; STREET: 1800 M Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5869
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/138,618
; FILING DATE: 06-May-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/975,080
; FILING DATE: 20-NOV-1997
; APPLICATION NUMBER: US 60/031,435
; FILING DATE: 20-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler, Reid G.
; REGISTRATION NUMBER: 30,988
; REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-467-7000
; TELEFAX: 202-467-7176
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 142 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-10-138-618-34
Query Match 100.0%; Score 142; DB 14; Length 142;
Best Local Similarity 100.0%; Pred. No. 2.1e-133;
Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGAFTLPAMQPFLEKDHRISTFKWMPLEGCACTPERMAEAGFTICPTENEPDLAQCFPC 60
DB 1 MGAFTLPAMQPFLEKDHRISTFKWMPLEGCACTPERMAEAGFTICPTENEPDLAQCFPC 60
QY 61 FKELEGWEPDDDPFIEEHKHSKSSGCAFLSVKQFEEITLGEFLKIDREBAKXIAKETNNK 120

DB 61 FKELEGWEPDDDPFIEEHKHSKSSGCAFLSVKQFEEITLGEFLKIDREBAKXIAKETNNK 120
QY 121 KKEFEETAKVRRRAIEQLAAMD 142
DB 121 KKEFEETAKVRRRAIEQLAAMD 142

RESULT 2
US-10-665-975-2
; Sequence 2, Application US/10665975
; Publication No. US20040138119A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Tamm, Ingo
; TITLE OF INVENTION: USE OF HEPATITIS VIRUS B X-INTERACTING
; PROTEIN (HBXIP) IN MODULATION OF APOPTOSIS
; FILE REFERENCE: BURHAM, 005A
; CURRENT APPLICATION NUMBER: US/10/665,975
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: 60/412,109
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-665-975-2

Query Match 100.0%; Score 142; DB 16; Length 142;
Best Local Similarity 100.0%; Pred. No. 2.1e-133;
Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAFTLPAMQPFLEKDHRISTFKWMPLEGCACTPERMAEAGFTICPTENEPDLAQCFPC 60
DB 1 MGAFTLPAMQPFLEKDHRISTFKWMPLEGCACTPERMAEAGFTICPTENEPDLAQCFPC 60
QY 61 FKELEGWEPDDDPFIEEHKHSKSSGCAFLSVKQFEEITLGEFLKIDREBAKXIAKETNNK 120
DB 61 FKELEGWEPDDDPFIEEHKHSKSSGCAFLSVKQFEEITLGEFLKIDREBAKXIAKETNNK 120
QY 121 KKEFEETAKVRRRAIEQLAAMD 142
DB 121 KKEFEETAKVRRRAIEQLAAMD 142

RESULT 3
US-10-408-765A-2210
; Sequence 2210, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088,465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2210
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-2210

Query Match 90.1%; Score 128; DB 16; Length 142;
Best Local Similarity 100.0%; Pred. No. 1.9e-119;

Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGAPTLPPAMQPLKDRISTFKWMPLESCACTPERMAEAGFIHCPTENEPDLAQCFC 60
Db 1 MGAPTLPPAMQPLKDRISTFKWMPLESCACTPERMAEAGFIHCPTENEPDLAQCFC 60

Qy 61 FKELGEMEPDDPIEHHKSSGCAFLSVKQPEELTL 120
Db 61 FKELGEMEPDDPIEHHKSSGCAFLSVKQPEELTLGFLDLDEPRANKIARETNK 120

Qy 121 KKEFEETA 128
Db 121 KKEFEETA 128

RESULT 4
US-09-965-967-23
Sequence 23, Application US/09965967
Patent No. US2002017557A1
GENERAL INFORMATION:
APPLICANT: Shi, Yigong
TITLE OF INVENTION: Compositions And Methods For Regulating Apoptosis
FILE REFERENCE: PU-0031 (01-1739-1)
CURRENT APPLICATION NUMBER: US/09/965,967
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: 60/236,574
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/256,830
PRIOR FILING DATE: 2000-12-20
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 23
LENGTH: 98
TYPE: PRT
ORGANISM: Homo sapiens
US-09-965-967-23

Query Match 69.0%; Score 98; DB 9; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.1e-89;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGAPTLPPAMQPLKDRISTFKWMPLESCACTPERMAEAGFIHCPTENEPDLAQCFC 60
Db 1 MGAPTLPPAMQPLKDRISTFKWMPLESCACTPERMAEAGFIHCPTENEPDLAQCFC 60

Qy 61 FKELGEMEPDDPIEHHKSSGCAFLSVKQPEELTL 98
Db 61 FKELGEMEPDDPIEHHKSSGCAFLSVKQPEELTL 98

RESULT 5
US-10-138-618-4
Sequence 4, Application US/10138618
Publication No. US20030100525A1
GENERAL INFORMATION:
APPLICANT: Altieri, Dario C.
TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
CELLULAR APOPTOSIS, AND ITS MODULATION
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 N Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,618

FILING DATE: 06-May-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/975,080
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: US 60/031,435
FILING DATE: 20-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7176
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-138-618-4

Query Match 14.1%; Score 20; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 65 EGMEPDPIEHHKSSGSC 84
Db 1 EGMEPDPIEHHKSSGSC 20

RESULT 6
US-10-138-618-3
Sequence 3, Application US/10138618
Publication No. US20030100525A1
GENERAL INFORMATION:
APPLICANT: Altieri, Dario C.
TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
CELLULAR APOPTOSIS, AND ITS MODULATION
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 N Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,618
FILING DATE: 06-May-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/975,080
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: US 60/031,435
FILING DATE: 20-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7176
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>

TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 3
US-10-138-618-3

Query Match 12.0%; Score 17; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 APTLPAMQPLKDHRI 19
Db 1 APTLPAMQPLKDHRI 17

RESULT 7
US-10-291-607-1
; Sequence 1, Application US/10291607
; Publication No. US20030143232A1
; GENERAL INFORMATION:
; APPLICANT: Altieri, Dario C.
; TITLE OF INVENTION: Methods for Selectively Modulating Survivin Apoptosis
; FILE REFERENCE: 44574-5063-US
; CURRENT APPLICATION NUMBER: US/10/291,607
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US/09/515,514
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (7)
; OTHER INFORMATION: PHOSPHORYLATION
US-10-291-607-1

Query Match 12.0%; Score 17; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 LEGCACTPERMAAGFI 44
Db 1 LEGCACTPERMAAGFI 17

RESULT 8
US-10-291-607-12
; Sequence 12, Application US/10291607
; Publication No. US20030143232A1
; GENERAL INFORMATION:
; APPLICANT: Altieri, Dario C.
; TITLE OF INVENTION: Methods for Selectively Modulating Survivin Apoptosis
; FILE REFERENCE: 44574-5063-US
; CURRENT APPLICATION NUMBER: US/10/291,607
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US/09/515,514
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Survivin phosphorylation motif
US-10-291-607-12

Query Match 6.3%; Score 9; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 31 CACTPERMA 39
Db 1 CACTPERMA 9

RESULT 9
US-10-291-607-13
; Sequence 13, Application US/10291607
; Publication No. US20030143232A1
; GENERAL INFORMATION:
; APPLICANT: Altieri, Dario C.
; TITLE OF INVENTION: Methods for Selectively Modulating Survivin Apoptosis
; FILE REFERENCE: 44574-5063-US
; CURRENT APPLICATION NUMBER: US/10/291,607
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US/09/515,514
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: Survivin phosphorylation motif
US-10-291-607-13

Query Match 6.3%; Score 9; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 CACTPERMA 39
Db 1 CACTPERMA 9

RESULT 10
US-10-424-599-148276
; Sequence 148276, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yinhua
; APPLICANT: Cao Yongsuei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285664
; SEQ ID NO 148276
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1) (68)
; OTHER INFORMATION: unsure at all Xaa locations
; OTHER INFORMATION: Clone ID: PAT_MRT3847_104915C.1.pcp
US-10-424-599-148276

Query Match 4.9%; Score 7; DB 12; Length 68;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 KVRRAIE 136
Db 14 KVRRAIE 20

RESULT 11
US-09-864-761-38999
Sequence 38999, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 38999
LENGTH: 73
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO ACO05840.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.1
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 5.7
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9
OTHER INFORMATION: SWISSPROT HIT: P47825, EVALUATE 1.10e+00
OTHER INFORMATION: EST_HUMAN HIT: AM361877.1, EVALUATE 4.00e-30
US-09-864-761-38999

Query Match

4.9%; Score 7; DB 9; Length 73;

Best Local Similarity 100.0%; Pred. No. 45;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 111 NRIKET 117
DB 1 NRIKET 7
RESULT 12
US-10-424-599-178983
Sequence 178983, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J
APPLICANT: Kovalic, David K
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 178983
LENGTH: 99
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_132638C.1.pcp
US-10-424-599-178983
Query Match
Best Local Similarity 100.0%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 97 TLGEFLK 103
DB 17 TLGEFLK 23
RESULT 13
US-09-933-767-450
Sequence 450, Application US/09933767
Publication No. US20030181632A1
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: P2007P2
CURRENT APPLICATION NUMBER: US/09/933,767
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: PCT/US01/05614
PRIOR FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: 60/184,836
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/193,170
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 09/205,258
PRIOR FILING DATE: 1998-12-04
PRIOR APPLICATION NUMBER: PCT/US98/11422
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/048,885
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/049,375
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,881
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,880
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,896
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/049,020
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,876

PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,895
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,884
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,894
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,971
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,964
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,882
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,899
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,893
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,900
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,901
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,892
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,915
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/049,019
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,970
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,972
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,916
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/049,373
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,875
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/049,374
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,917
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,949
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,974
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,883
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,897
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,898
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,962
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,963
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,877
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,878
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/068,054
PRIOR FILING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: 60/068,064
PRIOR FILING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: 60/068,053
PRIOR FILING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: 60/070,923
PRIOR FILING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: 60/073,160
PRIOR FILING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: 60/073,159
PRIOR FILING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: 60/073,165
PRIOR FILING DATE: 1998-01-30

PRIOR APPLICATION NUMBER: 60/073,164
PRIOR FILING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: 60/085,925
PRIOR FILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: 60/085,921
PRIOR FILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: 60/085,923
PRIOR FILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: 60/085,922
PRIOR FILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: 60/092,921
PRIOR FILING DATE: 1998-07-15
PRIOR APPLICATION NUMBER: 60/094,657
PRIOR FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1245
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 450
LENGTH: 101
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (44)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (46)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (77)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (78)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (101)
OTHER INFORMATION: Xaa equals stop translation
US-09-933-767-450

Query Match 4.9%; Score 7; DB 10; Length 101;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 FLKDRI 19
DB 22 FLKDRI 28

RESULT 14
US-10-004-860-450
Sequence 450, Application US/10004860
Publication No. US20030065160A1
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: P2007P1
CURRENT APPLICATION NUMBER: US/10/004,860
CURRENT FILING DATE: 2001-12-07
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 450
LENGTH: 101
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (44)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FEATURE:
NAME/KEY: SITE
LOCATION: (46)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FEATURE:

NAME/KEY: SITE
LOCATION: (77)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FEATURE:
NAME/KEY: SITE
LOCATION: (78)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FEATURE:
NAME/KEY: SITE
LOCATION: (101)
OTHER INFORMATION: Xaa equals stop translation
US-10-004-860-450

Query Match 4.9%; Score 7; DB 12; Length 101;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 FLDHRI 19
Db 22 FLDHRI 28

RESULT 15
US-10-023-282-450
Sequence 450, Application US/10023282
Publication No. US20030092893A1
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: P2007P1
CURRENT APPLICATION NUMBER: US/10/023,282
EARLIER FILING DATE: 2001-12-20
EARLIER APPLICATION NUMBER: 09/205,258
EARLIER FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-06-04
EARLIER APPLICATION NUMBER: 60/048,895
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,375
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,881
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,880
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,896
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,020
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,876
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,895
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,884
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,894
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,971
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,882
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,899
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,893
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,900
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,901
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,892
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,915

EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,019
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,970
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,972
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,916
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,373
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,875
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,374
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,917
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,949
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,883
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,897
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,898
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,962
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,963
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,877
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,878
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/070,923
EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 450
LENGTH: 101
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (44)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FEATURE:
NAME/KEY: SITE
LOCATION: (46)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FEATURE:
NAME/KEY: SITE
LOCATION: (77)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FEATURE:
NAME/KEY: SITE
LOCATION: (78)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FEATURE:
NAME/KEY: SITE
LOCATION: (101)
OTHER INFORMATION: Xaa equals stop translation
US-10-023-282-450

Query Match 4.9%; Score 7; DB 14; Length 101;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 FLKDRI 19
Db 22 FLKDRI 28

RESULT 16

US-10-424-599-209010
; Sequence 209010, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 209010
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_30764C.1.pep
US-10-424-599-209010

Query Match 4.9%; Score 7; DB 12; Length 126;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 112 KIARETN 118
Db 37 KIARETN 43

RESULT 17

US-10-437-963-116190
; Sequence 116190, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204366
; SEQ ID NO 116190
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_19714C.1.pep
US-10-437-963-116190

Query Match 4.9%; Score 7; DB 16; Length 176;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 APTLPPA 9
Db 97 APTLPPA 103

RESULT 18

US-10-282-122A-60941
; Sequence 60941, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60941
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
US-10-282-122A-60941

Query Match 4.9%; Score 7; DB 12; Length 179;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 TAKVRR 133
Db 36 TAKVRR 42

RESULT 19

US-10-282-122A-57125
; Sequence 57125, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant

```

; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57125
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
; US-10-282-122A-57125

Query Match
Best Local Similarity 100.0%; Pred. No. 97;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 TAKKVR 133
DB 39 TAKKVR 45

RESULT 20
US-10-282-122A-57761
; Sequence 57761, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57125
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
; US-10-282-122A-57125

```

```

; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57761
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Enterococcus faecium
; US-10-282-122A-57761

Query Match
Best Local Similarity 4.9%; Score 7; DB 12; Length 182;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 TAKKVR 133
DB 39 TAKKVR 45

RESULT 21
US-10-424-599-245457
; Sequence 245457, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 245457
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_6367C.1.pep
; US-10-424-599-245457

Query Match
Best Local Similarity 4.9%; Score 7; DB 12; Length 185;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 120 KKKFEE 126
DB 43 KKKFEE 49

RESULT 22
US-09-815-242-10698
; Sequence 10698, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.

```

APPLICANT: Carr, Grant J.
 APPLICANT: Yamamoto, Robert T.
 TITLE OF INVENTION: Identification of Essential Genes in
 FILE REFERENCE: ELITRA.011A
 CURRENT APPLICATION NUMBER: US/09/815,242
 CURRENT FILING DATE: 2001-03-21
 PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206,848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/269,308
 PRIOR FILING DATE: 2001-02-16
 NUMBER OF SEQ ID NOS: 14110
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO: 10698
 LENGTH: 194
 TYPE: PRF
 ORGANISM: Enterococcus faecalis
 US-09-815-242-10698

Query Match 4.9%; Score 7; DB 9; Length 194;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 TAKYVR 133
 DB 51 TAKYVR 57

RESULT 23
 US-10-335-977-7963
 Sequence 7963, Application US/10335977
 Publication No. US20040052799A1
 GENERAL INFORMATION:
 APPLICANT: DOUGLAS SMITH et al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
 RELATING TO HELICOBACTER PYLORI FOR
 DIAGNOSTICS AND THERAPEUTICS
 NUMBER OF SEQUENCES: 10031
 CORRESPONDENCE ADDRESS:
 ADDRESSER: LAHYE & COCKFIELD
 STREET: 28 State Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109-1875
 COMPUTER READABLE FORM:
 MEDIUM TYPE: CD-ROM ISO9660
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: Windows NT 4.0
 SOFTWARE: UNIX
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/335,977
 FILING DATE: 30-Dec-2002
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/993,002
 FILING DATE: 17-Dec-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Mandragouras, Amy E.
 REGISTRATION NUMBER: 36,207
 REFERENCE/DOCKET NUMBER: GTN-018
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)227-7400

TELEFAX: (617)742-4214
 INFORMATION FOR SEQ ID NO: 7963:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 199 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHEICAL: YES
 ORIGINAL SOURCE:
 ORGANISM: Helicobacter pylori
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (8) LOCATION 1...199
 SEQUENCE DESCRIPTION: SEQ ID NO: 7963:
 US-10-335-977-7963

Query Match 4.9%; Score 7; DB 12; Length 199;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 ELTLGRF 101
 DB 98 ELTLGRF 104

RESULT 24
 US-10-335-977-7964
 Sequence 7964, Application US/10335977
 Publication No. US20040052799A1
 GENERAL INFORMATION:
 APPLICANT: DOUGLAS SMITH et al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
 RELATING TO HELICOBACTER PYLORI FOR
 DIAGNOSTICS AND THERAPEUTICS
 NUMBER OF SEQUENCES: 10031
 CORRESPONDENCE ADDRESS:
 ADDRESSER: LAHYE & COCKFIELD
 STREET: 28 State Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109-1875
 COMPUTER READABLE FORM:
 MEDIUM TYPE: CD-ROM ISO9660
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: Windows NT 4.0
 SOFTWARE: UNIX
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/335,977
 FILING DATE: 30-Dec-2002
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/993,002
 FILING DATE: 17-Dec-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Mandragouras, Amy E.
 REGISTRATION NUMBER: 36,207
 REFERENCE/DOCKET NUMBER: GTN-018
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)227-7400
 TELEFAX: (617)742-4214
 INFORMATION FOR SEQ ID NO: 7964:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 203 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHEICAL: YES
 ORIGINAL SOURCE:
 ORGANISM: Helicobacter pylori
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (8) LOCATION 1...203
 SEQUENCE DESCRIPTION: SEQ ID NO: 7964:
 US-10-335-977-7964

US-10-335-977-7964

Query Match
Best Local Similarity 100.0%; Score 7; DB 12; Length 203;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 ELTLGER 101
DB 102 ELTLGER 108

RESULT 25

US-10-424-599-243648
; Sequence 243648, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 243648
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_62040C.1.pcp
US-10-424-599-243648

Query Match
Best Local Similarity 100.0%; Score 7; DB 12; Length 259;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 RAKXKIA 114
DB 70 RAKXKIA 76

RESULT 26

US-10-424-599-147883
; Sequence 147883, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 147883
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(311)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_104560C.1.pcp
US-10-424-599-147883

Query Match
Best Local Similarity 100.0%; Score 7; DB 12; Length 311;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 KYRAIE 136

DB 137 KYRAIE 143

RESULT 27

US-10-425-114-50128
; Sequence 50128, Application US/10425114
; Publication No. US2004003488BA1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 50128
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700682056_FLI.pcp
US-10-425-114-50128

Query Match
Best Local Similarity 100.0%; Score 7; DB 12; Length 311;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 KYRAIE 136
DB 138 KYRAIE 144

RESULT 28

US-10-369-493-13992
; Sequence 13992, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianning
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 13992
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Pseudomonas fluorescens
US-10-369-493-13992

Query Match
Best Local Similarity 100.0%; Score 7; DB 15; Length 382;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 AIEQLAA 140
DB 18 AIEQLAA 24

```

RESULT 29
US-10-424-599-154013
; Sequence 154013, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 154013
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_110095C.1.pep
US-10-424-599-154013

```

```

Query Match          4.9%; Score 7; DB 12; Length 388;
Best Local Similarity 100.0%; Pred.No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      124 FEETAKK 130
DB      187 FEETAKK 193

```

```

RESULT 30
US-10-424-599-248527
; Sequence 248527, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 248527
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(415)
; OTHER INFORMATION: unsure at all Xaa locations
; OTHER INFORMATION: Clone ID: PAT_MRT3847_6644C.1.pep
US-10-424-599-248527

```

```

Query Match          4.9%; Score 7; DB 12; Length 415;
Best Local Similarity 100.0%; Pred.No. 2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      128 AKVRRRA 134
DB      159 AKVRRRA 165

```

```

RESULT 31
US-10-421-654-28
; Sequence 28, Application US/10421654
; Publication No. US20040005604A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Gramatikova, Svetlana
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Lam, David E.
; APPLICANT: Barton, Nelson R.
; TITLE OF INVENTION: PHOSPHOLIPASES, NUCLEIC ACIDS ENCODING THEM AND
; TITLE OF INVENTION: METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 09010-094001
; CURRENT APPLICATION NUMBER: US/10/421,654
; CURRENT FILING DATE: 2003-04-21
; PRIOR APPLICATION NUMBER: US 60/374,313
; PRIOR FILING DATE: 2002-04-19
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
US-10-421-654-28

```

```

Query Match          4.9%; Score 7; DB 15; Length 428;
Best Local Similarity 100.0%; Pred.No. 2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      36 ERWAEAG 42
DB      373 ERWAEAG 379

```

```

RESULT 32
US-10-421-654-44
; Sequence 44, Application US/10421654
; Publication No. US20040005604A1
; GENERAL INFORMATION:
; APPLICANT: Gramatikova, Svetlana
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Lam, David E.
; APPLICANT: Barton, Nelson R.
; TITLE OF INVENTION: PHOSPHOLIPASES, NUCLEIC ACIDS ENCODING THEM AND
; TITLE OF INVENTION: METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 09010-094001
; CURRENT APPLICATION NUMBER: US/10/421,654
; CURRENT FILING DATE: 2003-04-21
; PRIOR APPLICATION NUMBER: US 60/374,313
; PRIOR FILING DATE: 2002-04-19
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
US-10-421-654-44

```

```

Query Match          4.9%; Score 7; DB 15; Length 428;
Best Local Similarity 100.0%; Pred.No. 2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      36 ERWAEAG 42
DB      373 ERWAEAG 379

```

```

RESULT 33
US-10-369-493-10000
; Sequence 10000, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.

```

APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 10000
LENGTH: 475
TYPE: PRT
ORGANISM: magnetite-containing magnetic coccus
US-10-369-493-10000

Query Match 4.9%; Score 7; DB 15; Length 475;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 131 VRAIEQ 137
Db 284 VRAIEQ 290

RESULT 34

US-10-437-963-192686
Sequence 192686, Application US/10437963
Publication NO. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 192686
LENGTH: 610
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(610)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_88895C.1.pap
US-10-437-963-192686

Query Match 4.9%; Score 7; DB 16; Length 610;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 APTLPPA 9
Db 81 APTLPPA 87

RESULT 35

US-10-369-493-21957
Sequence 21957, Application US/10369493
Publication NO. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 21957
LENGTH: 744
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-10-369-493-21957

Query Match 4.9%; Score 7; DB 15; Length 744;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 94 EELTLGE 100
Db 587 EELTLGE 593

RESULT 36

US-10-437-963-201149
Sequence 201149, Application US/10437963
Publication NO. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 201149
LENGTH: 751
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(751)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_96551C.1.pap
US-10-437-963-201149

Query Match 4.9%; Score 7; DB 16; Length 751;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 77 HKHSSG 83
Db 175 HKHSSG 181

RESULT 37

US-10-437-963-180519
Sequence 180519, Application US/10437963
Publication NO. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua

```

; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 180519
; LENGTH: 802
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_77882C.1.pep
US-10-437-963-180519

Query Match
Best Local Similarity 4.9%; Score 7; DB 16; Length 802;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 ATEQLAA 140
DB 301 ATEQLAA 307

RESULT 38
US-10-128-714-3257
; Sequence 3257, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Hu, Wengqi
; APPLICANT: Tishoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Broshkin, Alexey M
; APPLICANT: Lemieux, Sebastien M
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
; FILE REFERENCE: 10182-018-999
; CURRENT APPLICATION NUMBER: US/10/128,714
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/285,697
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: US 60/287,066
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/295,890
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/303,899
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/316,362
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 8603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3257
; LENGTH: 838
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-128-714-3257

Query Match
Best Local Similarity 4.9%; Score 7; DB 14; Length 838;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 94 EELTIGE 100
DB 11 EELTIGE 17

RESULT 39
US-09-932-183A-2
```

```

; Sequence 2, Application US/0932183A
; Patent No. US20020127641A1
; GENERAL INFORMATION:
; APPLICANT: Estell, David A.
; TITLE OF INVENTION: Proteases From Gram-Positive Organisms
; FILE REFERENCE: GC0394C1-US
; CURRENT APPLICATION NUMBER: US/09/932,183A
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US 09/308,375
; PRIOR FILING DATE: 1998-05-14
; PRIOR APPLICATION NUMBER: PCT/US98/18828
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: EP9719636.4
; PRIOR FILING DATE: 1997-09-15
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 2285
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-09-932-183A-2

Query Match
Best Local Similarity 4.9%; Score 7; DB 9; Length 2285;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 RRAIEQL 138
DB 184 RRAIEQL 190

RESULT 40
US-10-083-768-130
; Sequence 130, Application US/10083768
; Publication No. US20030158116A1
; GENERAL INFORMATION:
; APPLICANT: Dower, William J.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Cwiria, Steven E.
; APPLICANT: Duffin, David J.
; APPLICANT: Gates, Christian
; APPLICANT: Haselden, Sherrill S.
; APPLICANT: Matheakis, Larry C.
; APPLICANT: Schatz, Peter J.
; APPLICANT: Wagstrom, Christopher R.
; APPLICANT: Wrighton, Nicholas C.
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
; FILE REFERENCE: THROMBOPOIETIN RECEPTOR
; CURRENT APPLICATION NUMBER: 232
; CORRESPONDENCE ADDRESS:
; ADDRESS: Glaxo Wellcome
; STREET: Five Moore Drive, P.O. Box 13398
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/083,768
; FILING DATE: 27-Feb-2002
; ATTORNEY/AGENT INFORMATION:
; NAME: Hrubiec, Robert T.
; REGISTRATION NUMBER: 36,392
; REFERENCE/DOCKET NUMBER: PK3065USM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-248-1000
; INFORMATION FOR SEQ ID NO: 130:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
```


TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 130:
US-10-083-768-130

Query Match 4.2%; Score 6; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 TLGEFL 102
Db 2 TLGEFL 7

RESULT 41
US-09-939-980-380
Sequence 380, Application US/09939980
Patent No. US2002008234A1
GENERAL INFORMATION:
APPLICANT: Black, Michael
Burnham, Martin
Hodgson, John
Knowles, David
Loretto, Michael
Nicholas, Richard
Prett, Julie
Reichard, Richard
Rosenberg, Martin
Ward, Judith
TITLE OF INVENTION: No. US2002008234A1 Prokaryotic Polynucleotides,
Polypeptides and Their Uses
NUMBER OF SEQUENCES: 534
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/939,980
FILING DATE: 27-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/936,165
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Gimm, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P50549
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 380:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Protein
SEQUENCE DESCRIPTION: SEQ ID NO: 380:
US-09-939-980-380

Query Match 4.2%; Score 6; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 2,1e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 109 AKNKIA 114
Db 9 AKNKIA 14

RESULT 42
US-09-989-919-109
Sequence 109, Application US/09989919
Patent No. US2002016344A1
GENERAL INFORMATION:
APPLICANT: Macina, Roberto
APPLICANT: Recipon, Heeye
APPLICANT: Pluta, Jason
APPLICANT: Ghosh, Malavika
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Colon Specific Genes and Prot
FILE REFERENCE: DEX-0289
CURRENT APPLICATION NUMBER: US/09/989,919
CURRENT FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 60/252,505
PRIOR FILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 124
SOFTWARE: PatentIn version 3.1
SEQ ID NO 109
LENGTH: 36
TYPE: PRT
ORGANISM: Homo sapien
US-09-989-919-109

Query Match 4.2%; Score 6; DB 9; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 LSVKKQ 92
Db 21 LSVKKQ 26

RESULT 43
US-10-424-599-262708
Sequence 262708, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J
APPLICANT: Kovalic, David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
Fate Reference: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 262708
LENGTH: 42
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_79247C.1.pep
US-10-424-599-262708

Query Match 4.2%; Score 6; DB 12; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 TFKXWP 26
Db 36 TFKXWP 41

Query Match 4.2%; Score 6; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 2,1e+02;

RESULT 44
US-10-424-599-276718
; Sequence 276718, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 276718
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_91897C.1.pep
US-10-424-599-276718

Query Match
Best Local Similarity 4.2%; Score 6; DB 12; Length 52;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 117 TNNKKX 122
DB 11 TNNKKX 16

RESULT 45
US-10-425-114-68762
; Sequence 68762, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 68762
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLMO17127B08_FLI.pep
US-10-425-114-68762

Query Match
Best Local Similarity 4.2%; Score 6; DB 12; Length 52;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 118 NNRKKE 123
DB 16 NNRKKE 21

RESULT 46
US-09-860-352A-11
; Sequence 11, Application US/09860352A
; Patent No. US20020132785A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Curtis, Rory

APPLICANT: Welch, Nadine
; TITLE OF INVENTION: 13305 NOVEL PROTEIN KINASE MOLECULES AND
; TITLE OF INVENTION: USES THEREFOR
; FILE REFERENCE: 38155-20016.00
; CURRENT APPLICATION NUMBER: US/09/860,352A
; CURRENT FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 60/205,301
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus amino acid
US-09-860-352A-11

Query Match
Best Local Similarity 4.2%; Score 6; DB 9; Length 55;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LPPAWQ 11
DB 41 LPPAWQ 46

RESULT 47
US-10-424-599-152902
; Sequence 152902, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 152902
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_109094C.1.pep
US-10-424-599-152902

Query Match
Best Local Similarity 4.2%; Score 6; DB 12; Length 55;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 APTLPP 8
DB 38 APTLPP 43

RESULT 48
US-10-410-764-98
; Sequence 98, Application US/10410764
; Publication No. US2004000564A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Macbeth, Kyle J.
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Welch, Nadine S.
; APPLICANT: Olandt, Peter J.
; APPLICANT: Tsai, Peng-Ying
; APPLICANT: Kapeller-Libermann, Rosana

Tue Aug 17 05:54:49 2004

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; APPLICANT: Carroll, Joseph M.
; TITLE OF INVENTION: 26199, 33530, 33949, 47148, 50226,
; TITLE OF INVENTION: 58764, 62113, 32144, 32235, 23565, 13305, 14911, 86216,
; TITLE OF INVENTION: 25206 AND 8843 MOLECULES AND USES THEREFOR
; FILE REFERENCE: MP03-0520NMIM
; CURRENT APPLICATION NUMBER: US/10/410,764
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: US 09/924,358
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/229,300
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: US 10/350,553
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: US 60/351,572
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: US 09/966,614
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US 60/238,054
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: US 10/281,094
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/347,815
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 10/076,535
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/269,440
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 98
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amino acid consensus sequence
US-10-410-764-98

Query Match      4.2%; Score 6; DB 15; Length 55;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 LPPAMQ 11
        |||||
Db      41 LPPAMQ 46

RESULT 49
US-10-424-599-158384
; Sequence 158384, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 158384
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MFT3847_114039C.1 pep
US-10-424-599-158384

Query Match      4.2%; Score 6; DB 12; Length 56;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      3 APTLPP 8
        |||||
Db      44 APTLPP 49

RESULT 50
US-10-424-599-252199
; Sequence 252199, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 252199
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MFT3847_69764C.1 pep
US-10-424-599-252199

Query Match      4.2%; Score 6; DB 12; Length 57;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      110 KNKIAK 115
        |||||
Db      11 KNKIAK 16

RESULT 51
US-10-125-258-62
; Sequence 62, Application US/10125258
; Publication No. US20030028920A1
; GENERAL INFORMATION:
; APPLICANT: Altier, Daniel J.
; APPLICANT: Herrmann, Rafael
; APPLICANT: Lu, Albert L.
; APPLICANT: McCutchen, Billy F.
; APPLICANT: Prensall, James K.
; APPLICANT: Weaver, Janine L.
; APPLICANT: Wong, James F. H.
; TITLE OF INVENTION: Antimicrobial Polypeptides and Their
; FILE REFERENCE: 35718/246215
; CURRENT APPLICATION NUMBER: US/10/125,258
; CURRENT FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: 60/285,355
; PRIOR FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 62
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Helicoverpa zea
US-10-125-258-62

Query Match      4.2%; Score 6; DB 14; Length 57;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      61 FKELEG 66
        |||||
Db      25 FKELEG 30
```

```

RESULT 52
US-10-424-599-167067
; Sequence 167067, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 167067
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_121876C.1.pep
US-10-424-599-167067

```

```

Query Match
Best Local Similarity 4.2%; Score 6; DB 12; Length 58;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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QY 120 KKKKEE 125
DB 26 KKKKEE 31

```

```

RESULT 53
US-10-424-599-271511
; Sequence 271511, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 271511
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_87192C.1.pep
US-10-424-599-271511

```

```

Query Match
Best Local Similarity 4.2%; Score 6; DB 12; Length 58;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 58 FFCFKE 63
DB 43 FFCFKE 48

```

```

RESULT 54
US-10-437-963-183020
; Sequence 183020, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua

```

```

; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 183020
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_8014C.1.pep
US-10-437-963-183020

```

```

Query Match
Best Local Similarity 4.2%; Score 6; DB 16; Length 58;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 86 FLSVKK 91
DB 13 FLSVKK 18

```

```

RESULT 55
US-10-424-599-194266
; Sequence 194266, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 194266
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_1744C.1.pep
US-10-424-599-194266

```

```

Query Match
Best Local Similarity 4.2%; Score 6; DB 12; Length 62;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 12 PFLKDH 17
DB 52 PFLKDH 57

```

```

RESULT 56
US-10-424-599-237412
; Sequence 237412, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599

```

```

; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 237412
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(63)
; OTHER INFORMATION: unsure at all xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_56408C.1.pcp
US-10-424-599-237412

Query Match
Best Local Similarity 100.0%; Score 6; DB 12; Length 63;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 118 NNNKKE 123
Db 12 NNNKKE 17

RESULT 57
US-10-125-258-61
; Sequence 61, Application US/10125258
; Publication No. US20030028920A1
; GENERAL INFORMATION:
; APPLICANT: Altier, Daniel J.
; APPLICANT: Herrmann, Rafael
; APPLICANT: Lu, Albert L.
; APPLICANT: McCutchen, Billy F.
; APPLICANT: Presnall, James K.
; APPLICANT: Weaver, Janine L.
; APPLICANT: Wong, James F. H.
; TITLE OF INVENTION: Antimicrobial Polypeptides and Their
; TITLE OF INVENTION: Uses
; FILE REFERENCE: 35718/246215
; CURRENT APPLICATION NUMBER: US/10/125,258
; CURRENT FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: 60/285,355
; PRIOR FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: FastSeq For Windows Version 4.0
; SEQ ID NO 61
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Helicoverpa zea
US-10-125-258-61

Query Match
Best Local Similarity 100.0%; Score 6; DB 14; Length 63;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 FKELEG 66
Db 25 FKELEG 30

RESULT 58
US-10-425-114-54599
; Sequence 54599, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovacic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
```

```

; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 54599
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Zea mays subsp. mexicana
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMOTEOSINTE105D05_FLI.pcp
US-10-425-114-54599

Query Match
Best Local Similarity 100.0%; Score 6; DB 12; Length 64;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 VRRATE 136
Db 26 VRRATE 31

RESULT 59
US-09-764-881-122
; Sequence 122, Application US/09764881
; Publication No. US20030125246A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTO7
; CURRENT APPLICATION NUMBER: US/09/764,881
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 122
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-881-122

Query Match
Best Local Similarity 100.0%; Score 6; DB 10; Length 65;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 KKEFER 126
Db 20 KKEFER 25

RESULT 60
US-09-764-875-1113
; Sequence 1113, Application US/09764875
; Publication No. US20040018969A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTO2
; CURRENT APPLICATION NUMBER: US/09/764,875
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1249
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1113
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-875-1113

Query Match
Best Local Similarity 100.0%; Score 6; DB 11; Length 65;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 KKEFER 126
Db 20 KKEFER 25
```

Db 20 KKEEFE 25

RESULT 61

US-10-424-599-281627
; Sequence 281627, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 281627
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(65)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_9632C.1.pep
US-10-424-599-281627

Query Match

Best Local Similarity 4.2%; Score 6; DB 12; Length 65;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 FLSVKK 91
Db 32 FLSVKK 37

RESULT 62

US-09-764-881-122
; Sequence 122, Application US/09764891
; Publication No. US20020086821A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT207
; CURRENT APPLICATION NUMBER: US/09/764,881
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 122
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-881-122

Query Match

Best Local Similarity 4.2%; Score 6; DB 12; Length 65;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 KKEEFE 126
Db 20 KKEEFE 25

RESULT 63

US-10-242-747-122
; Sequence 122, Application US/10242747
; Publication No. US20040005577A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

; FILE REFERENCE: PT207C1
; CURRENT APPLICATION NUMBER: US/10/242,747
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 09/764,881
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 122
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-242-747-122

Query Match

Best Local Similarity 4.2%; Score 6; DB 15; Length 65;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 KKEEFE 126
Db 20 KKEEFE 25

RESULT 64

US-10-158-057-235
; Sequence 235, Application US/10158057
; Publication No. US20040014039A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P0205C1
; CURRENT APPLICATION NUMBER: US/10/158,057
; CURRENT FILING DATE: 2002-06-12
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 235
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-158-057-235

Query Match

Best Local Similarity 4.2%; Score 6; DB 15; Length 65;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 KKEEFE 126
Db 20 KKEEFE 25

RESULT 65

US-10-424-599-199019
; Sequence 199019, Application US/10424599

```

; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 199019
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_21739C.1.pep
US-10-424-599-199019

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Query Match      4.2%; Score 6; DB 12; Length 66;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      84 CAPLSV 89
Db      60 CAPLSV 65

```

```

RESULT 66
US-10-424-599-167398
; Sequence 167398, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 167398
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_122178C.1.pep
US-10-424-599-167398

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Query Match      4.2%; Score 6; DB 12; Length 67;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      15 KDHRIS 20
Db      50 KDHRIS 55

```

```

RESULT 67
US-10-424-599-153000
; Sequence 153000, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B

```

```

; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 153000
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_109183C.1.pep
US-10-424-599-153000

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Query Match      4.2%; Score 6; DB 12; Length 69;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      86 FLSVKK 91
Db      38 FLSVKK 43

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```

RESULT 68
US-10-437-963-141151
; Sequence 141151, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Bardazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 141151
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(74)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_42283C.1.pep
US-10-437-963-141151

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Query Match      4.2%; Score 6; DB 16; Length 74;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      7 PPAWOP 12
Db      62 PPAWOP 67

```

```

RESULT 69
US-10-282-122A-45175
; Sequence 45175, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John

```

```

; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45175
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-10-282-122A-45175

Query Match          4.2%  Score 6;  DB 12;  Length 75;
Best Local Similarity 100.0%;  Pred. No. 4.6e+02;
Matches 6;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY      125 EETAKK 130
Db      14 EETAKK 19

RESULT 70
US-10-437-963-182219
; Sequence 182219, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 182219
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(76)
; OTHER INFORMATION: unsure at all Xaa locations
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; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_79427C.1.pep
US-10-437-963-182219

Query Match          4.2%  Score 6;  DB 16;  Length 76;
Best Local Similarity 100.0%;  Pred. No. 4.6e+02;
Matches 6;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY      4 PTLPPA 9
Db      47 PTLPPA 52

RESULT 71
US-10-424-599-144105
; Sequence 144105, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 144105
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(77)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_101139C.1.pep
US-10-424-599-144105

Query Match          4.2%  Score 6;  DB 12;  Length 77;
Best Local Similarity 100.0%;  Pred. No. 4.7e+02;
Matches 6;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY      3 APTLPP 8
Db      65 APTLPP 70

RESULT 72
US-10-424-599-199222
; Sequence 199222, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 199222
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(82)
; OTHER INFORMATION: Clone ID: PAT_MRT3847_21921C.1.pep
US-10-424-599-199222

Query Match          4.2%  Score 6;  DB 12;  Length 82;
```


Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 LDRERA 109
|||||
Db 47 LDRERA 52

RESULT 73

US-10-424-599-152919
; Sequence 152919, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 152919
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_109109C.1.pbp
US-10-424-599-152919

Query Match
Best Local Similarity 100.0%; Score 6; DB 12; Length 84;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 TPERMA 39
|||||
Db 73 TPERMA 78

RESULT 74

US-10-424-599-232417
; Sequence 232417, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 232417
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_51897C.1.pbp
US-10-424-599-232417

Query Match
Best Local Similarity 100.0%; Score 6; DB 12; Length 84;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 APTLPP 8
|||||
Db 52 APTLPP 57

RESULT 75

US-10-424-599-216095
; Sequence 216095, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 216095
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_37163C.1.pbp
US-10-424-599-216095

Query Match
Best Local Similarity 100.0%; Score 6; DB 12; Length 85;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 RERAXN 111
|||||
Db 11 RERAXN 16

Search completed: August 11, 2004, 14:30:41
Job time : 48 secs

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OM protein - protein search, using sw model

Run on: August 11, 2004, 14:22:47 / Search time 19 Seconds

(without alignments)
385.836 Million cell updates/sec

Title: US-09-690-825-34

Perfect score: 142
Sequence: 1 MGAPLPPAWQPLKQHRIS.....EPEETAKVRALEQLAAMD 142

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 389414 seqs, 51625871 residues

Word size: 0

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database:

1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCUTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfillset1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	142	100.0	142	US-08-975-080-34	Sequence 34, Appl1
2	142	100.0	142	US-09-283-144-3	Sequence 3, Appl1
3	37	26.1	37	US-09-283-144-15	Sequence 15, Appl1
4	20	14.1	20	US-08-975-080-4	Sequence 4, Appl1
5	17	12.0	17	US-08-975-080-3	Sequence 3, Appl1
6	17	12.0	17	US-09-515-514-1	Sequence 1, Appl1
7	9	6.3	9	US-09-515-514-12	Sequence 12, Appl1
8	9	6.3	9	US-09-515-514-13	Sequence 13, Appl1
9	9	6.3	9	US-09-205-258-450	Sequence 450, App
10	7	4.9	130	US-09-732-210-281	Sequence 281, App
11	7	4.9	167	US-09-107-532A-5332	Sequence 5332, Ap
12	7	4.9	186	US-09-107-532A-5027	Sequence 5027, Ap
13	7	4.9	208	US-09-134-000C-4317	Sequence 4317, Ap
14	7	4.9	258	US-09-134-000C-3780	Sequence 3780, Ap
15	7	4.9	307	US-09-475-316A-70	Sequence 70, Appl1
16	7	4.9	307	US-09-704-640-70	Sequence 70, Appl1
17	7	4.9	309	US-09-475-316A-72	Sequence 72, Appl1
18	7	4.9	309	US-09-704-640-72	Sequence 72, Appl1
19	7	4.9	313	US-09-475-316A-62	Sequence 62, Appl1
20	7	4.9	313	US-09-704-640-62	Sequence 62, Appl1
21	7	4.9	314	US-09-475-316A-65	Sequence 65, Appl1
22	7	4.9	314	US-09-475-316A-118	Sequence 118, App
23	7	4.9	314	US-09-704-640-66	Sequence 66, Appl1
24	7	4.9	314	US-09-704-640-118	Sequence 118, App
25	7	4.9	418	US-09-252-991A-25075	Sequence 25075, A
26	7	4.9	580	US-09-107-532A-5734	Sequence 5734, Ap
27	7	4.9	2285	US-09-308-375-2	Sequence 2, Appl1

28	6	4.2	11	3	US-08-928-383B-5	Sequence 5, Appl1
29	6	4.2	12	2	US-08-764-640-130	Sequence 130, App
30	6	4.2	12	3	US-08-973-225-130	Sequence 130, App
31	6	4.2	12	3	US-09-244-298A-130	Sequence 130, App
32	6	4.2	12	3	US-09-516-704-130	Sequence 130, App
33	6	4.2	12	4	US-09-549-090-130	Sequence 130, App
34	6	4.2	12	4	US-09-832-230A-130	Sequence 130, App
35	6	4.2	24	1	US-08-185-433-13	Sequence 13, App
36	6	4.2	30	4	US-08-936-165A-380	Sequence 380, App
37	6	4.2	58	4	US-09-621-976-6592	Sequence 6992, App
38	6	4.2	80	4	US-09-328-352-4702	Sequence 4702, App
39	6	4.2	93	4	US-09-107-532A-3689	Sequence 3689, App
40	6	4.2	95	4	US-09-252-991A-19558	Sequence 19558, A
41	6	4.2	97	4	US-09-134-001C-5653	Sequence 5653, App
42	6	4.2	99	4	US-09-621-976-7607	Sequence 7607, App
43	6	4.2	130	4	US-09-489-039A-12130	Sequence 12130, A
44	6	4.2	133	4	US-09-252-991A-17914	Sequence 17914, A
45	6	4.2	134	4	US-09-800-729-141	Sequence 141, App
46	6	4.2	135	4	US-09-328-352-4961	Sequence 4961, App
47	6	4.2	141	4	US-09-732-210-545	Sequence 545, App
48	6	4.2	148	1	US-07-998-003A-36	Sequence 36, Appl1
49	6	4.2	148	1	US-08-453-274B-36	Sequence 36, Appl1
50	6	4.2	148	1	US-08-453-695A-36	Sequence 36, Appl1
51	6	4.2	148	1	US-08-468-347-22	Sequence 22, Appl1
52	6	4.2	148	1	US-08-268-161A-36	Sequence 36, Appl1
53	6	4.2	148	2	US-08-467-389-22	Sequence 22, Appl1
54	6	4.2	148	2	US-08-779-379-22	Sequence 22, Appl1
55	6	4.2	148	2	US-08-469-218-22	Sequence 22, Appl1
56	6	4.2	148	2	US-08-453-702A-36	Sequence 36, Appl1
57	6	4.2	148	3	US-09-228-152-22	Sequence 22, Appl1
58	6	4.2	148	3	US-09-699-633-36	Sequence 36, Appl1
59	6	4.2	148	5	PCT-US93-12588-36	Sequence 36, Appl1
60	6	4.2	148	5	PCT-US95-08071-36	Sequence 36, Appl1
61	6	4.2	153	1	US-08-226-264-26	Sequence 26, Appl1
62	6	4.2	153	4	US-09-738-946-4	Sequence 4, Appl1
63	6	4.2	155	4	US-09-732-210-1644	Sequence 1644, App
64	6	4.2	163	4	US-09-134-000C-4018	Sequence 4018, App
65	6	4.2	175	2	US-08-809-267-5	Sequence 5, Appl1
66	6	4.2	175	5	PCT-US95-13622A-5	Sequence 5, Appl1
67	6	4.2	181	4	US-09-252-991A-32676	Sequence 32676, A
68	6	4.2	182	4	US-09-328-352-4216	Sequence 4216, App
69	6	4.2	194	4	US-09-107-532A-6802	Sequence 6802, App
70	6	4.2	204	4	US-09-328-352-6654	Sequence 6654, App
71	6	4.2	207	4	US-09-328-352-6654	Sequence 6654, App
72	6	4.2	248	4	US-09-252-991A-32920	Sequence 32920, A
73	6	4.2	251	4	US-09-252-991A-32676	Sequence 32676, A
74	6	4.2	252	4	US-09-543-681A-6028	Sequence 6028, App
75	6	4.2	260	4	US-09-252-991A-17964	Sequence 17964, A
76	6	4.2	263	4	US-09-489-039A-10079	Sequence 10079, A
77	6	4.2	265	4	US-09-543-681A-8110	Sequence 8110, App
78	6	4.2	267	4	US-09-976-594-212	Sequence 212, App
79	6	4.2	286	4	US-09-172-952-31	Sequence 31, Appl1
80	6	4.2	290	4	US-09-134-000C-5874	Sequence 5874, App
81	6	4.2	301	4	US-09-352-991A-18771	Sequence 18771, A
82	6	4.2	308	4	US-09-489-039A-11473	Sequence 11473, A
83	6	4.2	320	4	US-09-543-681A-5877	Sequence 5877, App
84	6	4.2	325	3	US-09-108-020-49	Sequence 49, App
85	6	4.2	330	4	US-09-679-279-10	Sequence 10, Appl1
86	6	4.2	333	4	US-09-134-000C-5637	Sequence 5637, App
87	6	4.2	335	3	US-09-446-504-80	Sequence 80, Appl1
88	6	4.2	335	4	US-09-712-266-80	Sequence 80, Appl1
89	6	4.2	340	4	US-09-543-681A-4968	Sequence 4968, App
90	6	4.2	342	1	US-08-854-196-2	Sequence 2, Appl1
91	6	4.2	342	3	US-09-064-033-2	Sequence 2, Appl1
92	6	4.2	342	4	US-09-118-464-3	Sequence 3, Appl1
93	6	4.2	342	4	US-09-291-046-2	Sequence 2, Appl1
94	6	4.2	348	1	US-08-843-521-6	Sequence 6, Appl1
95	6	4.2	348	2	US-08-953-041-2	Sequence 2, Appl1
96	6	4.2	348	3	US-09-159-417-2	Sequence 2, Appl1
97	6	4.2	348	3	US-09-012-877-6	Sequence 6, Appl1
98	6	4.2	355	4	US-08-630-915A-192	Sequence 192, App
99	6	4.2	361	3	US-09-041-718-4	Sequence 4, Appl1
100	6	4.2	364	4	US-09-134-000C-4030	Sequence 4030, App

Db 1 MGAPLPPAWQPLKDHRISTFKWMPFLGCACTPER 37

RESULT 4

US-08-975-080-4
Sequence 4, Application US/08975080
Patent No. 6245523
GENERAL INFORMATION:
APPLICANT: Altieri, Dario C.
TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
CELLULAR APOPTOSIS, AND ITS MODULATION
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,080
FILING DATE: 20-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/031,435
FILING DATE: 20-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7176
TELEFAX: 202-467-7000
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-975-080-4

Query Match 14.1%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1e-13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 EGWEPDDPIEHHKXSSGC 84
Db 1 EGWEPDDPIEHHKXSSGC 20

RESULT 5
US-08-975-080-3
Sequence 3, Application US/08975080
Patent No. 6245523
GENERAL INFORMATION:
APPLICANT: Altieri, Dario C.
TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
CELLULAR APOPTOSIS, AND ITS MODULATION
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,080
FILING DATE: 20-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/031,435
FILING DATE: 20-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7176
TELEFAX: 202-467-7000
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-975-080-3

Query Match 12.0%; Score 17; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 APTLPPAWQPLKDHRI 19
Db 1 APTLPPAWQPLKDHRI 17

RESULT 6
US-09-515-514-1
Sequence 1, Application US/09515514
Patent No. 6509162
GENERAL INFORMATION:
APPLICANT: Altieri, Dario C.
TITLE OF INVENTION: Methods for Selectively Modulating Survivin Apoptosis
FILE REFERENCE: 44574-5063-US
CURRENT APPLICATION NUMBER: US/09/515,514
CURRENT FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 17
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (7)
OTHER INFORMATION: PHOSPHORYLATION
US-09-515-514-1

Query Match 12.0%; Score 17; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 LBGACTPERMAEGR 44
Db 1 LBGACTPERMAEGR 17

RESULT 7
US-09-515-514-12
Sequence 12, Application US/09515514
Patent No. 6509162
GENERAL INFORMATION:
APPLICANT: Altieri, Dario C.

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; TITLE OF INVENTION: Methods for Selectively Modulating Survivin Apoptosis
; FILE REFERENCE: 44574-5063-US
; CURRENT APPLICATION NUMBER: US/09/515,514
; CURRENT FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Survivin phosphorylation motif
US-09-515-514-12

Query Match      6.3%; Score 9; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      31 CACTPERMA 39
Db      1 CACTPERMA 9

RESULT 8
US-09-515-514-13
; Sequence 13, Application US/09515514
; Patent No. 6509162
; GENERAL INFORMATION:
; APPLICANT: Altieri, Dario C.
; TITLE OF INVENTION: Methods for Selectively Modulating Survivin Apoptosis
; FILE REFERENCE: 44574-5063-US
; CURRENT APPLICATION NUMBER: US/09/515,514
; CURRENT FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: Survivin phosphorylation motif
US-09-515-514-13

Query Match      6.3%; Score 9; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      31 CACTPERMA 39
Db      1 CACTPERMA 9

RESULT 9
US-09-205-258-450
; Sequence 450, Application US/09205258
; Patent No. 6528174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; SOFTWARE: PatentIn Ver. 2.0
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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,863
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
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SEQ ID NO 450
LENGTH: 101
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (44)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FEATURE:
NAME/KEY: SITE
LOCATION: (46)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FEATURE:
NAME/KEY: SITE
LOCATION: (77)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FEATURE:
NAME/KEY: SITE
LOCATION: (78)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FEATURE:
NAME/KEY: SITE
LOCATION: (101)
OTHER INFORMATION: Xaa equals stop translation
US-09-205-258-450

Query Match 4.9%; Score 7; DB 4; Length 101;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 13 FLKDRI 19
Db 22 FLKDRI 28

RESULT 10
US-09-732-210-281
Sequence 281; Application US/09732210
Patent No. 6573361
GENERAL INFORMATION:
APPLICANT: Bunkers, Greg J.
APPLICANT: Liang, Jihong
APPLICANT: Miltanck, Cindy A.
APPLICANT: Seale, Jeffrey W.
APPLICANT: Mu, Yonnie S.
TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
FILE REFERENCE: 38-21(15036)B
CURRENT APPLICATION NUMBER: US/09/732, 210
CURRENT FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 60/169,513
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: US 60/169,340
PRIOR FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 1753
SEQ ID NO 281
LENGTH: 130
TYPE: PRT
ORGANISM: Caenorhabditis elegans
US-09-732-210-281

Query Match 4.9%; Score 7; DB 4; Length 130;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 94 EELTGE 100
Db 47 EELTGE 53

RESULT 11
US-09-107-532A-5332
Sequence 5332; Application US/09107532A
Patent No. 6583275

GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107, 532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneka
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-8277
TELEFAX: (781)893-5007
INFORMATION FOR SEQ ID NO: 5332:
SEQUENCE CHARACTERISTICS:
LENGTH: 167 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...167
SEQUENCE DESCRIPTION: SEQ ID NO: 5332:
US-09-107-532A-5332

Query Match 4.9%; Score 7; DB 4; Length 167;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 131 VRAAEQ 137
Db 145 VRAAEQ 151

RESULT 12
US-09-107-532A-5027
Sequence 5027; Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:

MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneka
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 5027:
SEQUENCE CHARACTERISTICS:
LENGTH: 186 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc.feature
LOCATION: (B) LOCATION 1..186
SEQUENCE DESCRIPTION: SEQ ID NO: 5027:
US-09-107-532A-5027

Query Match 4.9%; Score 7; DB 4; Length 186;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 TAKVRR 133
DB 43 TAKVRR 49

RESULT 13
US-09-134-000C-4317
Sequence 4317, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4317
LENGTH: 208
TYPE: PRT
ORGANISM: Enterococcus faecalis
US-09-134-000C-4317

Query Match 4.9%; Score 7; DB 4; Length 208;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 TAKVRR 133
DB 65 TAKVRR 71

RESULT 14
US-09-134-000C-3780
Sequence 3780, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3780
LENGTH: 258
TYPE: PRT
ORGANISM: Enterococcus faecalis
US-09-134-000C-3780

Query Match 4.9%; Score 7; DB 4; Length 258;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EETAKKV 131
DB 171 EETAKKV 177

RESULT 15
US-09-475-316A-70
Sequence 70, Application US/09475316A
Patent No. 6210942
GENERAL INFORMATION:
APPLICANT: Lewis, No. 6210942man G.
APPLICANT: Davin, Laurence B.
APPLICANT: Dinkova-Kostova, Albena T.
APPLICANT: Fujita, Masayuki
APPLICANT: Gang, David R.
APPLICANT: Sakkenen, Simo
APPLICANT: Ford, Joshua D
TITLE OF INVENTION: RECOMBINANT PINORESINOL/LARICRESINOL REDUCTASES,
FILE REFERENCE: WSR-1-13793
CURRENT APPLICATION NUMBER: US/09/475,316A
CURRENT FILING DATE: 1999-12-30
PRIOR APPLICATION NUMBER: 09/307,653
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: PCT/US97/20391
PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: 60/054,380
PRIOR FILING DATE: 1997-07-31
PRIOR APPLICATION NUMBER: 60/030,522
PRIOR FILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 122
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 70
LENGTH: 307
TYPE: PRT
ORGANISM: Tsuga heterophylla
US-09-475-316A-70

Query Match 4.9%; Score 7; DB 3; Length 307;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 KVRRAIE 136
DB 135 KVRRAIE 141

RESULT 16


```
US-09-704-640-70
; Sequence 70, Application US/09704640
; Patent No. 6635459
; GENERAL INFORMATION:
; APPLICANT: Lewis, No. 6635459man G.
; APPLICANT: Davin, Laurence B.
; APPLICANT: Dinkova-Kostova, Albena T.
; APPLICANT: Fujita, Masayuki
; APPLICANT: Gang, David R.
; APPLICANT: Sarkanen, Simo
; APPLICANT: Ford, Joshua D
; TITLE OF INVENTION: RECOMBINANT PINOSESINOL/LARICRESINOL REDUCTASE,
; FILE REFERENCE: MSUR-1-16492
; CURRENT APPLICATION NUMBER: US/09/704,640
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: 09/475,316
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: 09/307,653
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: PCT/US97/20391
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: 60/054,380
; PRIOR FILING DATE: 1997-07-31
; PRIOR APPLICATION NUMBER: 60/030,522
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 70
; LENGTH: 307
; TYPE: PRT
; ORGANISM: Tsuga heterophylla
US-09-704-640-70
```

```
Query Match          4.9%; Score 7; DB 4; Length 307;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
CY      130 KVRRAIE 136
        |||||
Db       135 KVRRAIE 141
```

```
RESULT 17
US-09-475-316A-72
; Sequence 72, Application US/09475316A
; Patent No. 6210942
; GENERAL INFORMATION:
```

```
; APPLICANT: Lewis, No. 6210942man G.
; APPLICANT: Davin, Laurence B.
; APPLICANT: Dinkova-Kostova, Albena T.
; APPLICANT: Fujita, Masayuki
; APPLICANT: Gang, David R.
; APPLICANT: Sarkanen, Simo
; APPLICANT: Ford, Joshua D
; TITLE OF INVENTION: RECOMBINANT PINOSESINOL/LARICRESINOL REDUCTASES,
; FILE REFERENCE: MSUR-1-13793
; CURRENT APPLICATION NUMBER: US/09/475,316A
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: 09/307,653
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: PCT/US97/20391
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: 60/054,380
; PRIOR FILING DATE: 1997-07-31
; PRIOR APPLICATION NUMBER: 60/030,522
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 72
; LENGTH: 309
; TYPE: PRT
```

```
US-09-475-316A-72
; Sequence 72, Application US/09475316A
; Patent No. 6210942
; GENERAL INFORMATION:
; APPLICANT: Lewis, No. 6210942man G.
; APPLICANT: Davin, Laurence B.
; APPLICANT: Dinkova-Kostova, Albena T.
; APPLICANT: Fujita, Masayuki
; APPLICANT: Gang, David R.
; APPLICANT: Sarkanen, Simo
; APPLICANT: Ford, Joshua D
; TITLE OF INVENTION: RECOMBINANT PINOSESINOL/LARICRESINOL REDUCTASES,
; FILE REFERENCE: MSUR-1-13793
; CURRENT APPLICATION NUMBER: US/09/475,316A
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: 09/307,653
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: PCT/US97/20391
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: 60/054,380
; PRIOR FILING DATE: 1997-07-31
; PRIOR APPLICATION NUMBER: 60/030,522
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 72
; LENGTH: 309
; TYPE: PRT
```

```
; ORGANISM: Tsuga heterophylla
US-09-475-316A-72
```

```
Query Match          4.9%; Score 7; DB 3; Length 309;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
CY      130 KVRRAIE 136
        |||||
Db       137 KVRRAIE 143
```

```
RESULT 18
US-09-704-640-72
; Sequence 72, Application US/09704640
; Patent No. 6635459
; GENERAL INFORMATION:
; APPLICANT: Lewis, No. 6635459man G.
; APPLICANT: Davin, Laurence B.
; APPLICANT: Dinkova-Kostova, Albena T.
; APPLICANT: Fujita, Masayuki
; APPLICANT: Gang, David R.
; APPLICANT: Sarkanen, Simo
; APPLICANT: Ford, Joshua D
; TITLE OF INVENTION: RECOMBINANT PINOSESINOL/LARICRESINOL REDUCTASE,
; FILE REFERENCE: MSUR-1-16492
; CURRENT APPLICATION NUMBER: US/09/704,640
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: 09/475,316
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: 09/307,653
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: PCT/US97/20391
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: 60/054,380
; PRIOR FILING DATE: 1997-07-31
; PRIOR APPLICATION NUMBER: 60/030,522
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 72
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Tsuga heterophylla
US-09-704-640-72
```

```
Query Match          4.9%; Score 7; DB 4; Length 309;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
CY      130 KVRRAIE 136
        |||||
Db       137 KVRRAIE 143
```

```
RESULT 19
US-09-475-316A-62
; Sequence 62, Application US/09475316A
; Patent No. 6210942
; GENERAL INFORMATION:
; APPLICANT: Lewis, No. 6210942man G.
; APPLICANT: Davin, Laurence B.
; APPLICANT: Dinkova-Kostova, Albena T.
; APPLICANT: Fujita, Masayuki
; APPLICANT: Gang, David R.
; APPLICANT: Sarkanen, Simo
; APPLICANT: Ford, Joshua D
; TITLE OF INVENTION: RECOMBINANT PINOSESINOL/LARICRESINOL REDUCTASES,
; FILE REFERENCE: MSUR-1-13793
; CURRENT APPLICATION NUMBER: US/09/475,316A
; PRIOR FILING DATE: 1999-12-30
```

;; PRIOR APPLICATION NUMBER: 09/307,653
;; PRIOR FILING DATE: 1999-05-07
;; PRIOR APPLICATION NUMBER: PCT/US97/20391
;; PRIOR FILING DATE: 1997-11-07
;; PRIOR APPLICATION NUMBER: 60/054,380
;; PRIOR FILING DATE: 1997-07-31
;; PRIOR APPLICATION NUMBER: 60/030,522
;; PRIOR FILING DATE: 1996-11-08
;; NUMBER OF SEQ ID NOS: 122
;; SOFTWARE: Patentln Ver. 2.0
;; SEQ ID NO: 62
;; LENGTH: 313
;; TYPE: PRT
;; ORGANISM: Thuja plicata
US-09-475-316A-62

Query Match 4.9%; Score 7; DB 3; Length 313;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 130 KVRRAIE 136
Db 140 KVRRAIE 146

RESULT 20
US-09-704-640-62
;; Sequence 62, Application US/09704640
;; Patent No. 6635459
;; GENERAL INFORMATION:
;; APPLICANT: Lewis, No. 6635459man G.
;; APPLICANT: Davin, Laurence B. Albena T.
;; APPLICANT: Dinkova-Kostova, Albena T.
;; APPLICANT: Fujita, Masayuki
;; APPLICANT: Gang, David R.
;; APPLICANT: Sarkanen, Simo
;; APPLICANT: Ford, Joshua D
;; TITLE OF INVENTION: RECOMBINANT PINORESINOL/LARICRESINOL REDUCTASE,
;; TITLE OF INVENTION: RECOMBINANT DIRIGENT PROTEIN AND METHODS OF USE
;; FILE REFERENCE: MSUR-1-16492
;; CURRENT APPLICATION NUMBER: US/09/704,640
;; CURRENT FILING DATE: 2000-11-02
;; PRIOR APPLICATION NUMBER: 09/475,316
;; PRIOR FILING DATE: 1999-12-30
;; PRIOR APPLICATION NUMBER: 09/307,653
;; PRIOR FILING DATE: 1999-05-07
;; PRIOR APPLICATION NUMBER: PCT/US97/20391
;; PRIOR FILING DATE: 1997-11-07
;; PRIOR APPLICATION NUMBER: 60/054,380
;; PRIOR FILING DATE: 1997-07-31
;; PRIOR APPLICATION NUMBER: 60/030,522
;; PRIOR FILING DATE: 1996-11-08
;; NUMBER OF SEQ ID NOS: 122
;; SOFTWARE: Patentln Ver. 2.0
;; SEQ ID NO: 62
;; LENGTH: 313
;; TYPE: PRT
;; ORGANISM: Thuja plicata
US-09-704-640-62

Query Match 4.9%; Score 7; DB 4; Length 313;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 130 KVRRAIE 136
Db 140 KVRRAIE 146

RESULT 21
US-09-475-316A-66
;; Sequence 66, Application US/09475316A
;; Patent No. 6210942

;; GENERAL INFORMATION:
;; APPLICANT: Lewis, No. 6210942man G.
;; APPLICANT: Davin, Laurence B. Albena T.
;; APPLICANT: Dinkova-Kostova, Albena T.
;; APPLICANT: Fujita, Masayuki
;; APPLICANT: Gang, David R.
;; APPLICANT: Sarkanen, Simo
;; APPLICANT: Ford, Joshua D
;; TITLE OF INVENTION: RECOMBINANT PINORESINOL/LARICRESINOL REDUCTASES,
;; TITLE OF INVENTION: RECOMBINANT DIRIGENT PROTEINS AND METHODS OF USE
;; FILE REFERENCE: MSUR-1-13793
;; CURRENT APPLICATION NUMBER: US/09/475,316A
;; CURRENT FILING DATE: 1999-12-30
;; PRIOR APPLICATION NUMBER: 09/307,653
;; PRIOR FILING DATE: 1999-05-07
;; PRIOR APPLICATION NUMBER: PCT/US97/20391
;; PRIOR FILING DATE: 1997-11-07
;; PRIOR APPLICATION NUMBER: 60/054,380
;; PRIOR FILING DATE: 1997-07-31
;; PRIOR APPLICATION NUMBER: 60/030,522
;; PRIOR FILING DATE: 1996-11-08
;; NUMBER OF SEQ ID NOS: 122
;; SOFTWARE: Patentln Ver. 2.0
;; SEQ ID NO: 66
;; LENGTH: 314
;; TYPE: PRT
;; ORGANISM: Thuja plicata
US-09-475-316A-66

Query Match 4.9%; Score 7; DB 3; Length 314;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 130 KVRRAIE 136
Db 140 KVRRAIE 146

RESULT 22
US-09-475-316A-118
;; Sequence 118, Application US/09475316A
;; Patent No. 6210942
;; GENERAL INFORMATION:
;; APPLICANT: Lewis, No. 6210942man G.
;; APPLICANT: Davin, Laurence B. Albena T.
;; APPLICANT: Dinkova-Kostova, Albena T.
;; APPLICANT: Fujita, Masayuki
;; APPLICANT: Gang, David R.
;; APPLICANT: Sarkanen, Simo
;; APPLICANT: Ford, Joshua D
;; TITLE OF INVENTION: RECOMBINANT PINORESINOL/LARICRESINOL REDUCTASES,
;; TITLE OF INVENTION: RECOMBINANT DIRIGENT PROTEINS AND METHODS OF USE
;; FILE REFERENCE: MSUR-1-13793
;; CURRENT APPLICATION NUMBER: US/09/475,316A
;; CURRENT FILING DATE: 1999-12-30
;; PRIOR APPLICATION NUMBER: 09/307,653
;; PRIOR FILING DATE: 1999-05-07
;; PRIOR APPLICATION NUMBER: PCT/US97/20391
;; PRIOR FILING DATE: 1997-11-07
;; PRIOR APPLICATION NUMBER: 60/054,380
;; PRIOR FILING DATE: 1997-07-31
;; PRIOR APPLICATION NUMBER: 60/030,522
;; PRIOR FILING DATE: 1996-11-08
;; NUMBER OF SEQ ID NOS: 122
;; SOFTWARE: Patentln Ver. 2.0
;; SEQ ID NO: 118
;; LENGTH: 314
;; TYPE: PRT
;; ORGANISM: Schisandra chinensis
US-09-475-316A-118

Query Match 4.9%; Score 7; DB 3; Length 314;
Best Local Similarity 100.0%; Pred. No. 26;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 130 KVRRAIE 136
Db 142 KVRRAIE 148

RESULT 23

US-09-704-640-66
; Sequence 66, Application US/09704640
; Patent No. 6635459
; GENERAL INFORMATION:
; APPLICANT: Lewis, No. 6635459man G.
; APPLICANT: Davin, Laurence B.
; APPLICANT: Dinkova-Kostova, Albena T.
; APPLICANT: Fujita, Masayuki
; APPLICANT: Gang, David R.
; APPLICANT: Sarkanen, Simo
; APPLICANT: Ford, Joshua D
; TITLE OF INVENTION: RECOMBINANT PINORESINOL/LARICRESINOL REDUCTASE,
; FILE REFERENCE: WSUR-1-16492
; CURRENT APPLICATION NUMBER: US/09/704,640
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: 09/475,316
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: 09/307,653
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: PCT/US97/20391
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: 60/054,380
; PRIOR FILING DATE: 1997-07-31
; PRIOR APPLICATION NUMBER: 60/030,522
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Thruja plicata
US-09-704-640-66

Query Match 4.9%; Score 7; DB 4; Length 314;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 KVRRAIE 136
Db 140 KVRRAIE 146

RESULT 24

US-09-704-640-118
; Sequence 118, Application US/09704640
; Patent No. 6635459
; GENERAL INFORMATION:
; APPLICANT: Lewis, No. 6635459man G.
; APPLICANT: Davin, Laurence B.
; APPLICANT: Dinkova-Kostova, Albena T.
; APPLICANT: Fujita, Masayuki
; APPLICANT: Gang, David R.
; APPLICANT: Sarkanen, Simo
; APPLICANT: Ford, Joshua D
; TITLE OF INVENTION: RECOMBINANT PINORESINOL/LARICRESINOL REDUCTASE,
; FILE REFERENCE: WSUR-1-16492
; CURRENT APPLICATION NUMBER: US/09/704,640
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: 09/475,316
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: 09/307,653
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: PCT/US97/20391

; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: 60/054,380
; PRIOR FILING DATE: 1997-07-31
; PRIOR APPLICATION NUMBER: 60/030,522
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 118
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Schisandra chinensis
US-09-704-640-118

Query Match 4.9%; Score 7; DB 4; Length 314;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 KVRRAIE 136
Db 142 KVRRAIE 148

RESULT 25
US-09-252-991A-25075
; Sequence 25075, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25075
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25075

Query Match 4.9%; Score 7; DB 4; Length 418;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PAMQPL 14
Db 406 PAMQPL 412

RESULT 26
US-09-107-532A-5734
; Sequence 5734, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>

SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICANT: Robert W. Finberg, Jeffrey M. Bergelson,
APPLICANT: and Marshall S. Horwitz
FILING DATE: 30-Jun-1998
TITLE OF INVENTION: CAR, A No. 6210921el Cocksackievirus and Adenovirus
TITLE OF INVENTION: Receptor
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,383B
FILING DATE: 12-SEP-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,100
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: DEN-020
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...580
SEQUENCE DESCRIPTION: SEQ ID NO: 5734:
US-09-107-532A-5734

Query Match 4.9%; Score 7; DB 4; Length 580;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 NKIAKET 117
DB 227 NKIAKET 233

RESULT 27
US-09-308-375-2
Sequence 2, Application US/09308375
Patent No. 6300117
GENERAL INFORMATION:
APPLICANT: Genencor International, Inc.
TITLE OF INVENTION: Proteases From Gram-Positive Organisms
FILE REFERENCE: GC394-PCT
CURRENT APPLICATION NUMBER: US/09/308,375
CURRENT FILING DATE: 1999-05-14
EARLIER APPLICATION NUMBER: EP9719636.4
EARLIER FILING DATE: 1997-03-15
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 2285
TYPE: PRT
ORGANISM: Bacillus subtilis
US-09-308-375-2

Query Match 4.9%; Score 7; DB 4; Length 2285;
Best Local Similarity 100.0%; Pred. No. 14e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 RRAIEQL 138
DB 184 RRAIEQL 190

RESULT 28
US-08-928-383B-5
Sequence 5, Application US/08928383B
Patent No. 6210921

GENERAL INFORMATION:
APPLICANT: Robert W. Finberg, Jeffrey M. Bergelson,
APPLICANT: and Marshall S. Horwitz
FILING DATE: 30-Jun-1998
TITLE OF INVENTION: CAR, A No. 6210921el Cocksackievirus and Adenovirus
TITLE OF INVENTION: Receptor
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,383B
FILING DATE: 12-SEP-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,100
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: DEN-020
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-928-383B-5

Query Match 4.2%; Score 6; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PTLPPA 9
DB 5 PTLPPA 10

RESULT 29
US-08-764-640-130
Sequence 130, Application US/08764640
Patent No. 5869451
Patent No. 5869451 5837683
GENERAL INFORMATION:
APPLICANT: Dower, William J.
APPLICANT: Bartlett, Ronald W.
APPLICANT: Cwila, Steven E.
APPLICANT: Gates, Christian
APPLICANT: Schatz, Peter J.
APPLICANT: Balasubramanian, Palaniappan
APPLICANT: Magstrom, Christopher R.
APPLICANT: Hendren, Richard W.
APPLICANT: Depina, Randolph B.
APPLICANT: Podduburi, Surekha
APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398

CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,640
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 130:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-764-640-130

Query Match 4.2%; Score 6; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 TLGEFL 102
Db 2 TLGEFL 7

RESULT 30
US-08-973-225-130
Sequence 130, Application US/08973225A
Patent No. 6083913
GENERAL INFORMATION:
APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
Gates, Christian
Haselden, Sherill S.
Matheakis, Larry C.
Schatz, Peter J.
Wagstrom, Christopher R.
Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
THROMBOPOIETIN RECEPTOR
NUMBER OF SEQUENCES: 232
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,225A
FILING DATE: 04-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392

REFERENCE/DOCKET NUMBER: PK3065USW
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 130:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 130:
US-08-973-225-130

Query Match 4.2%; Score 6; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 TLGEFL 102
Db 2 TLGEFL 7

RESULT 31
US-09-244-298A-130
Sequence 130, Application US/09244298A
Patent No. 6121238
GENERAL INFORMATION:
APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
Schatz, Peter J.
Palaniappan
Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Henderson, Richard W.
Depina, Richard B.
Podduri, Surekha
APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
RECEPTOR
NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/244,298A
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 130:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-244-298A-130

Query Match 4.2%; Score 6; DB 3; Length 12;

Best Local Similarity 100.0%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 TLGEFL 102
Db 2 TLGEFL 7

RESULT 32
US-09-516-704-130

; Sequence 130, Application US/09516704

; Patent No. 6251864

; GENERAL INFORMATION:

; APPLICANT: Dower, William J.

; Barrett, Ronald W.

; Cwirla, Steven E.

; Gates, Christian

; Schatz, Peter J.

; Balasubramanian, Palaniappan

; Magstrom, Christopher R.

; Hendren, Richard W.

; Depinche, Randolph B.

; Podduturi, Surekha

; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A RECEPTOR

; NUMBER OF SEQUENCES: 244

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Glaxo Wellcome

; STREET: Five Moore Drive, P.O. Box 13398

; CITY: Research Triangle Park

; STATE: NC

; COUNTRY: USA

; ZIP: 27709

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/516,704

; FILING DATE: 01-Mar-2000

; CLASSIFICATION: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Hrubiec, Robert T.

; REGISTRATION NUMBER: 36,392

; REFERENCE/DOCKET NUMBER: PK3261

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 919-248-1000

; INFORMATION FOR SEQ ID NO: 130:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 12 amino acids

; TYPE: amino acid

; STRANDEDNESS: <Unknown>

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 130:

; US-09-516-704-130

; Query Match 4.2%; Score 6; DB 3; Length 12;

; Best Local Similarity 100.0%; Pred. No. 17;

; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 TLGEFL 102
Db 2 TLGEFL 7

RESULT 33

US-09-549-090-130

; Sequence 130, Application US/09549090

; Patent No. 6465430

; GENERAL INFORMATION:

; APPLICANT: Dower, William J.

; Barrett, Ronald W.

; Cwirla, Steven E.

; Duffin, David J.

; Gates, Christian

; Haselden, Sheril S.

; Matheakis, Larry C.

; Schatz, Peter J.

; Magstrom, Christopher R.

; Wrighton, Nicholas C.

; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A THROMBOPOIETIN RECEPTOR

; NUMBER OF SEQUENCES: 232

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Glaxo Wellcome

; STREET: Five Moore Drive, P.O. Box 13398

; CITY: Research Triangle Park

; STATE: NC

; COUNTRY: USA

; ZIP: 27709

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/549,090

; FILING DATE: 13-Apr-2000

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/973,225

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Hrubiec, Robert T.

; REGISTRATION NUMBER: 36,392

; REFERENCE/DOCKET NUMBER: PK3065USW

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 919-248-1000

; INFORMATION FOR SEQ ID NO: 130:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 12 amino acids

; TYPE: amino acid

; STRANDEDNESS: <Unknown>

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 130:

; US-09-549-090-130

; Query Match 4.2%; Score 6; DB 4; Length 12;

; Best Local Similarity 100.0%; Pred. No. 17;

; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 TLGEFL 102
Db 2 TLGEFL 7

RESULT 34
US-09-832-230A-130

; Sequence 130, Application US/09832230A

; Patent No. 6506362

; GENERAL INFORMATION:

; APPLICANT: Dower, William J et al

; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A RECEPTOR

; NUMBER OF SEQUENCES: 244

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Glaxo Wellcome

; STREET: Five Moore Drive, P.O. Box 13398

; CITY: Research Triangle Park

; STATE: NC

; COUNTRY: USA

; ZIP: 27709

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/832,230A
FILING DATE: 10-Apr-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 130:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 130:
US-09-832-230A-130

Query Match
Best Local Similarity 100.0%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 TLGEFL 102
Db 2 TLGEFL 7

RESULT 35
US-08-185-432-13
Sequence 13, Application US/08185432
Patent No. 5750652
GENERAL INFORMATION:
APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Bussseau, Isabelle
APPLICANT: Diederich, Robert J.
APPLICANT: Xu, Tian
APPLICANT: Matsuno, Kenji
TITLE OF INVENTION: DELTEx PROTEINS, NUCLEIC ACIDS, AND
NUMBER OF SEQUENCES: 23
CURRENT APPLICATION DATA:
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,432
FILING DATE: 21-JAN-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: amino acid

TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-185-432-13

Query Match
Best Local Similarity 100.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 APTLP 8
Db 2 APTLP 7

RESULT 36
US-08-936-165A-380
Sequence 380, Application US/08936165A
Patent No. 6348382
GENERAL INFORMATION:
APPLICANT: Black, Michael
APPLICANT: Burnham, Martin
APPLICANT: Hodgson, John
APPLICANT: Knowles, David
APPLICANT: Lonetto, Michael
APPLICANT: Nicholas, Richard
APPLICANT: Pratt, Julie
APPLICANT: Reichard, Richard
APPLICANT: Rosenberg, Martin
APPLICANT: Ward, Judith
TITLE OF INVENTION: No. 6348382el Prokaryotic polynucleotides,
NUMBER OF SEQUENCES: 334
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/936,165A
FILING DATE: 24-SEP-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/027,032
FILING DATE: 24-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimm, Edward R.
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P50549
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 380:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-936-165A-380

Query Match
Best Local Similarity 100.0%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 AKKTA 114
|||||

Db 9 AKKIA 14

RESULT 37

US-09-621-976-6992
; Sequence 6992, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTS and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 6992
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-6992

Query Match 4.2%; Score 6; DB 4; Length 58;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 OPELKD 16
Db 21 QPFLKD 26

RESULT 38

US-09-328-352-4702
; Sequence 4702, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Bleton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4702
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4702

Query Match 4.2%; Score 6; DB 4; Length 80;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 125 EETAKK 130
Db 19 EETAKK 24

RESULT 39

US-09-107-532A-3689
; Sequence 3689, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts

COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:
NAME: Arinello, Pamela Deneke
REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 3689:
SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids

TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
HYPOTHETICAL: YES

ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium

FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...93

SEQUENCE DESCRIPTION: SEQ ID NO: 3689:
US-09-107-532A-3689

Query Match 4.2%; Score 6; DB 4; Length 93;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 90 KKOFER 95
Db 30 KKOFER 35

RESULT 40
US-09-252-991A-19558
; Sequence 19558, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196-136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19558
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19558

Query Match 4.2%; Score 6; DB 4; Length 95;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 117 TNNKKX 122

Db 30 TNNKKK 35

RESULT 41
US-09-134-001C-5653
Sequence 5653, Application US/09134001C
Patent No. 6380370

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-09
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 5653
LENGTH: 97
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5653

Query Match 4.2%; Score 6; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 KXKIAK 115
Db 91 KXKIAK 96

RESULT 42

US-09-621-976-7607
Sequence 7607, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET-054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 7607
LENGTH: 99
TYPE: PRT
ORGANISM: Homo sapiens
US-09-621-976-7607

Query Match 4.2%; Score 6; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 KXSSG 83
Db 19 KXSSG 24

RESULT 43
US-09-489-039A-12130
Sequence 12130, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 12130
LENGTH: 130
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12130

Query Match 4.2%; Score 6; DB 4; Length 130;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 133 RATEOL 138
Db 32 RATEOL 37

RESULT 44
US-09-252-991A-17914
Sequence 17914, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 17914
LENGTH: 133
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17914

Query Match 4.2%; Score 6; DB 4; Length 133;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 KVRRAI 135
Db 7 KVRRAI 12

RESULT 45
US-09-800-729-141
Sequence 141, Application US/09800729
Patent No. 6605592
GENERAL INFORMATION:
APPLICANT: N. et al.
TITLE OF INVENTION: 32 Human secreted proteins
FILE REFERENCE: P2044P1
CURRENT APPLICATION NUMBER: US/09/800,729
CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: PCT/US00/26013
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 60/155,709
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 217
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 141
LENGTH: 134
TYPE: PRT
ORGANISM: Homo sapiens
US-09-800-729-141

Query Match 4.2%; Score 6; DB 4; Length 134;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 128 AKVRR 133
 DB 123 AKVRR 128

RESULT 46
 US-09-328-352-4961
 ; Sequence 4961, Application US/09328352
 ; Patent No. 6562958
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary L. Breton et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
 ; FILE REFERENCE: GTC99-039A
 ; CURRENT APPLICATION NUMBER: US/09/328,352
 ; NUMBER OF SEQ ID NOS: 04
 ; SEQ ID NO 4961
 ; LENGTH: 135
 ; TYPE: PRT
 ; ORGANISM: Acinetobacter baumannii
 US-09-328-352-4961

Query Match 4.2%; Score 6; DB 4; Length 135;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 129 KKVRR 134
 DB 60 KKVRR 65

RESULT 47
 US-09-732-210-545
 ; Sequence 545, Application US/09732210
 ; Patent No. 6573361
 ; GENERAL INFORMATION:
 ; APPLICANT: Bunkers, Greg J.
 ; APPLICANT: Liang, Jihong
 ; APPLICANT: Mitnick, Candy A.
 ; APPLICANT: Seale, Jeffrey W.
 ; APPLICANT: Wu, Yonnie S.
 ; TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
 ; FILE REFERENCE: 38-21(15036)B
 ; CURRENT APPLICATION NUMBER: US/09/732,210
 ; CURRENT FILING DATE: 2000-12-07
 ; PRIOR APPLICATION NUMBER: US 60/169,513
 ; PRIOR FILING DATE: 1999-12-07
 ; PRIOR APPLICATION NUMBER: US 60/169,340
 ; PRIOR FILING DATE: 1999-12-07
 ; NUMBER OF SEQ ID NOS: 1753
 ; SEQ ID NO 545
 ; LENGTH: 141
 ; TYPE: PRT
 ; ORGANISM: Helicobacter pylori
 US-09-732-210-545

Query Match 4.2%; Score 6; DB 4; Length 141;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 110 KVKIAR 115
 DB 94 KVKIAR 99

RESULT 48
 US-07-998-003A-36
 ; Sequence 36, Application US/07998003A

Patent No. 5643781
 ; GENERAL INFORMATION:
 ; APPLICANT: Suzuki, Shintaro
 ; TITLE OF INVENTION: Protocadherin Materials and Methods
 ; NUMBER OF SEQUENCES: 107
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, &
 ; STREET: 20 South Clark Street
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60603
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/998,003A
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: No. 5643781and, Greta E.
 ; REGISTRATION NUMBER: 35,302
 ; REFERENCE/DOCKET NUMBER: 30903
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312/346-5750
 ; TELEFAX: 312/984-9740
 ; INFORMATION FOR SEQ ID NO: 36:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 148 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-07-998-003A-36

Query Match 4.2%; Score 6; DB 1; Length 148;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 103 KLDRR 108
 DB 107 KLDRR 112

RESULT 49
 US-08-453-274B-36
 ; Sequence 36, Application US/08453274B
 ; Patent No. 5663300
 ; GENERAL INFORMATION:
 ; APPLICANT: Suzuki, Shintaro
 ; TITLE OF INVENTION: Protocadherin Materials and Methods
 ; NUMBER OF SEQUENCES: 107
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: United States of America
 ; ZIP: 60606-6402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/453,274B
 ; FILING DATE: 30-MAY-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: No. 5663300and, Greta E.

REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32660
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 148 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-453-274B-36

Query Match 4.2%; Score 6; DB 1; Length 148;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 KLDRE 108
Db 107 KLDRE 112

RESULT 50
US-08-453-695A-36
Sequence 36, Application US/08453695A
Patent No. 5708143
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: Protocadherin Materials and Methods
NUMBER OF SEQUENCES: 115
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, &
ADDRESS: Borun
STREET: 233 South Wacker, 6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,695A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: No. 5708143and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32658
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 148 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-453-695A-36

Query Match 4.2%; Score 6; DB 1; Length 148;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 KLDRE 108
Db 107 KLDRE 112

RESULT 51
US-08-468-347-22
Sequence 22, Application US/08468347
Patent No. 5783421
GENERAL INFORMATION:
APPLICANT: Zeelon, Elsha P.
APPLICANT: Werber, Moshe M.
APPLICANT: Levamou, Avigdor
TITLE OF INVENTION: NOVEL POLYPEPTIDE HAVING FACTOR Xa
TITLE OF INVENTION: INHIBITORY ACTIVITY
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,347
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/225,442
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0317/43020-A/JFW/EAB
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550
TELEFAX: 212-664-0525
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 148 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
FEATURE:
NAME/KEY: Protein
LOCATION: 1..148
US-08-468-347-22

Query Match 4.2%; Score 6; DB 1; Length 148;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 RISTF 23
Db 135 RISTF 140

RESULT 52
US-08-268-161A-36
Sequence 36, Application US/08268161A
Patent No. 5798224
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: Protocadherin Materials and Methods
NUMBER OF SEQUENCES: 115
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, &
ADDRESS: Borun

STREET: 233 South Wacker, 6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/268,161A
APPLICATION NUMBER: US/08/268,161A
FILING DATE: June 27, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Young J. Suh
REGISTRATION NUMBER: P-41,337
REFERENCE/DOCKET NUMBER: 27866/32149
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 148 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-268-161A-36

Query Match 4.2%; Score 6; DB 1; Length 148;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 KIDRRR 108
Db 107 KIDRRR 112

RESULT 53
US-08-467-389-22
Sequence 22, Application US/08467389
Patent No. 5824641
GENERAL INFORMATION:
APPLICANT: Zeelon, Elisha P.
APPLICANT: Werber, Moshe M.
APPLICANT: Levaton, Avigdor
TITLE OF INVENTION: NOVEL POLYPEPTIDE HAVING FACTOR Xa
TITLE OF INVENTION: INHIBITORY ACTIVITY
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,389
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/225,442
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0317/43020-A/JPM/EAB

TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550
TELEFAX: 212-664-0525
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 148 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
FEATURE:
NAME/KEY: Protein
LOCATION: 1..148
US-08-467-389-22

Query Match 4.2%; Score 6; DB 2; Length 148;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 RISTRK 23
Db 135 RISTRK 140

RESULT 54
US-08-779-379-22
Sequence 22, Application US/08779379
Patent No. 5858970
GENERAL INFORMATION:
APPLICANT: Zeelon, Elisha P.
APPLICANT: Werber, Moshe M.
APPLICANT: Levaton, Avigdor
TITLE OF INVENTION: NOVEL POLYPEPTIDE HAVING FACTOR Xa
TITLE OF INVENTION: INHIBITORY ACTIVITY
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,379
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/225,442
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0317/43020-A/JPM/EAB
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550
TELEFAX: 212-664-0525
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 148 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

FEATURE:

NAME/KEY: Protein

LOCATION: 1..148

US-08-779-379-22

Query Match 4.2%; Score 6; DB 2; Length 148;

Best Local Similarity 100.0%; Pred.No.1.5e+02; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 0;

QY 18 RSTFK 23

Db 135 RSTFK 140

RESULT 55

US-08-469-219-22

Sequence 22, Application US/08469219

Patent No. 5863534

GENERAL INFORMATION:

APPLICANT: Zeelon, Elisha P.

APPLICANT: Werber, Moshe M.

APPLICANT: Levanon, Avigdor

TITLE OF INVENTION: NOVEL POLYPEPTIDE HAVING FACTOR Xa

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESSES:

ADDRESS: Cooper & Dunham

STREET: 30 Rockefeller Plaza

CITY: New York

STATE: New York

ZIP: 10112

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/469,219

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/225,442

FILING DATE: 08-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 0317/43020-A/JPM/EAB

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-977-9550

TELEFAX: 212-664-0525

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 148 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

FEATURE:

NAME/KEY: Protein

LOCATION: 1..148

US-08-469-219-22

Query Match 4.2%; Score 6; DB 2; Length 148;

Best Local Similarity 100.0%; Pred.No.1.5e+02; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 0;

QY 18 RSTFK 23

Db 135 RSTFK 140

RESULT 56

US-08-453-702A-36

Sequence 36, Application US/08453702A

Patent No. 5891706

GENERAL INFORMATION:

APPLICANT: Suzuki, Shintaro

TITLE OF INVENTION: Protocadherin Materials and Methods

NUMBER OF SEQUENCES: 115

CORRESPONDENCE ADDRESSES:

ADDRESS: Marshall, O'Toole, Gerstein, Murray, &

ADDRESS: Borun

STREET: 233 South Wacker, 6300 Sears Tower

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/453,702A

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: No. 5891706and, Greta E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 32657

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/474-6300

TELEFAX: 312/474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 36:

SEQUENCE CHARACTERISTICS:

LENGTH: 148 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-453-702A-36

Query Match 4.2%; Score 6; DB 2; Length 148;

Best Local Similarity 100.0%; Pred.No.1.5e+02; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 0;

QY 103 KLDRR 108

Db 107 KLDRR 112

RESULT 57

US-09-228-152-22

Sequence 22, Application US/09228152

Patent No. 6211341

GENERAL INFORMATION:

APPLICANT: Zeelon, Elisha P.

APPLICANT: Werber, Moshe M.

APPLICANT: Levanon, Avigdor

TITLE OF INVENTION: NOVEL POLYPEPTIDE HAVING FACTOR Xa INHIBITORY ACTIVITY

FILE REFERENCE: 430204ya

CURRENT APPLICATION NUMBER: US/09/228,152

CURRENT FILING DATE: 1999-01-11

NUMBER OF SEQ ID NOS: 25

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 22

LENGTH: 148

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Amino acid

OTHER INFORMATION: sequence of clone pSP65-Xa1-4.
US-09-228-152-22

Query Match 4.2%; Score 6; DB 3; Length 148;
Best Local Similarity 100.0%; Pred.No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 R1STFK 23
DB 135 R1STFK 140

RESULT 58
US-09-099-639-36

Sequence 36, Application US/09099639
Patent No. 6262237

GENERAL INFORMATION:

APPLICANT: Suzuki, Shintaro

TITLE OF INVENTION: Protocadherin Materials and Methods

NUMBER OF SEQUENCES: 115

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, &
STREET: 233 South Wacker, 6300 Sears Tower

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/099,639

FILING DATE: 18 JUN 1998

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/263,161

FILING DATE: 27 JUN 1994

ATTORNEY/AGENT INFORMATION:

NAME: Greta E. No. 6262237and

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 27865/34703

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/474-6300

TELEFAX: 312/474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 36:

SEQUENCE CHARACTERISTICS:

LENGTH: 148 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-099-639-36

Query Match 4.2%; Score 6; DB 3; Length 148;
Best Local Similarity 100.0%; Pred.No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 KLDRR 108
DB 107 KLDRR 112

RESULT 59

PCT-US93-12588-36

Sequence 36, Application PC/TUS9312588

GENERAL INFORMATION:

APPLICANT: Suzuki, Shintaro

TITLE OF INVENTION: Protocadherin Materials and Methods

NUMBER OF SEQUENCES: 107

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, &
ADDRESS: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/12588

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/998,003

FILING DATE: 29 DEC 1992

ATTORNEY/AGENT INFORMATION:

NAME: Noland, Greta E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 31811

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/474-6300

TELEFAX: 312/474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 36:

SEQUENCE CHARACTERISTICS:

LENGTH: 148 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US93-12588-36

Query Match 4.2%; Score 6; DB 5; Length 148;
Best Local Similarity 100.0%; Pred.No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 KLDRR 108
DB 107 KLDRR 112

RESULT 60

PCT-US95-08071-36

Sequence 36, Application PC/TUS9508071

GENERAL INFORMATION:

APPLICANT: Suzuki, Shintaro

TITLE OF INVENTION: Protocadherin Materials and Methods

NUMBER OF SEQUENCES: 115

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, &
STREET: 6300 Sears Tower, 233 S. Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/08071

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/12588

FILING DATE: 23 DEC 1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/998,003
FILING DATE: 29 DEC 1992
ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32149
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 148 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-08071-36

Query Match 4.2%; Score 6; DB 5; Length 148;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 KLDPR 108
Db 107 KLDPR 112

RESULT 61
US-08-226-264-26
Sequence 26, Application US/08226264
Patent No. 5801017
GENERAL INFORMATION:
APPLICANT: Weider, Moshe M.
APPLICANT: Zeelon, Elisha P.
APPLICANT: Levanon, Avigdor
APPLICANT: Guy, Rachel
APPLICANT: Goldusc, Arie
APPLICANT: Rigbi, Meir
APPLICANT: Panel, Amos
APPLICANT: Fischer, Meir
TITLE OF INVENTION: PRODUCTION OF RECOMBINANT FACTOR XA
TITLE OF INVENTION: INHIBITORS OF LEBCH HIRUDO MEDICINALIS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESSES:
ADDRESS: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/226,264
FILING DATE: 08-APR-94
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 4001-A/JPW/GJG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
TELEX:
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 153 amino acids
TYPE: amino acid
STRANDEDNESS: unknown

TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-226-264-26

Query Match 4.2%; Score 6; DB 1; Length 153;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 RISTFK 23
Db 140 RISTFK 145

RESULT 62
US-09-738-946-4
Sequence 4, Application US/09738946
Patent No. 6579701
GENERAL INFORMATION:
APPLICANT: EXELIXIS, INC.
TITLE OF INVENTION: DROSOPHILA HOMOLOGUES OF GENES AND PROTEINS IMPLICATED IN CANCER
TITLE OF INVENTION: METHODS OF USE
FILE REFERENCE: EX00-043C
CURRENT APPLICATION NUMBER: US/09/738,946
CURRENT FILING DATE: 2000-12-14
PRIOR APPLICATION NUMBER: 60/170,832
PRIOR FILING DATE: 1999-12-14
PRIOR APPLICATION NUMBER: 60/170,838
PRIOR FILING DATE: 1999-12-14
PRIOR APPLICATION NUMBER: 60/178,580
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/185,879
PRIOR FILING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: 60/185,880
PRIOR FILING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: 60/186,150
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 60/189,701
PRIOR FILING DATE: 2000-03-15
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Version 3.0
SEQ ID NO: 4
LENGTH: 153
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-738-946-4

Query Match 4.2%; Score 6; DB 4; Length 153;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 MAAEAF 43
Db 51 MAAEAF 56

RESULT 63
US-09-732-210-1644
Sequence 1644, Application US/09732210
Patent No. 6573361
GENERAL INFORMATION:
APPLICANT: Bunkers, Greg J.
APPLICANT: Liang, Jihong
APPLICANT: Mittenck, Cindy A.
APPLICANT: Seale, Jeffrey W.
APPLICANT: Wu, Yonnie S.
TITLE OF INVENTION: Anti-fungal Proteins and Methods for their Use
FILE REFERENCE: 38-21(15036)B
CURRENT APPLICATION NUMBER: US/09/732,210
CURRENT FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 60/169,513

PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: US 60/169,340
PRIOR FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 1753
SEQ ID NO 1644
LENGTH: 155
TYPE: PR
ORGANISM: Thermus aquaticus (subsp. thermophilus)
US-09-732-210-1644

Query Match 4.2%; Score 6; DB 4; Length 155;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 36 ERWAA 41
DB 141 ERWAA 146

RESULT 64
US-09-134-000C-4018
Sequence 4018, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patent in version 3.1
SEQ ID NO 4018
LENGTH: 163
TYPE: PR
ORGANISM: Enterococcus faecalis
US-09-134-000C-4018

Query Match 4.2%; Score 6; DB 4; Length 163;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 126 ERAKV 131
DB 84 ERAKV 89

RESULT 65
US-08-809-267-5
Sequence 5, Application US/08809267
Patent No. 5861296
GENERAL INFORMATION:
APPLICANT: LENNOX, Tricia L.
APPLICANT: SLATKO, Barton E.
APPLICANT: SEARS, Lauren E.
TITLE OF INVENTION: PURIFIED THERMOSTABLE INORGANIC
TITLE OF INVENTION: PYROPHOSPHATASE OBTAINABLE FROM THERMOCOCCUS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEW ENGLAND BIOLABS, INC.
STREET: 32 TOZER ROAD
CITY: BEVERLY
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 01915
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,267
FILING DATE: 12-MAR-1997
CLASSIFICATION: 433
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13662
FILING DATE:
APPLICATION NUMBER: US 08/329,721
FILING DATE: 25-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, GREGORY D.
REGISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: NEB-105-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 927-5054
TELEFAX: (508) 927-1705
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-809-267-5

Query Match 4.2%; Score 6; DB 2; Length 175;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 107 ERAKN 112
DB 170 ERAKN 175

RESULT 66
PCT-US95-13662A-5
Sequence 5, Application PC/TUS9513662A
GENERAL INFORMATION:
APPLICANT: LENNOX, Tricia L.
APPLICANT: SLATKO, Barton E.
APPLICANT: SEARS, Lauren E.
TITLE OF INVENTION: PURIFIED THERMOSTABLE INORGANIC
TITLE OF INVENTION: PYROPHOSPHATASE OBTAINABLE FROM THERMOCOCCUS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEW ENGLAND BIOLABS, INC.
STREET: 32 TOZER ROAD
CITY: BEVERLY
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 01915
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13662A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/329,721
FILING DATE: 25-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, GREGORY D.
REGISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: NEB-105-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 927-5054
TELEFAX: (508) 927-1705
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:

LENGTH: 175 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
PCT-US95-13662A-5

Query Match
Best Local Similarity 100.0%; Score 6; DB 5; Length 175;
Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 ERAKX 112
Db 170 ERAKX 175

RESULT 67
US-09-252-991A-16898
Sequence 16898, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252.991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 16898
LENGTH: 181
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16898

Query Match
Best Local Similarity 100.0%; Score 6; DB 4; Length 181;
Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 APTLP 8
Db 130 APTLP 135

RESULT 68
US-09-328-352-4216
Sequence 4216, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Berton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328.352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4216
LENGTH: 182
TYPE: PRT
ORGANISM: Acinetobacter baumannii
US-09-328-352-4216

Query Match
Best Local Similarity 100.0%; Score 6; DB 4; Length 182;
Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 ETLTG 100
Db 50 ETLTG 55

RESULT 69
US-09-107-532A-6802
Sequence 6802, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
CORRESPONDENCE ADDRESS: ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
ADDRESS: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354

COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107.532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneka
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 6802:
SEQUENCE CHARACTERISTICS:
LENGTH: 194 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...194
SEQUENCE DESCRIPTION: SEQ ID NO: 6802:

US-09-107-532A-6802

Query Match
Best Local Similarity 100.0%; Score 6; DB 4; Length 194;
Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 126 ETKKV 131
Db 119 ETKKV 124

RESULT 70
US-09-252-991A-16813
Sequence 16813, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252.991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 16813
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16813

Query Match 4.2%; Score 6; DB 4; Length 204;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FILPPA 9
Db 80 FILPPA 85

RESULT 71
US-09-328-352-6654
; Sequence 6654, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6654
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6654

Query Match 4.2%; Score 6; DB 4; Length 207;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 120 KKKKFE 125
Db 7 KKKKFE 12

RESULT 72
US-09-252-991A-32926
; Sequence 32926, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 32926
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; NAME/KEY: UNSURE
; LOCATION: (216)
; OTHER INFORMATION: Identity of amino acid at the above locations are unknown.
US-09-252-991A-32926

Query Match 4.2%; Score 6; DB 4; Length 248;

Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 RMAEAG 42
Db 147 RMAEAG 152

RESULT 73
US-09-252-991A-32676
; Sequence 32676, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 32676
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32676

Query Match 4.2%; Score 6; DB 4; Length 251;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 128 AKKVR 133
Db 106 AKKVR 111

RESULT 74
US-09-543-681A-6028
; Sequence 6028, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 6028
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-6028

Query Match 4.2%; Score 6; DB 4; Length 252;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 AKKXIA 114
Db 60 AKKXIA 65

RESULT 75
US-09-252-991A-17964
; Sequence 17964, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:

```

APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIORITY APPLICATION NUMBER: US 60/074,768
PRIORITY FILING DATE: 1998-02-18
PRIORITY APPLICATION NUMBER: US 60/094,190
PRIORITY FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 17964
LENGTH: 260
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17964

```

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Query Match Similarity 4.2% Score 6; DB 4; Length 260;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 PPAWOP 12
    |||||
Db 45 PPAWOP 50

```

Search completed: August 11, 2004, 14:26:02
Job time : 21 secs

Tue Aug 17 05:54:50 2004

us-09-690-825-34.oligo.rge

Page 1

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 16, 2004, 00:14:49 ; Search time 3668 Seconds
(without alignments)
1668.648 Million cell updates/sec

Title: US-09-690-825-34

Perfect score: 142
Sequence: 1 MGAPLTPKMPQPLKDHRLS.....EFFEPAKVRRAIRQLAAMD 142

Scoring table: OLIGO

Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 2167151695 residues

Word size: 1
Total number of hits satisfying chosen parameters: 6934737

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Command line parameters:

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-NOSM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
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Database:

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2: gb_hg: *
3: gb_in: *
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5: gb_ov: *
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7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_ses: *
12: gb_sy: *
13: gb_un: *
14: gb_vl: *
15: em_ba: *
16: em_fun: *
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19: em_mu: *
20: em_om: *
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22: em_ov: *
23: em_pat: *
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25: em_pl: *
26: em_ro: *
27: em_ses: *
28: em_un: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	142	100.0	426	6	AR184473 Sequence
2	142	100.0	426	6	BD167854 Survivin
3	142	100.0	426	6	BD185366 Survivin
4	142	100.0	1619	6	AR099347 Sequence
5	142	100.0	1619	6	BD273550 Antisense
6	142	100.0	1619	6	AR181635 Sequence
7	142	100.0	1619	6	AX775129 Sequence
8	142	100.0	1619	6	AX779941 Sequence
9	142	100.0	1629	9	AF077350 Homo sapi
10	142	100.0	1643	9	BC034148 Homo sapi
11	142	100.0	1653	9	BC008718 Homo sapi
12	107	75.4	1111	9	HUMMRNASBQ
13	107	75.4	1165	6	AR097642 Sequence
14	107	75.4	1165	6	AR154345 Sequence
15	106	74.6	1330	4	AB095108 Canis fam
16	93	65.5	740	6	AR270355 Sequence
17	76	53.5	399	6	AX86452 Sequence
18	76	53.5	399	6	BD026062 Sequence
19	74	52.1	600	9	AB028869 Homo sapi
20	73	51.4	1339	9	BC000784 Homo sapi
21	68	47.9	463	6	AX778483 Sequence
22	58	40.8	794	4	AP195781 Sus scrofa
23	41	28.9	924	10	AF077349 Mus muscu
24	41	28.9	955	6	AR181548 Sequence
25	41	28.9	955	6	AB013819 Mus muscu
26	41	28.9	3352	10	BC004702 Mus muscu
27	39	27.5	903	10	AF276775 Rattus no
28	39	27.5	14796	6	AR157507 Sequence
29	39	27.5	14796	6	AR181541 Sequence
30	39	27.5	14796	6	AX333491 Sequence
31	39	27.5	14796	6	AX334154 Sequence
32	39	27.5	14796	6	AX336483 Sequence
33	39	27.5	14796	6	AX410775 Sequence
34	39	27.5	14796	6	BD192864 Survivin
35	39	27.5	14796	6	HSU75285 Sequence
36	39	27.5	154840	2	AC032035 Homo sapien
37	39	27.5	209751	9	AC087645 Homo sapi
38	37	26.1	417	6	AR184472 Sequence
39	37	26.1	154840	2	AC032035 Homo sapi
40	37	26.1	229426	2	AC010532 Homo sapi
41	34	23.9	779	10	CRUCIRA
42	34	23.9	9263	10	AF077351 Mus muscu
43	34	23.9	10074	10	AB036741 Mus muscu
44	34	23.9	10919	10	AF115517 Mus muscu
45	34	23.9	197194	2	AL954690 Mus muscu
46	34	23.9	203336	10	AL591433 Mouse DNA
47	20	14.1	143111	2	AC143833 Macaca mu
48	19	13.4	138875	2	AC142802 Macaca mu
49	19	13.4	186874	2	AC142803 Macaca mu
50	15	10.6	229426	2	AC010532 Homo sapi

51	13	9.2	772	5	AY174765
52	13	9.2	207347	2	AC141438 Mus muscu
53	12	8.5	483	5	AF442492 Xenopus 1
54	12	8.5	483	5	AF442492 Xenopus 1
55	12	8.5	503	5	AF332051 Gallus ga
56	12	8.5	555	5	AF332051 Gallus ga
57	12	8.5	773	5	AF332051 Gallus ga
58	10	7.0	230800	10	AY100633 Xenopus 1
59	10	7.0	26342	2	ALB31742 Mouse DNA
60	9	6.3	30	6	AC109663 Rattus no
61	9	6.3	30	6	AX412099 Sequence
62	9	6.3	316	5	AX923830 Sequence
63	9	6.3	445	5	AF377322 Gallus ga
64	9	6.3	489	5	AF377322 Gallus ga
65	9	6.3	489	5	AF377322 Gallus ga
66	9	6.3	104435	9	AY057058 Dario rer
67	9	6.3	136470	2	AC107911 Homo sapi
68	9	6.3	146515	2	AC016292 Homo sapi
69	9	6.3	180849	2	AC145222 Medicago
70	9	6.3	184592	2	AC146981 Homo sapi
71	9	6.3	184717	9	AC009717 Homo sapi
72	9	6.3	188476	10	AC009717 Homo sapi
73	9	6.3	194837	10	AC122238 Homo sapi
74	9	6.3	199590	2	AC122238 Homo sapi
75	9	6.3	202366	2	ALB07066 Mus muscu
76	9	6.3	205117	2	ALB05939 Mus muscu
77	9	6.3	220069	10	AC124809 Mus muscu
78	9	6.3	226529	2	AT732470 Mouse DNA
79	9	6.3	228077	2	EX571968 Dario rer
80	9	6.3	240200	2	AC130552 Rattus no
81	9	6.3	261484	2	AC122075 Rattus no
82	9	6.3	323459	2	AC095477 Rattus no
83	8	5.6	26	6	AC119555 Rattus no
84	8	5.6	293	6	AR181551 Sequence
85	8	5.6	293	6	AR421862 Sequence
86	8	5.6	326	6	BD117415 EST and e
87	8	5.6	326	6	AR421901 Sequence
88	8	5.6	337	6	BD117454 EST and e
89	8	5.6	337	6	AR421887 Sequence
90	8	5.6	342	6	BD117440 EST and e
91	8	5.6	342	6	AR421870 Sequence
92	8	5.6	346	6	BD117423 EST and e
93	8	5.6	346	6	AR421946 Sequence
94	8	5.6	349	6	BD117499 EST and e
95	8	5.6	349	6	AR421878 Sequence
96	8	5.6	351	6	BD117431 EST and e
97	8	5.6	351	6	AR421923 Sequence
98	8	5.6	357	6	BD117476 EST and e
99	8	5.6	357	6	AR421910 Sequence
100	8	5.6	361	6	BD117463 EST and e
					AR421895 Sequence

ALIGNMENTS

RESULT 1
 AR184473
 LOCUS AR184473 426 bp DNA linear PAT 20-APR-2002
 DEFINITION Sequence 2 from patent US 6346389.
 ACCESSION AR184473
 VERSION AR184473.1 GI:20230438
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 426)
 AUTHORS Altherr,D.C.
 TITLE Method for selectively modulating the interactions between survivin
 and tubulin
 JOURNAL Patent: US 6346389-A 2 12-FEB-2002;
 FEATURES
 Location/Qualifiers
 1..426
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN		US-09-690-825-34 (1-142) x AR184473 (1-426)
Alignment Scores:		
Pred. No.:	2.1e-157	Length: 426
Score:	142.00	Matches: 142
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	100.00%	Indels: 0
DB:	6	Gaps: 0
US-09-690-825-34 (1-142) x AR184473 (1-426)		
QY	1	MetGlyAlaProThrIleuProProAlaITrGlnProPheLeuIysAspHisArgIleSer 20
DB	1	ATGGGTCGCCCGAGCGTTGCCCCCTGCTGCGAGCCCTTCTCAAGACCAACCCATCTCT 60
QY	21	ThrPheIysAsnTPRProPheLeuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 40
DB	61	ACATTCAGAACTGGCTCTTGGAGGCTGGCGCTGCAACCCCGAGCGGATGGCCGAG 120
QY	41	AlaGlyPheIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 60
DB	121	GCTGGCTTCATCCACCTGCCCTCCCTGAGAACGACCCAGCTGGCCCGAGTCTTCTTCTGC 180
QY	61	PheIleGluIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 80
DB	181	TTCAAGAGCTGAGAGGCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
QY	81	SerSerGlyCysAlaPheLeuSerValIleIleIleIleIleIleIleIleIleIleIleIleIle 100
DB	241	TCCGCGCGCTGGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 300
QY	101	PheLeuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 120
DB	301	TTTTTGAACTGACAG 360
QY	121	IleIleGluIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 140
DB	361	AAGAAAGATTTTAAAGAACTGCAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
QY	141	MetAsp 142
DB	421	ATGAGT 426
RESULT 2		
BD167854		
LOCUS BD167854 426 bp DNA linear PAT 17-JAN-2003		
DEFINITION Survivin-like polypeptide and its DNA.		
ACCESSION BD167854		
VERSION BD167854.1 GI:27873666		
KEYWORDS		
SOURCE Homo sapiens (human)		
ORGANISM Homo sapiens		
REFERENCE 1 (bases 1 to 426)		
AUTHORS Tanaka,H. and Kaieda,I.		
TITLE Survivin-like polypeptide and its DNA		
JOURNAL Patent: WO 0233071-A 6 25-APR-2002;		
TAKEDA CHEMICAL INDUSTRIES LTD,HIROSHI TANAKA,ISAO KAIEDA		
OS Homo sapiens (human)		
PN WO 0233071-A/6		
PD 25-APR-2002		
PF 16-OCT-2001 WO 2001JP009071		
PR 17-OCT-2000 JP 00P 316721,20-DEC-2000 JP 00P 366809 PI		
HIROSHI TANAKA,ISAO KAIEDA		
PC C12N15/09,C12N15/12,C07K14/47,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC		
10, C12P21/02,C07K16/18,C12Q1/02,C12Q1/68,G01N33/15,G01N33/50, PC		
A61K31/711, A61K38/17,A61K39/395,A61K48/00,A61P35/00,A61P43/00 CC		
Survivin-like polypeptide and its DNA		

FEATURES
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 Location/Qualifiers
 1..426
 /organism="Homo sapiens (human)"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

ORIGIN

Alignment Scores:
 Pred. No.: 2,1e-157 Length: 426
 Score: 142.00 Matches: 142
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-690-825-34 (1-142) x BD167854 (1-426)

QY 1 MetGLYAlaProThLeuProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
 Db 1 ATGGGTGCCCGACGTTGCGCCCTGCGTGGACGCTTTCTCAAGACCAACCGATCTCT 60
 QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
 Db 61 ACATTCAAGAACTGGCGCTTTCTTGGAGGCGCTGCGCTTCCACCCCGAGCGGATGCGCGAG 120
 QY 41 AlaGlyPheIleHisCysPProThrGlnLysGlnProAspLeuAlaGlnCysPhePheCys 60
 Db 121 GCTGGCTTCATCACTGACGCTCCCACTGAGAACGACGACCTGGCCCACTTTCTTCTGCG 180
 QY 61 PheLysGluLeuGluGlyTTPGluProAspAspProIleGluGluHisLysLysHis 80
 Db 181 TTCAGAGGAGCTGGAAGCTGGAGGCAATGACGACCCCATGAGGAAACATTAATAAACCAT 240
 QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
 Db 241 TGGTCGGGTGGCGCTTCTCTCTGTCAGAGACGCTTGAAGAAATTACCTTTGCTGGA 300
 QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
 Db 301 TTTTGAACCTGACGAGAGAAAGACCAAGAAATTCAGAAAGGAAACCAACAAATPAG 360
 QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAla 140
 Db 361 AAGAAAGANTTTGAGGAAACCTGCGAAGAAAGTGGCCCTGCGCATGAGCACTGCTGCC 420
 QY 141 MetAsp 142
 Db 421 ATGGAT 426

RESULT 3
 BD185366 426 bp DNA linear PAT 17-JUN-2003
 LOCUS Survivin-like polypeptide and its DNA.
 DEFINITION BD185366
 ACCESSION BD185366.1 GI:31877566
 VERSION JP 2002355062-A/6.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 426)

REFERENCE
 AUTHORS Tanaka,H. and Kaleda,I.
 TITLES Survivin-like polypeptide and its DNA
 JOURNAL Patent: JP 2002355062-A 6 10-DEC-2002;
 TAKEEDA CHEMICAL INDUSTRIES LTD
 OS Homo sapiens (human)
 PN JP 2002355062-A/6
 PD 10-DEC-2002
 PF 16-OCT-2001 JP 2001318533
 PI HIROSHI TANAKA, ISAO KALEDA

PC C12N15/09,A61K31/7088,A61K38/55,A61K39/395,A61K39/395,A61K46/00,A61P35/00,PC
 PC A61P43/00,A61P43/00,C07K14/82,C07K16/32,C12N1/15,C12N1/19,PC
 C12N1/21,
 PC C12N5/10,C12P21/02,C12Q1/02,C12Q1/68,G01N33/15,G01N33/50,PC
 G01N33/53,
 PC G01N33/53,G01N33/56,G01N33/574,C12N15/00,C12N5/00,A61K37/64
 CC Survivin-like polypeptide and its DNA
 FH key
 FT source
 FT source
 Location/Qualifiers
 1..426
 /organism="Homo sapiens (human)"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

ORIGIN

Alignment Scores:
 Pred. No.: 2,1e-157 Length: 426
 Score: 142.00 Matches: 142
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-690-825-34 (1-142) x BD185366 (1-426)

QY 1 MetGLYAlaProThLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
 Db 1 ATGGGTGCCCGACGTTGCGCCCTGCGTGGACGCTTTCTCAAGACCAACCGATCTCT 60
 QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
 Db 61 ACATTCAAGAACTGGCGCTTTCTTGGAGGCGCTGCGCTTCCACCCCGAGCGGATGCGCGAG 120
 QY 41 AlaGlyPheIleHisCysPProThrGlnLysGlnProAspLeuAlaGlnCysPhePheCys 60
 Db 121 GCTGGCTTCATCACTGACGCTCCCACTGAGAACGACGACCTGGCCCACTTTCTTCTGCG 180
 QY 61 PheLysGluLeuGluGlyTTPGluProAspAspProIleGluGluHisLysLysHis 80
 Db 181 TTCAGAGGAGCTGGAAGCTGGAGGCAATGACGACCCCATGAGGAAACATTAATAAACCAT 240
 QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
 Db 241 TGGTCGGGTGGCGCTTCTCTCTGTCAGAGACGCTTGAAGAAATTACCTTTGCTGGA 300
 QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
 Db 301 TTTTGAACCTGACGAGAGAAAGACCAAGAAATTCAGAAAGGAAACCAACAAATPAG 360
 QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAla 140
 Db 361 AAGAAAGANTTTGAGGAAACCTGCGAAGAAAGTGGCCCTGCGCATGAGCACTGCTGCC 420
 QY 141 MetAsp 142
 Db 421 ATGGAT 426

RESULT 4
 AR099347 1619 bp DNA linear PAT 14-FEB-2001
 LOCUS Sequence 1 from patent US 6077709.
 DEFINITION AR099347
 ACCESSION AR099347.1 GI:12809113
 VERSION AR099347.1
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.
 1 (bases 1 to 1619)
 REFERENCE
 AUTHORS Bennett,C.Frank,, Ackermann,E.J., Swayze,E.E. and Cowsett,L.M.
 TITLES Antisense modulation of Survivin expression

JOURNAL Patent: US 6077709-A 1-20-JUN-2000;
FEATURES Location/Qualifiers
source 1..1619
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:
Pred. No.: 7.81e-157 Length: 1619
Score: 142.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-690-825-34 (1-142) x AR099347 (1-1619)

QY 1 MetGlyAlaProThrLeuProProAlaATPGlnProPheLeuLysAspHisArgIleSer 20
Db 50 ATGGGTCCTCCGACGCTGGCCCTGCTGCGACGCTTTCTCAAGACACCGCATCTCT 109
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
Db 110 ACATTCAAGAACTGGCCCTTTCTTGAGGGCTGGCTGACCCCGAGGGATGGCCGAG 169
QY 41 AlaGlyPheLeuHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
Db 170 GCTGGCTTCACTACGACGCTGGCCCACTGAGAACGAGCAGACTGGCCAGTGTCTTCTGC 229
QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHisLysLysHis 80
Db 230 TTCAAGAGCTGGAAGCTGGGAGCGAGTACGACCCCATAGAGAACATTAAGAT 289
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluLeuThrLeuGlyGlu 100
Db 290 TCGTCCGCTTGGCTTCTTCTTCTGCAAGAGCGATTGAAGATTAACTTGGTGA 349
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120
Db 350 TTTTGAACCTGACAGAGAAAGAGCCAGAACAAATTGCAAGAAACCAACATTAAG 409
QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAlaAla 140
Db 410 AAGAAAGAAATTGAGAGAACTGCAAGAAAGTGGCCGTCATGACACACTGGCTGCC 469
QY 141 MetAsp 142
Db 470 ATGGAT 475

RESULT 5
BD273550 1619 bp DNA linear PAT 17-JUL-2003
LOCUS Antisense modulation of survivin expression.
DEFINITION BD273550
ACCESSION BD273550.1 GI:33083318
VERSION 1
KEYWORDS UP 2002539073-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1619)
REFERENCE
AUTHORS Bennett, F. C., Ackermann, E. J., Swazy, E. E. and Cowsett, L. M.
TITLE Antisense modulation of survivin expression
JOURNAL Patent: JP 2002539073-A 1 19-NOV-2002;
OS ISIS PHARMACEUTICALS INC
OS Homo sapiens (human)
PN JP 2002539073-A/1
PD 19-NOV-2002
PF 23-SEP-1999 JP 2000572239
PR 29-SEP-1998 US 09/163162, 05-APR-1999 US 09/286407 PI
FRANK C BENNETT, ELIZABETH J ACKERMANN, ERIC E SWAYZE, LEX M PI
COMSERT
PC C07H21/04, A61K31/7088, A61K31/712, A61K48/00, A61S35/00 CC

Antisense modulation of survivin expression
FH Key Location/Qualifiers
FT CDS (50)..(478).
source 1..1619
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN

Alignment Scores:
Pred. No.: 7.81e-157 Length: 1619
Score: 142.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-690-825-34 (1-142) x BD273550 (1-1619)

QY 1 MetGlyAlaProThrLeuProProAlaATPGlnProPheLeuLysAspHisArgIleSer 20
Db 50 ATGGGTCCTCCGACGCTGGCCCTGCTGCGACGCTTTCTCAAGACACCGCATCTCT 109
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
Db 110 ACATTCAAGAACTGGCCCTTTCTTGAGGGCTGGCTGACCCCGAGGGATGGCCGAG 169
QY 41 AlaGlyPheLeuHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
Db 170 GCTGGCTTCACTACGACGCTGGCCCACTGAGAACGAGCAGACTGGCCAGTGTCTTCTGC 229
QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHisLysLysHis 80
Db 230 TTCAAGAGCTGGAAGCTGGGAGCGAGTACGACCCCATAGAGAACATTAAGAT 289
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluLeuThrLeuGlyGlu 100
Db 290 TCGTCCGCTTGGCTTCTTCTTCTGCAAGAGCGATTGAAGATTAACTTGGTGA 349
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120
Db 350 TTTTGAACCTGACAGAGAAAGAGCCAGAACAAATTGCAAGAAACCAACATTAAG 409
QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAlaAla 140
Db 410 AAGAAAGAAATTGAGAGAACTGCAAGAAAGTGGCCGTCATGACACACTGGCTGCC 469
QY 141 MetAsp 142
Db 470 ATGGAT 475

RESULT 6
AR181635 1619 bp DNA linear PAT 20-APR-2002
LOCUS Sequence 97 from patent US 6335194.
DEFINITION AR181635
ACCESSION AR181635
VERSION 1
KEYWORDS AR181635.1 GI:20223849
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE
AUTHORS Bennett, F. C., Ackermann, E. J., Swazy, E. E. and Cowsett, L. M.
TITLE Antisense modulation of survivin expression
JOURNAL Patent: US 6335194-A 97 01-JAN-2002;
OS ISIS PHARMACEUTICALS INC
OS Homo sapiens (human)
PN JP 2002539073-A/1
PD 19-NOV-2002
PF 23-SEP-1999 JP 2000572239
PR 29-SEP-1998 US 09/163162, 05-APR-1999 US 09/286407 PI
FRANK C BENNETT, ELIZABETH J ACKERMANN, ERIC E SWAYZE, LEX M PI
COMSERT
PC C07H21/04, A61K31/7088, A61K31/712, A61K48/00, A61S35/00 CC

Alignment Scores:
Pred. No.: 7.81e-157 Length: 1619
Score: 142.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-690-825-34 (1-142) x BD273550 (1-1619)

QY 1 MetGlyAlaProThrLeuProProAlaATPGlnProPheLeuLysAspHisArgIleSer 20
Db 50 ATGGGTCCTCCGACGCTGGCCCTGCTGCGACGCTTTCTCAAGACACCGCATCTCT 109
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
Db 110 ACATTCAAGAACTGGCCCTTTCTTGAGGGCTGGCTGACCCCGAGGGATGGCCGAG 169
QY 41 AlaGlyPheLeuHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
Db 170 GCTGGCTTCACTACGACGCTGGCCCACTGAGAACGAGCAGACTGGCCAGTGTCTTCTGC 229
QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHisLysLysHis 80
Db 230 TTCAAGAGCTGGAAGCTGGGAGCGAGTACGACCCCATAGAGAACATTAAGAT 289
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluLeuThrLeuGlyGlu 100
Db 290 TCGTCCGCTTGGCTTCTTCTTCTGCAAGAGCGATTGAAGATTAACTTGGTGA 349
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120
Db 350 TTTTGAACCTGACAGAGAAAGAGCCAGAACAAATTGCAAGAAACCAACATTAAG 409
QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAlaAla 140
Db 410 AAGAAAGAAATTGAGAGAACTGCAAGAAAGTGGCCGTCATGACACACTGGCTGCC 469
QY 141 MetAsp 142
Db 470 ATGGAT 475

Pred. No.: 7.81e-157 Length: 1619
Score: 142.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-690-825-34 (1-142) x AR181635 (1-1619)

QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
Db 50 ATGGGTGCCCCGAGGTGGCCCCCTGGCGAGCCCTTCTCAAGAGCCACCGCATCTCT 109

QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
Db 110 ACATTCAAGAACTGGCCCTTCTTGAGGGCTGGCCCTGCACCCCGAGCGGATGGCCGAG 169

QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
Db 170 GCTGCTTCAATCCACTGCCCCACAGAGAGCCAGACTTGGCCCTGCTTCTCTGC 229

QY 61 PheLysGluLeuGluGlyTrpGluProAspAspAspProIleGluGluHis 80
Db 230 TTCAAGAGCTGGAAGCTGGAGCCAGATGACAGCCCATAGAGAACTATAAAGCAT 289

QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluLeuThrLeuGlyGlu 100
Db 290 TCGTCCGTTGCGCTTCTTCTCTGTCAGAGAGCATTTGAAGATTAACTTGGTGA 349

QY 101 PheLeuLysLeuAspArgGluThrAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
Db 350 TTTTGAAGACTGGACAGAGAAAGCCAGAAACAATTTGCAAGAGAAACCAATTAAG 409

QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAlaAla 140
Db 410 AAGAAAGAACTTTGAGAGAACTGCGAAGAAAGTGGCCGTCATCGAGCAGCTGCTGCC 469

QY 141 MetAsp 142
Db 470 ATGGAT 475

RESULT 7
LOCUS AX775129 1619 bp DNA linear PAT 09-JUL-2003
DEFINITION Sequence 445 from Patent WO03038129.
ACCESSION AX775129
VERSION AX775129.1 GI:32486645
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Raponi,M.
TITLE Methods for assessing and treating leukemia
JOURNAL Patent: WO 03038129-A 445 08-MAY-2003;
Ortho-Clinical Diagnostics, Inc. (US)
FEATURES
source 1..1619
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores: 7.81e-157 Length: 1619
Pred. No.: 142.00 Matches: 142
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
US-09-690-825-34 (1-142) x AX775129 (1-1619)

QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
Db 50 ATGGGTGCCCCGAGGTGGCCCCCTGGCGAGCCCTTCTCAAGAGCCACCGCATCTCT 109

QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
Db 110 ACATTCAAGAACTGGCCCTTCTTGAGGGCTGGCCCTGCACCCCGAGCGGATGGCCGAG 169

QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
Db 170 GCTGCTTCAATCCACTGCCCCACAGAGAGCCAGACTTGGCCCTGCTTCTCTGC 229

QY 61 PheLysGluLeuGluGlyTrpGluProAspAspAspProIleGluGluHis 80
Db 230 TTCAAGAGCTGGAAGCTGGAGCCAGATGACAGCCCATAGAGAACTATAAAGCAT 289

QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluLeuThrLeuGlyGlu 100
Db 290 TCGTCCGTTGCGCTTCTTCTCTGTCAGAGAGCATTTGAAGATTAACTTGGTGA 349

QY 101 PheLeuLysLeuAspArgGluThrAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
Db 350 TTTTGAAGACTGGACAGAGAAAGCCAGAAACAATTTGCAAGAGAAACCAATTAAG 409

QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAlaAla 140
Db 410 AAGAAAGAACTTTGAGAGAACTGCGAAGAAAGTGGCCGTCATCGAGCAGCTGCTGCC 469

QY 141 MetAsp 142
Db 470 ATGGAT 475

RESULT 8
LOCUS AX779941 1619 bp DNA linear PAT 14-JUL-2003
DEFINITION Sequence 2098 from Patent WO03039443.
ACCESSION AX779941
VERSION AX779941.1 GI:32696935
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Haeflrich,T., Schoch,C., Kern,W., Kohlmann,A., Schittiger,S.,
Dugas,M., Bils,R., Broze,B. and Wergenthaler,S.
TITLE Novel genetic markers for Leukemias
JOURNAL Patent: WO 03039443-A 2098 15-MAY-2003;
Deutsches Krebsforschungszentrum (DE);
Ludwig-Maximilian-Universitaet Muenchen
PD Dr. Dr. (DE); Schoch, Claudia (DE); Kern, Wolfgang (DE)

FEATURES
source 1..1619
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores: 7.81e-157 Length: 1619
Pred. No.: 142.00 Matches: 142
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
US-09-690-825-34 (1-142) x AX779941 (1-1619)

QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
Db 50 ATGGGTGCCCCGAGGTGGCCCCCTGGCGAGCCCTTCTCAAGAGCCACCGCATCTCT 109

QY 21 ThrPhelYsAsnTrpProPheLeuGluGlyCysAlaCysThrProGluuArgMetAlaGlu 40
 Db 110 ACATTCAAGAGACTGGCGCTTCTTGGAGGGCTCGGCTGACCCCGGAGGAGATGGCCAG 169
 QY 41 AlaGlyPheIleHisCysProThrGluuGluProAspLeuAlaGlnCysPhePheCys 60
 Db 170 GCTGGCTTCAATCCACTGCGCCCACTGGAACGAGCCAGATTGGCCAGGTTCTTCTGCG 229
 QY 61 PheYsGluLeuGluGluGlyTrpGluProAspAspAspProIleGluGluHisIleCysHis 80
 Db 230 TTCAAGAGAGCTGGAGAGCTGGAGAGCAGATGACGACCCCATAGAGAACTATAAAGCAT 289
 QY 81 SerSerGlyCysAlaPheLeuSerValIleYsYsGlnPheGluGluLeuThrLeuGlyGlu 100
 Db 290 TCGTCCGCTTGGCGCTTCTTCTGTCAGAAAGCAGTTTGAAGATTAACTTGTGTGA 349
 QY 101 PheLeuYsLeuAspArgGluuArgAlaYsAsnYsIleAlaYsGluThrAsnAsnYs 120
 Db 350 TTTTAAACTGGACAGAGAAAGCCAGAAACAAATTGCCAAGAAACCAACATATAG 409
 QY 121 LysYsGluPheGluGluGluThrAlaYsYsValArgArgAlaIleGluGluLeuAlaAla 140
 Db 410 AAGAAAGAAATTGAGAGAACTGCGAAGAAAGTCCCGCTGCATGACAGCTGGCTGCC 469
 QY 141 MetAsp 142
 Db 470 ATGGAT 475
 RESULT 9
 AF077350 1629 bp mRNA linear PRI 14-DEC-2000
 LOCUS Homo sapiens inhibitor of apoptosis homolog mRNA, complete cds.
 DEFINITION AF077350
 ACCESSION AF077350.1 GI:4959078
 VERSION
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1629)
 AUTHORS Uren,A.G., Wong,L., Pakusch,M., Fowler,K.J., Burrows,F.J.,
 Vaux,D.L. and Choo,K.H.
 TITLE Survival and the inner centromere protein INCENP show similar
 cell-cycle localization and gene knockout phenotype
 JOURNAL Curr. Biol. 10 (21), 1319-1328 (2000)
 MEDLINE 20538917
 PUBMED 11084331
 REFERENCE 2 (bases 1 to 1629)
 AUTHORS Uren,A.G. and Vaux,D.L.
 TITLE Direct Submision
 JOURNAL Submitted (02-OCT-1997) Molecular Cancer Division, The Walter and
 Eliza Hall Institute, Royal Parade, Parkville, Vic 3052, Australia
 FEATURES
 source location/Qualifiers
 1..1629
 /organism="Homo sapiens"
 /mol_type="mRNA"
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 /clone="IMAGE consortium clone ID 590560"
 /tissue_type="pancreatic adenocarcinoma"
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 /note="TAP; contains single baculovirus TAP repeat (BIR)
 motif"
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 /db_xref="GI:4959079"
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 HCPTENEPDLNOCFCFKELEGGMRPDDPIFEHKKSSGCAFYSVKQFELTGEPL
 KLDREKAKIAKETNNKKSEFEETAKKVRATLQLAAMD"
 ORIGIN
 Alignment Scores: 7.85e-157 Length: 1629
 Pred. No.:

Score: 142.00 Matches: 142
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0
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 QY 1 MetGlyAlaPheProThrPheProPheAlaTrpGlnProPheLeuYsAspHisArgIleSer 20
 Db 25 ATGGAGTCCCGAGCGTTGGCCCCCTGCTGCGACCCCTTCTCAAGAGACACCGCATCTT 84
 QY 21 ThrPhelYsAsnTrpProPheLeuGluGlyCysAlaCysThrProGluuArgMetAlaGlu 40
 Db 85 ACATTCAAGAGACTGGCGCTTCTTGGAGGGCTCGGCTGACCCCGGAGGAGATGGCCAG 144
 QY 41 AlaGlyPheIleHisCysProThrGluuGluProAspLeuAlaGlnCysPhePheCys 60
 Db 145 GCTGGCTTCAATCCACTGCGCCCACTGGAACGAGCCAGATTGGCCAGGTTCTTCTGCG 204
 QY 61 PheYsGluLeuGluGluGlyTrpGluProAspAspAspProIleGluGluHisIleCysHis 80
 Db 205 TTCAAGAGAGCTGGAGAGCTGGAGAGCAGATGACGACCCCATAGAGAACTATAAAGCAT 264
 QY 81 SerSerGlyCysAlaPheLeuSerValIleYsYsGlnPheGluGluLeuThrLeuGlyGlu 100
 Db 265 TCGTCCGCTTGGCGCTTCTTCTGTCAGAAAGCAGTTTGAAGATTAACTTGTGTGA 324
 QY 101 PheLeuYsLeuAspArgGluuArgAlaYsAsnYsIleAlaYsGluThrAsnAsnYs 120
 Db 325 TTTTAAACTGGACAGAGAAAGCCAGAAACAAATTGCCAAGAAACCAACATATAG 384
 QY 121 LysYsGluPheGluGluGluThrAlaYsYsValArgArgAlaIleGluGluLeuAlaAla 140
 Db 385 AAGAAAGAAATTGAGAGAACTGCGAAGAAAGTCCCGCTGCATGACAGCTGGCTGCC 444
 QY 141 MetAsp 142
 Db 445 ATGGAT 450
 RESULT 10
 BC034148 1643 bp mRNA linear PRI 12-NOV-2003
 LOCUS Homo sapiens baculoviral TAP repeat-containing 5 (survivin), mRNA
 DEFINITION BC034148
 ACCESSION BC034148
 VERSION BC034148.1 GI:21707886
 KEYWORDS MGC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1643)
 AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
 Klausner,R.D., Collins,F.S., Wagner,J., Shenmen,C.M., Schuler,G.D.,
 Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
 Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
 Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
 Stapleton,M., Soares,J.B., Bonaldi,M.F., Casavant,T.L.,
 Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Tosiyuki,S.,
 Carninci,F., Frange,C., Rana,S.S., Loquellano,N.A., Peters,G.J.,
 Abramson,R.D., Wuliany,S.J., Bosak,S.A., Meswan,P.J.,
 McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
 Morley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
 Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
 Fahey,J., Helton,E., Ketterman,M., Madan,A., Rodriguez,S.,
 Sanchez,A., Whitting,M., Madan,A., Young,A.C., Shechenko,Y.,
 Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
 Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
 Buetterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalins,D.E.,
 Scherch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
 TITLE Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 MEDLINE 22388257
 PUBMED 12477932
 REFERENCE 2 (bases 1 to 1643)
 AUTHORS Strausberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (02-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2550, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 COMMENT Contact: MGC help desk
 Email: cgaps-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: CLONTECH Laboratories, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www-shgc.stanford.edu>
 Contact: (Dickson, Mark) mcg@paxil.stanford.edu
 R. M. Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
 Series: IPAL Plate: 41 Row: h Column: 21.

FEATURES

SOURCE

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/db_xref="taxon:9606"

/clone="MGC:32768 IMAGE:4656567"

/tissue_type="Lung, mucopidermoid carcinoma"

/clone_id="NTH_MGC_59"

/lab_host="DH10B"

/note="Vector: pDNR-LIB"

1. 1643

/gene="BIRC5"

/note="synonyms: API4, SURVIVIN, EPR-1"

/db_xref="locusid:333"

/db_xref="WIM:603552"

45. 473

/codon_start=1

/product="baculoviral IAP repeat-containing protein 5"

/protein_id="AAH34148.1"

/db_xref="GI:21707887"

/db_xref="locusid:333"

/translation="MGAPLTPAMQPLKDHRISTPKMPLLEGCACTPERMAEAFI HCFTEHPDLAQCFPCFKELEGWEDDPIFEHKKSSGCAFLSKVQFELTIGFEL KUDREKANKAKETNNKKKEFEETAKKVRATIQDLAMD"

84. 305

/note="3IR; Region: Baculoviral inhibition of apoptosis protein repeat"

/db_xref="CDD:smat00238"

misc_feature

ORIGIN

Alignment Scores:

Pred. No.: 7,92e-157 Length: 1643
 Score: 142.00 Matches: 142
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-690-825-34 (1-142) x BC034148 (1-1643)

QY 1 MetGtYAlAPrOThrLeuPrOProAlATrPqInPrOphLeuLeuAspHisArgIleSer 20
 DB 45 ATGGGAGCCCGACGCTGGCCCTGGCTGGACGCTTTCTCAAGACACCGCATCTCT 104
 QY 21 ThrPhLeuAsnTrpPrOphLeuGluGlyCYsAlaCYsThPrGrgIuArgMetAlaGlu 40
 DB 105 ACATTCAGAAAGTGGCCCTTTGGAGGGCTGGCTGCACCCGAGCGGATGGCCGAG 164

QY 41 AlaGlyPheIleHisCYsProThrcIuAsnGluProAspLeuAlaGlnCYsPhePheCYs 60
 DB 165 GCTGGCTTCATTCATCTGCCCTCCACTGAGAACAGCCAGACTGGCCCACTGTTCTTCG 224
 QY 61 PheLYSGluLeuGluGlyTrpGluProAspAspProIleGluGlnHisLYsHis 80
 DB 225 TTCAGAGAGCTGAGAGCTGGGAGCCAGATGCGACCCCATAGAGAACATAAAAAGCAT 284
 QY 81 SerSerGlyCYsAlaPheLeuSerValLYsGlnPheGluGluLeuThrcIuGlyGlu 100
 DB 285 TCGTCGGTTCGCTTCCTTCCTTCCTCAAGAGCGATTGAGAAATTAACTTGTGTGA 344
 QY 101 PheLeuLYsLeuAspArgGluArgAlaLYsAsnLYsIleAlaLYsGluThrAsnAsnLYs 120
 DB 345 TTTTGAAGACTGACAGAGAAAGACCAAGAACAAATTGCAAGAGAACCAATTAAG 404
 QY 121 LYsLYSGluPheGluGluThrAlaLYsLYsValArgArgAlaIleGluGlnLeuAla 140
 DB 405 AAGAAAGAAATTGAGAGAACTGCGAAGAAAGTCCGCGCATGACGACGCTGCTGC 464
 QY 141 MetAsp 142
 DB 465 ATGGAT 470

RESULT 11

BC008718

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

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Db 983 TGACCCCGAGGAGGATGCGGCTTCATCCATGCCCCCACTGAGAACGACCA 924

Qy 53 AspleuAlaGlnCysPhePheCysPheLysGluLeuGluGlyTTPGluProAspAspAsp 72

Db 923 GACTGGCCCGAGGTTTCTTCTCTTCAGAGACTGGAAGCTGGAGCGAGATGACGAC 864

Qy 73 ProLleGluGluHisLysLysHisSerSerGlyCysAlaPheLeuSerValLysLysGln 92

Db 863 CCGATAGAGAACTATAAAGCATTCGTCGGCTTCCTTCTCTCTGCAAGAAAGCAG 804

Qy 93 PheGluGluLeuThrLeuGlyGluPheLeuLysLeuAspArgGluArgAlaLysAsnLys 112

Db 803 TTTCAGAAATTAACCTTGTGTAATTTTGAACCTGACAGAAAGAACGCAAGAAACAA 744

Qy 113 IleAlaLysGluThrAsnAsnLysLysLysGluPheGluGluThrAlaLysValArg 132

Db 743 ATTGCAAGAAACCAACATAGAACAAAGAAATTGAGAAACTGGAAGAAAGTGGCC 684

Qy 133 ArgAlaLleGluGlnLeuAla 139

Db 683 CGTCCATCGAGCGCTGGCC 663

RESULT 13

AR097642/c 1165 bp DNA linear PAT 14-FEB-2001

LOCUS Sequence 1 from patent US 6072028.

DEFINITION AR097642

ACCESSION AR097642

VERSION AR097642.1 GI:12806372

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1165)

AUTHORS Altieri,D.C.

TITLE EPR-1 proteins, polypeptides, and nucleic acid molecules encoding same

JOURNAL Patent: US 6072028-A 1 06-JUN-2000;

FEATURES

source

1..1165

/organism="Unknown"

/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.: 8,85e-116 Length: 1165

Score: 107.00 Matches: 138

Percent Similarity: 99.28% Conservative: 0

Best Local Similarity: 99.28% Mismatches: 1

Query Match: 75.35% Indels: 1

Gaps: 0

US-09-690-825-34 (1-142) x AR097642 (1-1165)

Qy 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgLleSer 20

Db 1114 ATGGTGCCCGAGCTTGCCCTGCTGGAGCCCTTCTCAAGAACCAACCGCATCTCT 1055

Qy 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40

Db 1054 ACATTCAAGAACTGGCCCTTCTTGAGAGGCTGGCG-TGCACCCCGAGCGGATGGCCAG 996

Qy 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60

Db 995 GGTGCTTCATCATGCCCCCACTGAGAACGACGACCTGGCCCACTGTTCTTCTGCG 936

Qy 61 PheLysGluLeuGluGlyTTPGluProAspAspAspProLleGluGluHisLysHis 80

Db 935 TTCAGAGAACTGGAAGCTGGAGCCAGATGACGCCCATAGAGAACTATAAAGCAT 876

Qy 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100

Db 875 TCGTCCGTTGCGCTTCTTCTCTGCAAGAACGATTTGAAGAAATTAACCTTGTGAA 816

Qy 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120

Db 815 TTTTGAAACTGACAGACAGAAAGAGCCCAAGAACAAATTTGCAAGAGAAACCAACATTAAG 756

Qy 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaLleGluGlnLeuAla 139

Db 755 AAGAAAGAAATTTAGAGAAACTGCGAAGAAAGTGGCCCTGCAATGACGACTGGCC 699

RESULT 14

AR154245/c 1165 bp DNA linear PAT 08-AUG-2001

LOCUS Sequence 1 from patent US 6238875.

DEFINITION AR154245

ACCESSION AR154245

VERSION AR154245.1 GI:15122298

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1165)

AUTHORS Altieri,D.C.

TITLE Diagnostic methods useful in the characterization of lymphoproliferative disease characterized by increased EPR-1

JOURNAL Patent: US 6238875-A 1 29-MAY-2001;

FEATURES

source

1..1165

/organism="Unknown"

/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.: 8,85e-116 Length: 1165

Score: 107.00 Matches: 138

Percent Similarity: 99.28% Conservative: 0

Best Local Similarity: 99.28% Mismatches: 1

Query Match: 75.35% Indels: 1

Gaps: 0

US-09-690-825-34 (1-142) x AR154245 (1-1165)

Qy 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgLleSer 20

Db 1114 ATGGTGCCCGAGCTTGCCCTGCTGGAGCCCTTCTCAAGAACCAACCGCATCTCT 1055

Qy 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40

Db 1054 ACATTCAAGAACTGGCCCTTCTTGAGAGGCTGGCG-TGCACCCCGAGCGGATGGCCAG 996

Qy 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60

Db 995 GGTGCTTCATCATGCCCCCACTGAGAACGACGACGACTTGGCCCACTGTTCTTCTGCG 936

Qy 61 PheLysGluLeuGluGlyTTPGluProAspAspAspProLleGluGluHisLysHis 80

Db 935 TTCAGAGAACTGGAAGCTGGAGCCAGATGACGCCCATAGAGAACTATAAAGCAT 876

Qy 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100

Db 875 TCGTCCGTTGCGCTTCTTCTCTGCAAGAACGATTTGAAGAAATTAACCTTGTGAA 816

Qy 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120

Db 815 TTTTGAAACTGACAGACAGAAAGAGCCCAAGAACAAATTTGCAAGAGAAACCAACATTAAG 756

Qy 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaLleGluGlnLeuAla 139

Db 755 AAGAAAGAAATTTAGAGAAACTGCGAAGAAAGTGGCCCTGCAATGACGACTGGCC 699

RESULT 15

AB095108 1630 bp mRNA linear MAM 27-NOV-2002

LOCUS AB095108

DEFINITION Canis familiaris mRNA for survivin, complete cds.

ACCESSION AB095108

VERSION AB095108.1 GI:124636590

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
5'UTR
CDS
3'UTR
ORIGIN
Alignment Scores:
Pred. No.:
Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
US-09-690-825-34 (1-142) x AB095108 (1-1630)
QY 1 MetGlyAlaProThleuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
DB 55 ATGGGTGCCCCGACGTCCTGCTGCGACGCCCTTTCAGAGACACCGCATCTCT 114
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGlu-ArGmetAlaG1 40
DB 115 ACATTCAAGAACTGGCCCTTCTTGAGGGCTGCGCTGCACCCGGA-CCGGATGGGAGA 173
QY 40 uLaaglyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCy 60
DB 174 GGCCGGCTTCATCCACTGTCACAGAGACGACAGCTGGCCGCTGTTCTCTG 233
QY 60 sPheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHisLysLysH1 80
DB 234 CTTCAAGAGAGCTGGAAGCTGGAGCCAGATGATACCTTATAGAGGACATTAATAACA 293
QY 80 sSerGerglyCysAlaPheLeuSerValLysLysGlnPheGluLeuThrLeuGlyG1 100
DB 294 TTCATCTGGTGTGCTTCTTCTTCTGTCAGAGAGAGTTTAAAGATTAACCTTGGTGA 353
QY 100 uPheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAlu 120
DB 354 ATTTTGAAGACTGGAAG 413
QY 120 sLysLysGluPheGluGluGluThrAlaLysValArgArgAlaIleGluGluLeuAla1 140
DB 414 GAAGAAGAGATTGAGAGAACTGCGAGAGAAAGTGGCGCTGCCATCGAGAGAGCTGCTGC 473

QY 140 aMetAsp 142
DB 474 CATCGAT 480
RESULT 16
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
ORIGIN
Alignment Scores:
Pred. No.:
Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
US-09-690-825-34 (1-142) x AR270355 (1-740)
QY 12 ProPheLeuLysAspHisArgIleSerThrPheLysAsnTrpProPheLeuGluGlyCys 31
DB 51 CCTTTCTCAAGAGACACCGCATCTTCAATTCAGAACTGGCCCTTCTTGAGGGCTGC 110
QY 32 AlaCysThrProGluArgMetAlaGluAlaGlyPheIleHisCysProThrGlu-AsnG1 51
DB 111 GCCTGACACCCCGAGGAGATGGCCGAGGCTGCTTCATCTGCTGCTGCTGCTGCTG 169
QY 51 uProAspLeuAlaGlnCysPhePheCysPheLysGluLeuGluGlyTrpGluProAspAs 71
DB 170 GCCAGACTGGCCCATGTGTTCTTCTGCTTCAAGAGCTGGAAGCTGGAGACCGATGA 229
QY 71 pAspProIleGluGluHisLysLysHisSerGerglyCysAlaPheLeuSerValLysL 91
DB 230 CGACCCCATAG 289
QY 91 sGlnPheGluGluLeuThrLeuGlyGluPheLeuLysLeuAspArgGluArgAlaLysAs 111
DB 290 GCAGTTTGAAGATTTTACCTTGGTGATTTTGAAGCTGAGACAGAGAGAGAGAGAG 349
QY 111 nLysIleAlaLysGluThrAsnAsnLysLysLysGluPheGluGluThrAlaLysLysVa 131
DB 350 CAAATTTGCAAG 409
QY 131 lArgArgAlaIleGluGlnLeuAlaMetFsp 142
DB 410 GCGCGTGCATCGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 443
RESULT 17
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1
AUTHORS Dumas Milne Edwards, J.B., Duclert, A. and Giordano, J.Y.
TITLE Expressed sequence tags and encoded human proteins
JOURNAL Patent: EP 1033401-A 2315 06-SEP-2000;
Genet (FR)
FEATURES
source Location/Qualifiers
1..399
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
52..399
/note="unassigned protein product"
CDS
/codon_start=1
/protein_id="CA00590.1"
/db_xref="GI:40043628"
/translation="MGAPLTPAMQPLKDHRIKTPKMPLEGCACTEPNAAGPI
HPTENPDIAOCFPCFKELEWEPDDDDPIEEKKHSKSGCAFLSVKQFEELTIGFEL
KLDREKRNKRIAKE"
ORIGIN
Alignment Scores:
Pred. No.: 9,46e-80 Length: 399
Score: 76.00 Matches: 115
Percent Similarity: 98.29% Conservative: 0
Best Local Similarity: 98.29% Mismatches: 1
Query Match: 53.52% Indels: 2
Gaps: 0
US-09-690-825-34 (1-142) x AX886452 (1-399)
QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
DB 52 ATGGGTCGCCGACGCTTCCCTCCCTGCGACGCTTCTTCAAGACACCGCATCTCT 111
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 112 ACATTCAAGAACTGGCCCTTCTTGAGAGGCTGCGCCCTGCAACCCGAGCGGATGCGCAG 171
QY 41 AlaGlyPheIleHisCysProThrGluLysGlnProAspLeuAlaGlnCysPhePheCys 60
DB 172 GCTGCTTCATCCATCCGACCTGAGACGACGACGACCTGCGCCGCTGTTCTTCTGC 231
QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHis-LysLysHis 80
DB 232 TTCAAGAGAGCTGGAGAGCTGGAGACGATGACGACCCCATAGAGAGAA-TAAAAAGCA 290
QY 80 sSerSerGlyCysAlaPheLeuSerValLysGlnPheGluGluLeuThrLeuGlyGlu 100
DB 291 TTCGTCGCGTGGCGCTTCTTCTGTSAGAGAGAGTTGAGAGATTACGCTTGTA 350
QY 100 uPheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGlu 116
DB 351 ATTTTGAACCTGACAGAGAAAGGCCAAGAACAAATTGCAAGGAA 399
RESULT 18
LOCUS BD026062 399 bp DNA linear FAT 27-AUG-2002
DEFINITION Sequence tag and encoded human protein.
ACCESSION BD026062
VERSION BD026062.1 GI:22567285
KEYWORDS UP 2001269182-A/2308
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS Edwards, J.B.D.M., Duclair, E. and Jordan, J.Y.
TITLE Sequence tag and encoded human protein
JOURNAL Patent: JP 2001269182-A 2308 02-OCT-2001;
GENSET
COMMENT OS Homo sapiens (human)
PN JP 2001269182-A/2308
PD 02-OCT-2001

PF 24-FEB-2000 JP 2000118772
PR 26-FEB-1999 US 60/122487
PI JEAN BARDETIST DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
PJ JORDAN
PC C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC
C12N5/10,
PC C12P21/02, C12P21/08, C12Q1/68//G06F17/30, C12N15/00, C12N5/00, PC
G06F15/40
FEATURES
source Location/Qualifiers
FT CDS
1..399
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 9,46e-80 Length: 399
Score: 76.00 Matches: 115
Percent Similarity: 98.29% Conservative: 0
Best Local Similarity: 98.29% Mismatches: 1
Query Match: 53.52% Indels: 2
Gaps: 0
US-09-690-825-34 (1-142) x BD026062 (1-399)
QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
DB 52 ATGGGTCGCCGACGCTTCCCTCCCTGCGACGCTTCTTCAAGACACCGCATCTCT 111
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 112 ACATTCAAGAACTGGCCCTTCTTGAGAGGCTGCGCCCTGCAACCCGAGCGGATGCGCAG 171
QY 41 AlaGlyPheIleHisCysProThrGluLysGlnProAspLeuAlaGlnCysPhePheCys 60
DB 172 GCTGCTTCATCCATCCGACCTGAGACGACGACGACCTGCGCCGCTGTTCTTCTGC 231
QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHis-LysLysHis 80
DB 232 TTCAAGAGAGCTGGAGAGCTGGAGACGATGACGACCCCATAGAGAGAA-TAAAAAGCA 290
QY 80 sSerSerGlyCysAlaPheLeuSerValLysGlnPheGluGluLeuThrLeuGlyGlu 100
DB 291 TTCGTCGCGTGGCGCTTCTTCTGTSAGAGAGAGTTGAGAGATTACGCTTGTA 350
QY 100 uPheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGlu 116
DB 351 ATTTTGAACCTGACAGAGAAAGGCCAAGAACAAATTGCAAGGAA 399
RESULT 19
LOCUS AB028869 600 bp mRNA linear PRI 04-APR-2000
DEFINITION Homo sapiens mRNA for survivin-beta, complete cds.
ACCESSION AB028869
VERSION AB028869.1 GI:7416052
KEYWORDS survivin-beta.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS Kageyama, H., Islam, A., Takayasu, H. and Nakagawara, A.
TITLE An isoform of Survivin (Survivin-beta) which has 23 Amino Acids
JOURNAL Insertion into the BIR Domain
Unpublished
AUTHORS Kageyama, H., Islam, A. and Nakagawara, A.
REFERENCE Direct Submission
Submitted (11-JUN-1999) Akira Nakagawara, Chiba Cancer Center
Research Institute, Division of Biochemistry, 666-2 Nipona,

Chuch-Ku, Chiba, China 260-8717, Japan
E-mail: akiranak@chiba-cs.pref.chiba.jp,
Tel: 81-43-264-5431 (ex. 5201), Fax: 81-43-265-4459)
Location/Qualifiers

FEATURES

1..600

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/cell_line="CHP134"

/cell_type="neuroblastoma"

27..524

/codon_start=1

/product="survivin-beta"

/protein_id="BAA93676.1"

/db_xref="GI:7416053"

/translation="MSAPTLPPAPQPFLLKDRISTFQKWPPIEGCCTPERMAAGFI

HCPTENEPDLAQCFCEKELEGMEPPDDPIGGTVAACNTSTGGRGRTTRESHK

HSSGCAFLSVKKQFELTLGEPLKIDREKAKKIKETNNKKKEFEETAKXVRAIEQ

LAAMD"

CDS

/product="survivin-beta"

/protein_id="BAA93676.1"

/db_xref="GI:7416053"

/translation="MSAPTLPPAPQPFLLKDRISTFQKWPPIEGCCTPERMAAGFI

HCPTENEPDLAQCFCEKELEGMEPPDDPIGGTVAACNTSTGGRGRTTRESHK

HSSGCAFLSVKKQFELTLGEPLKIDREKAKKIKETNNKKKEFEETAKXVRAIEQ

LAAMD"

ORIGIN

Alignment Scores:

Pred. No.: 3,198-77 Length: 600
Score: 74.00 Matches: 74
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 52.11% Indels: 0
Gaps: 0

US-09-690-825-34 (1-142) x ABD28869 (1-600)

QY 1 MetGlyAlaProThrIleuProProAlaTTPGlnProPheLeuLysAspHisArgIleSer 20

Db 27 ATGGGTCGCCCGACGCTGGCCCTGCTGGACGCCCTTCTCAAGACACACCGCATCTCT 86

QY 21 ThrPheLysAsnTTPProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaIle 40

Db 87 ACATTAAAGAACTGGCCCTTCTTGGAGGCGCTGCGCTTCCACCCGACCGATGGCCAG 146

QY 41 AlaGlyPheIleHisCysProThrGluGlnGluProAspLeuAlaGlnCysPhePheCys 60

Db 147 GCTGGCTTATCATCATCGCCCACTGAGAACGAGCCAGCTTGGCCCACTGTTCTTCTG 206

QY 61 PheLysGluLeuGluGluGlyTTPGluProAspAspProIle 74

Db 207 TTCAGGAGCTGGAAGGCTGGAGGACGATGACGACCCCAT 248

RESULT 20

LOCUS BC000784 1539 bp mRNA linear PRI 16-SEP-2003

DEFINITION Homo sapiens baculoviral IAP repeat-containing 5 (survivin), mRNA

ACCESSION BC000784

VERSION BC000784.2 GI:34783885

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 1539)

Strausberg, R. L., Feingold, E. A., Grouse, L. H., Derge, J. G.,

Klauser, R. D., Collins, F. S., Wagner, J., Shenmen, C. M., Schuler, G. D.,

Altschul, S. F., Zeeberg, B., Buetow, K. H., Schaefer, C. F., Bhat, N. K.,

Hopkins, R. F., Jordan, H., Moore, T., Max, S. I., Wang, J., Heien, F.,

Diachenko, L., Marusina, K., Farmer, A. A., Rubin, G. M., Hong, L.,

Stapleton, M., Soares, M. B., Bonaldo, M. F., Casavant, T. L.,

Scheetz, T. E., Brownstein, M. J., Uedl, T. B., Toshiyuki, S.,

Carinini, P., Prange, C., Rana, S. S., Loguigliano, N. A., Peters, G. J.,

Abramsen, R. D., Mullaly, S. J., Bosak, S. A., McEwan, P. J.,

McKernan, R. J., Malek, J. A., Gunaratne, P. H., Richards, S.,

Worley, K. C., Hale, S., Garcia, A. M., Gay, L. J., Hulyk, S. M.,

Villalobon, D. K., Muzny, D. M., Sodergren, E. J., Lu, X., Gibbs, R. A.,

Fahney, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,

TITLE

JOURNAL

MEDLINE

PUBMED

AUTHORS

JOURNAL

REMARK

COMMENT

FEATURES

source

1..1539

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:3506845"

/tissue_type="Kidney, renal cell adenocarcinoma"

/clone_id="NH_MGC_14"

/lab_host="DH10B-R"

/note="Vector: pOTB7"

Alignment Scores:

Pred. No.: 1,218-75 Length: 1539
Score: 73.00 Matches: 73
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 51.41% Indels: 0
Gaps: 0

US-09-690-825-34 (1-142) x BC000784 (1-1539)

QY 1 MetGlyAlaProThrIleuProProAlaTTPGlnProPheLeuLysAspHisArgIleSer 20

Db 46 ATGGGTCGCCCGACGCTGGCCCTGCTGGACGCCCTTCTCAAGACACACCGCATCTCT 105

QY 21 ThrPheLysAsnTTPProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaIle 40

Db 106 ACATTAAAGAACTGGCCCTTCTTGGAGGCGCTGCGCTGACCCCGAGCGATGGCCAG 165

QY 41 AlaGlyPheIleHisCysProThrGluGlnGluProAspLeuAlaGlnCysPhePheCys 60

Db 166 GCTGGCTTATCATCATCGCCCACTGAGAACGAGCCAGCTTGGCCCACTGTTCTTCTG 225

QY 61 PheLysGluLeuGluGluGlyTTPGluProAspAspProIle 73

Db 226 TTCAGGAGCTGGAAGGCTGGAGGACGATGACGACCC 264

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Series: IRAP Plate: 7 Row: C Column: 10
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4502144.

Location/Qualifiers

1..1539

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:3506845"

/tissue_type="Kidney, renal cell adenocarcinoma"

/clone_id="NH_MGC_14"

/lab_host="DH10B-R"

/note="Vector: pOTB7"

Sanchez, A., Whiting, M., Madan, A., Young, A. C., Shevchenko, Y.,
Boutfield, G., Blakesley, R. W., Touchman, D. W., Green, E. D.,
Dickson, M. C., Rodriguez, A. C., Greenwood, J., Schmutz, J., Myers, R. M.,
Butterfield, Y. S., Krzyzanski, M. I., Skalska, U., Smalys, D. E.,
Schmerch, A., Schein, J. E., Jones, S. J., and Marra, M. A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

2 (bases 1 to 1539)

Strausberg, R.

Direct Submission

Submitted (15-NOV-2000) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

NH-MGC Project URL: <http://mgc.nci.nih.gov>
On Sep 16, 2003 this sequence version replaced gi:12653976.

Contact: MGC help desk

Email: cgabs-remail.nih.gov

Tissue Procurement: DCTD/DRP

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Institute for Systems Biology

<http://www.systemsbio.org>

Contact: madan@systemsbiology.org

Anup Madan, Jessica Fahney, Erin Helton, Mark Kettelman, Anuradha
Madan, Stephanie Rodriguez, Amy Sanchez and Michelle Whiting

RESULT 21
 AX778483 463 bp DNA linear PAT 14-JUL-2003
 LOCUS AX778483
 DEFINITION Sequence 640 from Patent WO03039443.
 ACCESSION AX778483
 VERSION AX778483.1 GI:32695477
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 AUTHORS Haferlach, T.; Schoch, C., Kern, W., Kohlmann, A., Schmittger, S.,
 Dugas, M., Ellis, R., Brors, B. and Mergenthaler, S.
 TITLE Novel genetic markers for leukemias
 JOURNAL Patent: WO 03039443-A 640 15-MAY-2003;
 Deutsches Krebsforschungszentrum (DE);
 Ludwig-Maximilian-Universitaet Muenchen (DE); Haferlach, Torsten,
 PD Dr. Dr. (DE); Schoch, Claudia (DE); Kern, Wolfgang (DE)
 FEATURES
 source Location/Qualifiers
 1..463
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
 ORIGIN
 Alignment Scores:
 Pred. No.: 2,85e-70 Length: 463
 Score: 68.00 Matches: 68
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 47.89% Indels: 0
 Gaps: 0
 DB: 6
 US-09-690-825-34 (1-142) x AX778483 (1-463)
 QY 75 GIUIGUHSLSYLSVSHSSESESCLYCYSAIAPHLEUSESEVALVLSYLSGIPHEGLU 94
 DB 245 GAGGAACATTAAGAACATTCCTCCGCTTCGCTTCCTTCCTTCGACAGACATTTTGA 304
 QY 95 GIULEUTHRLLEUGLYGIPHELEULYSLEUSPARGIUAARGAIALYSASNIYSIEII 114
 DB 305 GAATTAACCCCTTGCGAATTTTGAACCTGGACAGAGAAAGCCAGAACAAATTTGCA 364
 QY 115 LYSGLUUTTAASAAATLSYLSYLSYLSGIPHEGLUUTTRIALYLSVVAIARXGALA 134
 DB 365 AAGGAACCAACAAATTAAGAGAAAGATTGTGAGAACTGGAGAAAGTGGCGCGTGC 424
 QY 135 ILEGUINLEUALAIAIAMEKASP 142
 DB 425 ATCGAGCAGCTGCTGCCTCATGAT 448
 RESULT 22
 AF195781 794 bp mRNA linear MAM 07-SEP-2001
 LOCUS AF195781
 DEFINITION Sus scrofa apoptosis inhibitor survivin mRNA, complete cds.
 ACCESSION AF195781
 VERSION AF195781.1 GI:10443627
 KEYWORDS
 SOURCE Sus scrofa (pig)
 ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE
 AUTHORS Citera, S. and Fredholm, M.
 TITLE Isolation and mapping the pig homologs survivin (BIRC5) and
 effector cell protease receptor 1 (EPR1) genes
 JOURNAL Cytogenet. Cell Genet. 92 (3-4), 351-352 (2001)
 MEDLINE 21328903
 PUBMED 11435714
 REFERENCES 2 (bases 1 to 794)
 AUTHORS Citera, S. and Fredholm, M.
 TITLE Direct Submission

JOURNAL Submitted (18-OCT-1999) Animal Science and Animal Health, The Royal
 Veterinary and Agricultural University, Copenhagen, Denmark
 Frederiksberg C. 1870, Denmark
 FEATURES
 source Location/Qualifiers
 1..794
 /organism="Sus scrofa"
 /mol_type="mRNA"
 /db_xref="taxon:9823"
 /chromosome="12"
 /map="12q11-q15; ETR-1 encoded by complement strand"
 6..434
 /note="contains 1 BIR and 1 COOH-terminus coiled domain"
 /codon_start=1
 /product="apoptosis inhibitor survivin"
 /protein_id="AA01540.1"
 /db_xref="GI:10443628"
 /translation="MSAPSLPPAWQIYKDHRISTFKNMPFLGCACTPERMAAGFI
 HPTNEPDLACFCFPELEGEEDDDPIEHHKSGSCAFISVKQFESLTSEFL
 KDKERAKVKIAKETNNKQKEFEETAKVRCALGGLAASE"
 ORIGIN
 Alignment Scores:
 Pred. No.: 2,86e-58 Length: 794
 Score: 58.00 Matches: 58
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 40.85% Indels: 0
 Gaps: 0
 DB: 4
 US-09-690-825-34 (1-142) x AF195781 (1-794)
 QY 41 AIAAGIYPhelIshiscySProthrguAEngluProaspLeuAlaGInCysPhePheCys 60
 DB 126 GCCGTTTATCCACGCTGCCACTGAGAACGAGCCGATTTGGCTCAAGTTCTTCTGCC 185
 QY 61 PhelyGluLeuGluGlyTTPGluProaspPaspPricIleGluGluHisIshis 80
 DB 186 TTCAAAGAGCTGGAAGCTGGGAGCCAGACGAGACCCCATAGAAACATAAAAAGCAT 245
 QY 81 SerserGlyCYSAIAPHLEUSESEVALVLSYLSGIPHEGLUUTTRIALYLSVVAIARXGALA 134
 DB 246 TCATCCGTTGCTGCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTC 299
 RESULT 23
 AF077349 924 bp mRNA linear ROD 14-DEC-2000
 LOCUS AF077349
 DEFINITION Mus musculus inhibitor of apoptosis homolog mRNA, complete cds.
 ACCESSION AF077349
 VERSION AF077349.1 GI:4959076
 KEYWORDS
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE
 AUTHORS Dren, A.G., Wong, L., Pakusch, M., Fowler, K.J., Burrows, F.J.,
 Vaux, D.L. and Choo, K.H.
 TITLE Survivin and the inner centromere protein INCENP show similar
 cell-cycle localization and gene knockout phenotype
 JOURNAL Curr. Biol. 10 (21), 1319-1328 (2000)
 MEDLINE 20538917
 PUBMED 11084331
 REFERENCES 2 (bases 1 to 924)
 AUTHORS Dren, A.G. and Vaux, D.L.
 TITLE Direct Submission
 JOURNAL Submitted (10-SEP-1997) Molecular Cancer Division, The Walter and
 Eliza Hall Institute, Royal Parade, Parkville, Vic 3052, Australia
 FEATURES
 source Location/Qualifiers
 1..924
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="IWAGE Consortium Clone ID 422303"

CDS
/dev_stage="embryo; E13.5 - E14.5"
16..438
/note="IAP; contains single baculovirus IAP repeat (BIR)
motif"
/codon_start=1
/product="inhibitor of apoptosis homolog"
/protein_id="AAD34225.1"
/db_xref="GI:4959077"
/translation="MGAPALPOLIOLYLNRYIAFKWMPLEDCATPERMAAGFI
HCPTEHPDLAOCFFCFKELBEMEDDNIIEHRKHSPGCAFLTYKKOMBELTVSEFL
KIDROPARKKIATKNTNNKKEFEETAKTTRQSI EQLAA"

ORIGIN
Alignment Scores:
Pred. No.: 3,39e-38 Length: 924
Score: 41.00 Matches: 41
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 28.87% Indels: 0
DB: 10 Gaps: 0

US-09-690-825-34 (1-142) x AF077349 (1-924)

QY 31 Cy5A1Cy5ThPrGluArgMetAlaGluAlaGlyPheIleHisCy5ProThGluAsn 50
Db 106 TGGCGCTGCACCCAGAGGAATGGCGAGGCTGCTTCATCCACTGCCCTACCGAGAAC 165

QY 51 GluProAspLeuAlaGlnCy5PhePheCy5PheGlyGluLeuGluGlyTyrGluProAsp 70
Db 166 GAGCCGATTGGCCCAAGTGTTCCTTAAAGAAATGGAAAGCTGGGAACCCGAT 225

QY 71 Asp 71
Db 226 GAC 228

RESULT 24
AR181548
LOCUS AR181548 955 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 10 from patent US 6335194.
ACCESSION AR181548
VERSION AR181548.1 GI:20223762
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 955)
AUTHORS Bennett,C.,Frank., Ackermann,E.C., Swayze,E.E. and Cowsett,T.M.
TITLE Antisense modulation of survivin expression
JOURNAL Patent: US 6335194-A 10 01-JAN-2002;
FEATURES
source 1..955
Location/Qualifiers
/organism="Unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.: 3.5e-38 Length: 955
Score: 41.00 Matches: 41
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 28.87% Indels: 0
DB: 6 Gaps: 0

US-09-690-825-34 (1-142) x AR181548 (1-955)

QY 31 Cy5A1Cy5ThPrGluArgMetAlaGluAlaGlyPheIleHisCy5ProThGluAsn 50
Db 199 TGGCGCTGCACCCAGAGGAATGGCGAGGCTGCTTCATCCACTGCCCTACCGAGAAC 258

QY 51 GluProAspLeuAlaGlnCy5PhePheCy5PheGlyGluLeuGluGlyTyrGluProAsp 70
Db 259 GAGCCGATTGGCCCAAGTGTTCCTTAAAGAAATGGAAAGCTGGGAACCCGAT 318

QY 71 Asp 71
Db 319 GAC 321

RESULT 25
AB013819 955 bp mRNA linear ROD 25-FEB-1999
LOCUS AB013819
DEFINITION Mus musculus mRNA for TIAP, complete cds.
ACCESSION AB013819
VERSION AB013819.1 GI:3135206
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (sites)
AUTHORS Kobayashi,K., Hatano,M., Otaki,M., Ogasawara,T. and Tokuhisa,T.
TITLE Expression of a murine homologue of the inhibitor of apoptosis
protein is related to cell proliferation
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (4), 1457-1462 (1999)
MEDLINE 99145571
PubMed 9990045

REFERENCE 2 (bases 1 to 955)
AUTHORS Kobayashi,K., Otaki,M., Ogasawara,T. and Tokuhisa,T.
TITLE Direct Submission
JOURNAL Submitted (11-MAY-1998) Koichi Kobayashi, Chiba University Graduate
School of Medicine, Department of Developmental Genetics; Inohana
1-8-1, Chuo-ku, Chiba 260-8670, Japan
[E-mail:kobayashi@devgenol.m.chiba-u.ac.jp, Tel:81-43-226-2182]
COMMENT
Sequence updated (15-May-1998).
FEATURES
source 1..955
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/tissue_type="embryo"
/dev_stage="day16"
1..955
/gene="tiap"
/gene="tiap"
109..531
/note="IAP repeat"
/codon_start=1
/product="TIAP"
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/db_xref="GI:3135207"
/translation="MGAPALPOLIOLYLNRYIAFKWMPLEDCATPERMAAGFI
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KIDROPARKKIATKNTNNKKEFEETAKTTRQSI EQLAA"

ORIGIN
Alignment Scores:
Pred. No.: 3.5e-38 Length: 955
Score: 41.00 Matches: 41
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 28.87% Indels: 0
DB: 10 Gaps: 0

US-09-690-825-34 (1-142) x AB013819 (1-955)

QY 31 Cy5A1Cy5ThPrGluArgMetAlaGluAlaGlyPheIleHisCy5ProThGluAsn 50
Db 199 TGGCGCTGCACCCAGAGGAATGGCGAGGCTGCTTCATCCACTGCCCTACCGAGAAC 258

QY 51 GluProAspLeuAlaGlnCy5PhePheCy5PheGlyGluLeuGluGlyTyrGluProAsp 70
Db 259 GAGCCGATTGGCCCAAGTGTTCCTTAAAGAAATGGAAAGCTGGGAACCCGAT 318

QY 71 Asp 71
Db 319 GAC 321

RESULT 26
LOCUS BC004702 3352 bp mRNA linear ROD 03-OCT-2003
DEFINITION Mus musculus baculoviral IAP repeat-containing 5, mRNA (cDNA clone
MGC:5790 IMAGE:3499203), complete cds.
ACCESSION BC004702
VERSION BC004702.1 GI:13435665
KEYWORDS MGC.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, K.H., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heien, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Schaeetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, V.A., Gunaratne, P.H., Richards, S.,
Mortley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, K.S., Krzywinski, M.I., Skalska, U., Smallos, D.E.,
Scherer, A., Schein, J.E., Jones, S.J., and Warr, N.A.,
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
12477932
2 (bases 1 to 3352)
Strausberg, R.
Direct Submission
Submitted (21-MAR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2530,
USA
REMARK
COMMENT NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Louised, H.,
Kovits, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Naranvali,
A.N., Gibbs, R.A.
FEATURES
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="MGC:5790 IMAGE:3499203"
/tissue_type="mammary tumor; C3 (1)-Tag model. Infiltrating
ductal carcinoma. 5 month old virgin mouse."
/clone_id="NCI_CGAP_Mam6"

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1..3352
/gene="Birc5"
/note="synonyms: TIAP, AAC-11"
/db_xref="LocustID:11799"
/db_xref="MGI:1203517"
33..398
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/db_xref="GI:13435666"
/db_xref="LocustID:11799"
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HCPTEHPDIAQCFPCPKLESGWEDDNPRIEHRKHSQCAFLTVKQMEELVSEFL
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/note="BIR; Region: Baculoviral inhibition of apoptosis
protein repeat"
/db_xref="CD:smart00238"
misc_feature
Alignment Scores:
Pred. No.: 1.2e-37 Length: 3352
Score: 41.00 Matches: 41
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 28.87% Indels: 0
DB: 10 Gaps: 0
US-09-690-825-34 (1-142) x BC004702 (1-3352)
QY 31 CysAlaCysThrProGluArgMetAlaGluAlaGlyPheIleHisCysProThrGluAsn 50
Db 123 TGGCGCTGCACCCAGAGGAATGGCGAGCGCTGCCTCATCCATGCCCTACCGGAAC 182
QY 51 GluProAspLeuAlaGlnCysPhePheCysPheIleGluLeuGluGlyTyrGluProAsp 70
Db 183 GAACCTGATTGGCCCAAGGATTTTCCTTAAGAAATGGAAGCGTGGAGACCCGAT 242
QY 71 Asp 71
Db 243 GAC 245
RESULT 27
AF276775 903 bp mRNA linear ROD 12-JUL-2000
LOCUS AF276775
DEFINITION Rattus norvegicus survivin mRNA, complete cds.
ACCESSION AF276775
VERSION AF276775.1 GI:5050024
KEYWORDS
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
AUTHORS Chen, D., Cao, G., and Chen, J.
TITLE Molecular cloning and characterization of rat survivin
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 903)
AUTHORS Chen, D., Cao, G., and Chen, J.
TITLE Direct Submission
JOURNAL Submitted (09-JUN-2000) Neurology, University of Pittsburgh, 3500
Terrace Street, Pittsburgh, PA 15261, USA
FEATURES
Source
1..903
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
5..433
/codon_start=1

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/product="survivin"
/protein_id="AAF2586.1"
/db_xref="GI:9050025"
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KIDKQAKKIAKETNNKQKEFEETRTVROSIEQLALR"

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ORIGIN

Alignment Scores:

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Pred. No.: 7,48e-36 Length: 903
Score: 39.00 Matches: 39
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 27,46# Indels: 0
DB: 10 Gaps: 0

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US-09-690-825-34 (1-142) x AAF26775 (1-903)

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QY 33 CysThrProGluArgMetLacGluPheHleHisCysProThrGluAspGluPro 52
DB 101 TGAACCCCGAGCGAGCGAGGCTGGCTTCATCCAGTCCGACGAGATAGGCT 160

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QY 53 AspLeuAlaGlnCysPhePheCysPheLysGluLeuGluGlyTrpGluProAspAsp 71
DB 161 GATTGGCCCGAGTGTTCCTTCCTTTAAGAACTGGAAGGCTGGGAACCGGATGAC 217

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RESULT 28
AR157507 AR157507 14796 bp DNA linear PAT 17-OCT-2001
LOCUS AR157507 Sequence 35 from patent US 6245523.
DEFINITION AR157507
ACCESSION AR157507
VERSION AR157507.1 GI:16218452
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 14796)
AUTHORS Altieri,D.C.
TITLE Survivin, a protein that inhibits cellular apoptosis, and its
JOURNAL Patent: US 6245523-A 35 12-JUN-2001;
FEATURES
source Location/Qualifiers
1..14796
/organism="unknown"
/mol_type="unassigned DNA"

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ORIGIN

Alignment Scores:

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Pred. No.: 1.17e-34 Length: 14796
Score: 39.00 Matches: 39
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 27,46# Indels: 0
DB: 6 Gaps: 0

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US-09-690-825-34 (1-142) x AR157507 (1-14796)

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QY 75 GluGluHisLysLysHisSerSerGlyCysAlaPheLeuSerValLysGlnPheGlu 94
DB 5159 GAGGAACATTAATAAGCATTCGTCGGCTTCCTTCCTTCCTCAAGAGAGATTGAA 5218

```

```

QY 95 GluLeuThrLeuGluGluPheLeuLysLeuAspArgGluArgAlaLysAsnLysIle 113
DB 5219 GAATTAAACCTTGTTGAATTTTGAACCTGACAGAGAAAGCCCAACAAATT 5275

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RESULT 29
AR181541 AR181541 14796 bp DNA linear PAT 20-APR-2002
LOCUS AR181541 Sequence 3 from patent US 6335194.
DEFINITION AR181541
ACCESSION AR181541
VERSION AR181541.1 GI:20223755
KEYWORDS
SOURCE Unknown.

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ORGANISM

Unknown.

REFERENCE 1 (bases 1 to 14796)

AUTHORS Bennett,C.Frank., Ackermann,E.J., Swayze,E.B. and Cowseert,L.M.

TITLE Antisense modulation of survivin expression

JOURNAL Patent: US 6335194-A 3 01-JAN-2002;

FEATURES

Location/Qualifiers

source 1..14796

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:

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Pred. No.: 1.17e-34 Length: 14796
Score: 39.00 Matches: 39
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 27,46# Indels: 0
DB: 6 Gaps: 0

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US-09-690-825-34 (1-142) x AR181541 (1-14796)

```

QY 75 GluGluHisLysLysHisSerSerGlyCysAlaPheLeuSerValLysGlnPheGlu 94
DB 5159 GAGGAACATTAATAAGCATTCGTCGGCTTCCTTCCTTCCTCAAGAGAGATTGAA 5218

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QY 95 GluLeuThrLeuGluGluPheLeuLysLeuAspArgGluArgAlaLysAsnLysIle 113
DB 5219 GAATTAAACCTTGTTGAATTTTGAACCTGACAGAGAAAGCCCAACAAATT 5275

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```

RESULT 30
AX333491 AX333491 14796 bp DNA linear PAT 09-JAN-2002
LOCUS AX333491 Sequence 4000 from Patent WO0194629.
DEFINITION AX333491
ACCESSION AX333491
VERSION AX333491.1 GI:18124125
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

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Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1

Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
Horrigan,S., Soppet,D.R. and Weaver,Z.
Cancer gene determination and therapeutic screening using signature
gene sets

TITLE

Patent: WO 0194629-A 4000 13-DEC-2001;

JOURNAL

Avalon Pharmaceuticals (US)

FEATURES

source

Location/Qualifiers

1..14796

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Alignment Scores:

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Pred. No.: 1.17e-34 Length: 14796
Score: 39.00 Matches: 39
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 27,46# Indels: 0
DB: 6 Gaps: 0

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US-09-690-825-34 (1-142) x AX333491 (1-14796)

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QY 75 GluGluHisLysLysHisSerSerGlyCysAlaPheLeuSerValLysGlnPheGlu 94
DB 5159 GAGGAACATTAATAAGCATTCGTCGGCTTCCTTCCTTCCTCAAGAGAGATTGAA 5218

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QY 95 GluLeuThrLeuGluGluPheLeuLysLeuAspArgGluArgAlaLysAsnLysIle 113
DB 5219 GAATTAAACCTTGTTGAATTTTGAACCTGACAGAGAAAGCCCAACAAATT 5275

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RESULT 31
AX334154 14796 bp DNA linear PAT 09-JAN-2002
LOCUS AX334154
DEFINITION Sequence 4663 from Patent WO0194629.
ACCESSION AX334154
VERSION AX334154.1 GI:18124873
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horrigan, S., Soppet, D.R. and Weaver, Z.
TITLE Cancer gene determination and therapeutic screening using signature gene sets
JOURNAL Patent: WO 0194629-A 4663 13-DEC-2001;
FEATURES
LOCATION/Qualifiers
SOURCE 1. 14796
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 1.17e-34 Length: 14796
Score: 39.00 Matches: 39
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 27.46% Indels: 0
DB: 6 Gaps: 0
US-09-690-825-34 (1-142) x AX334154 (1-14796)

QY 75 GIUGLHISLYSHISSEISERGLYCYSALAPHELEUSERVALYSLYSGINPHEGLU 94
DB 5159 GAGGAAACATTAAGACATTCGCGGTTCCCTTCTCTCTCAAGACAGCTTGAA 5218

QY 95 GIULEUTHIRLEUGLYGHPHELEULYSLEUASPARGIUAIRGALALYSANLYSILE 113
DB 5219 GAATTAAACCTTGCGTAATTTTGAACCTGCAGAGAAAGCCAGAACAAATTT 5275

RESULT 32
AX336483 14796 bp DNA linear PAT 09-JAN-2002
LOCUS AX336483
DEFINITION Sequence 6992 from Patent WO0194629.
ACCESSION AX336483
VERSION AX336483.1 GI:18127202
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horrigan, S., Soppet, D.R. and Weaver, Z.
TITLE Cancer gene determination and therapeutic screening using signature gene sets
JOURNAL Patent: WO 0194629-A 6992 13-DEC-2001;
FEATURES
LOCATION/Qualifiers
SOURCE 1. 14796
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 1.17e-34 Length: 14796
Score: 39.00 Matches: 39
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 27.46% Indels: 0
DB: 6 Gaps: 0
US-09-690-825-34 (1-142) x AX336483 (1-14796)

Query Match: 27.46% Indels: 0
DB: 6 Gaps: 0
US-09-690-825-34 (1-142) x AX336483 (1-14796)

QY 75 GIUGLHISLYSHISSEISERGLYCYSALAPHELEUSERVALYSLYSGINPHEGLU 94
DB 5159 GAGGAAACATTAAGACATTCGCGGTTCCCTTCTCTCTCAAGACAGCTTGAA 5218

QY 95 GIULEUTHIRLEUGLYGHPHELEULYSLEUASPARGIUAIRGALALYSANLYSILE 113
DB 5219 GAATTAAACCTTGCGTAATTTTGAACCTGCAGAGAAAGCCAGAACAAATTT 5275

RESULT 33
AX410775 14796 bp DNA linear PAT 14-JUN-2002
LOCUS AX410775
DEFINITION Sequence 3422 from Patent WO0229103.
ACCESSION AX410775
VERSION AX410775.1 GI:21443480
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Alvares, C., Horne, D., Peres-da-Silva, S. and Vockley, J.G.
TITLE Gene expression profiles in liver cancer
JOURNAL Patent: WO 0229103-A 3422 11-APR-2002;
GENE LOGIC INC (US)
FEATURES
LOCATION/Qualifiers
SOURCE 1. 14796
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="EMBL/Genbank Accession No. U75285"

ORIGIN
Alignment Scores:
Pred. No.: 1.17e-34 Length: 14796
Score: 39.00 Matches: 39
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 27.46% Indels: 0
DB: 6 Gaps: 0
US-09-690-825-34 (1-142) x AX410775 (1-14796)

QY 75 GIUGLHISLYSHISSEISERGLYCYSALAPHELEUSERVALYSLYSGINPHEGLU 94
DB 5159 GAGGAAACATTAAGACATTCGCGGTTCCCTTCTCTCTCAAGACAGCTTGAA 5218

QY 95 GIULEUTHIRLEUGLYGHPHELEULYSLEUASPARGIUAIRGALALYSANLYSILE 113
DB 5219 GAATTAAACCTTGCGTAATTTTGAACCTGCAGAGAAAGCCAGAACAAATTT 5275

RESULT 34
BD192864 14796 bp DNA linear PAT 17-JUL-2003
LOCUS BD192864
DEFINITION Survivin, a protein that inhibits cellular apoptosis, and its modulation.
ACCESSION BD192864
VERSION BD192864.1 GI:33002603
KEYWORDS UP 2002514060-A/6.
SOURCE Cuphea hookeriana
ORGANISM Cuphea hookeriana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Myrtales; Lythraceae; Cuphea.

REFERENCE
AUTHORS Altieri, D.C.
TITLE Survivin, a protein that inhibits cellular apoptosis, and its
JOURNAL Patent: UP 2002514060-A 6 14-MAY-2002;
YALE UNIVERSITY

Journal of Cellular Biochemistry
Submitted (17-OCT-1996) Pathology, Boyer Center for Molecular
Medicine Rm 436B, Yale University School of Medicine, 295 Congress

JOURNAL
REFERENCE
2 (bases 1 to 154840)
Unpublished


```

TITLE
JOURNAL
REFERENCE
AUTHORS
Direct Submission
Submitted (15-JAN-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 209751)
Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
Barnett,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhalter,B.,
Camarda,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
Cook,A., Cooke,P., DeArrellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J.,
Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hafez,N.,
Hagge,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karakas,A., Kells,C., Landers,T., Levine,R.,
Lindblad-Toh,K., Liu,G., Maclean,C., Macdonald,P., Major,J.,
Maltews,C., McCarthy,M., Meldrum,J., Menes,L., Mhova,T.,
Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C.,
Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J.,
Peterson,K., Phunkhang,P., Pierre,N., Raymond,C., Retta,R.,
Rise,C., Rogov,P., Roman,J., Roy,A., Schner,S., Schupbak,R.,
Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Talamas,J., Testaye,S., Theodore,J., Topham,K.,
Travers,M., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X.,
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (16-JAN-2003) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
4 (bases 1 to 209751)
Birren,B., Nusbaum,C., Lander,E., Abouelheil,A., Allen,N.,
Anderson,S., Arachchi,H.M., Barnett,N., Bastien,V., Bloom,T.,
Boguslavsky,L., Boukhalter,B., Camarda,J., Chang,J., Choepel,Y.,
Collymore,A., Cook,A., Cooke,P., Corum,B., Erickson,J., Faro,S.,
Diaz,J.S., Dodge,S., Doolley,K., Dorris,L., Eriksson,J., Faro,S.,
Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J., Gardyna,S.,
Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B.,
Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karakas,A., Kells,C., Landers,T., Levine,R.,
Lindblad-Toh,K., Liu,G., Liu,A., Mabbitt,R., Maclean,C.,
Macdonald,P., Major,J., Manning,J., Mathews,C., McCarthy,M.,
Meldrum,J., Menes,L., Mhova,T., Mlenga,V., Murphy,T., Naylor,J.,
Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,
O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Schner,S., Schupbak,R., Seaman,S., Severy,P., Smith,C.,
Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,
Talamas,J., Testaye,S., Theodore,J., Topham,K., Travers,M.,
Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (05-FEB-2003) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Dec 20, 2002 this sequence version replaced gi:26190573.
All repeats were identified using RepeatMasker:
Smit,A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence.submissions@genome.wi.mit.edu
Project Information
Center project name: L11992
Center clone name: 213_G_17
FEATURES
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1..209751
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="17"
/map="17"
/clone="RP11-219G17"
/clone_11b="RP11-219G17 Human Male BAC"
repeat_region
95..232
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repeat_region
complement(634..972)
/rpt_family="AluSx"
complement(1653..1760)
/rpt_family="MER3A"
complement(1807..1886)
/rpt_family="MIR"
complement(2001..2312)
/rpt_family="AluDo"
2336..2636
/rpt_family="AluSx"
complement(3664..3706)
/rpt_family="AluDo"
3707..3993
/rpt_family="AluSx"
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5194..5371
/rpt_family="AluSg/X"
5606..5738
/rpt_family="FRAM"
complement(5739..5850)
/rpt_family="Alu"
complement(5865..5999)
/rpt_family="AluSg/X"
6293..6600
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complement(7562..7879)
/rpt_family="AluY"
8178..8326
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8327..8617
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8618..8721
/rpt_family="L1ME4a"
8799..9231
/rpt_family="L13"
9248..9488
/rpt_family="L13"
9996..10097
/rpt_family="AluSg/X"
complement(10100..10397)
/rpt_family="AluY"
10159..10164
/note="<30 qual SNCL region"
10399..10579
/rpt_family="AluSg/X"
10580..10908
/rpt_family="AluSx"
10909..10919
/rpt_family="AluSg/X"
11385..11522
/rpt_family="MIR"
complement(11696..11997)
/rpt_family="AluY"
complement(12826..12967)
/rpt_family="L1MC4"
complement(12968..13262)
/rpt_family="AluYb"
complement(13263..13344)
/rpt_family="L1MC4"
complement(13354..13532)
/rpt_family="AluYb"
complement(13533..13820)
/rpt_family="AluSx"
complement(13821..13890)
/rpt_family="L1MC4"
14283..14348
/rpt_family="MER45C"
complement(14349..14525)
/rpt_family="AluSg"
complement(14526..14828)
/rpt_family="AluY"
complement(14829..14962)

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repeat_region      /rpt_family="AlusG"
                    14963..14999
repeat_region      /rpt_family="MER45C"
                    15000..15299
repeat_region      /rpt_family="AlusX"
                    15303..15598
repeat_region      /rpt_family="AlusX"
                    15599..15752
repeat_region      /rpt_family="MER45C"
                    complement(16198..16332)
repeat_region      /rpt_family="WIR"
                    16832..16961
repeat_region      /rpt_family="WIR"
                    17736..17810
unare               /note="single clone coverage"
repeat_region      17794..17973
repeat_region      /rpt_family="CT-rich"
                    18235..18553
repeat_region      /rpt_family="AlusG"

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Alignment Scores:

Pred. No.:	1.59e-33	Length:	209751
Score:	39.00	Matches:	39
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	27.46%	Indels:	0
DB:	9	Gaps:	0

US-09-690-825-34 (1-142) x AC087645 (1-209751)

QY 75 GUGUHHSHLYSHSERSERGLYCSALAPHLEUSERVALLYSLYGLINPHAGLU 94
 DB 125460 GAGGACATMAAAGCATTCGCGCGTTCCGCTTCTGTCAGAGACAGTTGAA 125401

QY 95 GUGUHHSHLYSHSERSERGLYCSALAPHLEUSERVALLYSLYGLINPHAGLU 113
 DB 125400 GAATTAACCTTGGAATTTTGAACTGGACAGAAAGCCAGACAAATTT 125344

RESULT 38
 ARI84472 417 bp DNA linear PAT 20-APR-2002
 LOCUS ARI84472
 DEFINITION Sequence 1 from patent US 6346389.
 ACCESSION ARI84472.1 GI:20230437
 VERSION ARI84472.1
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 417)
 AUTHORS Aliteri,D.C.
 TITLE Method for selectively modulating the interactions between survivin
 and tubulin
 JOURNAL Patent: US 6346389-A 1 12-FEB-2002;
 FEATURES Location/Qualifiers
 source 1..417
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN
 Alignment Scores:
 Pred. No.: 7.9e-34 Length: 417
 Score: 37.00 Matches: 37
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 26.06% Indels: 0
 DB: 6 Gaps: 0

US-09-690-825-34 (1-142) x ARI84472 (1-417)
 QY 1 MEGUHALPPTHLEUPROPHALATPGINPROPHLEULEYASPHISARGLIESER 20
 DB 291 ATGGGCGCCGACGCTGGCCCTGCTGGACGCCCTTCTCAAGACCAACGCACTCTCT 350

QY 21 THRPHELYASNTTTPROPHLEUUGLYCYSAALACYSSTRNPROGLIATG 37
 DB 351 ACATTCAGACACTGCGCTTCTTGAGGGCTGCGCTGACACCCGACGCG 401

RESULT 39
 AC032035 154840 bp DNA linear HTG 08-SEP-2000
 LOCUS AC032035
 DEFINITION Homo sapiens chromosome 17 clone RP11-141D15 map 17, *** SEQUENCING
 IN PROGRESS ***, 18 unordered pieces.
 ACCESSION AC032035.3 GI:9994161
 VERSION AC032035
 KEYWORDS HTG; HTGS_PHASE1.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 154840)
 AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
 TITLE Homo sapiens chromosome 17, clone RP11-141D15
 JOURNAL Unpublished
 ORGANISM 2 (bases 1 to 154840)
 AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Adnan,H., Allen,N.,
 Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
 Boguslavsky,L., Boukhalter,B., Brown,A., Burkett,G.,
 Campolino,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
 Collymore,A., Cooke,P., DeArillano,K., Dewar,K., Diaz,J.S.,
 Dodge,S., Domino,M., Doyle,M., Ferreira,P., Fitzhugh,W., Gage,D.,
 Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
 Grand-pierre,N., Grant,G., Hagos,B., Harford,A., Horton,L.,
 Howard,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karakas,A.,
 Klein,U., Lacombe,K., Lamazares,R., Landers,T., Lechoczky,J.,
 Levine,R., Lien,C., Liu,G., Locke,K., Macdonald,P., Margus,N.,
 McCarthy,M., McEwan,P., McGuirk,A., McKernan,K., McNetters,R.,
 Melchior,J., Meneses,L., Mihova,T., Miranda,C., Mleaga,V., Morrow,J.,
 Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
 O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K., Pletzer,N.,
 Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
 Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
 Stange-Thomann,N., Stojanovic,N., Subramaniam,A., Talamas,J.,
 Testaye,S., Theodore,J., Tirrell,A., Travers,M., Triggillo,J.,
 Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
 Young,G., Zainoun,J., Zimmer,A. and Zody,M.

TITLE
 JOURNAL
 COMMENT
 Submitted (03-APR-2000) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141 USA.
 On Sep 8, 2000 this sequence version Replaced by: 7705196.
 All repeats were identified using RepeatMasker:
 http://ftp.genome.washington.edu/TM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIR
 Web site: http://www-seg.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu
 Project Information
 Center project name: L9138
 Center clone name: 141_D15

NOTE: This is a 'working draft' sequence. It currently
 consists of 18 contigs. The true order of the pieces
 is not known and their order in this sequence record is
 arbitrary. Gaps between the contigs are represented as
 runs of N, but the exact sizes of the gaps are unknown.
 This record will be updated with the finished sequence
 as soon as it is available and the accession number will
 be preserved.

Contig	Length
1	2373: contig of 2373 bp in length
2374	2473: gap of 100 bp
2474	4930: contig of 2457 bp in length
4931	5030: gap of 100 bp
5031	7215: contig of 2185 bp in length
7216	7315: gap of 100 bp
7316	9541: contig of 2226 bp in length

9542 9641: gap of 100 bp
* 9642 12211: contig of 2570 bp in length
* 12212 12311: gap of 100 bp
* 12312 14923: contig of 2612 bp in length
* 14924 15023: gap of 100 bp
* 15024 19094: contig of 4071 bp in length
* 19095 19194: gap of 100 bp
* 19195 22286: contig of 3092 bp in length
* 22287 22386: gap of 100 bp
* 22387 26147: contig of 3761 bp in length
* 26148 26247: gap of 100 bp
* 26248 31933: contig of 5566 bp in length
* 31934 32033: gap of 100 bp
* 32034 37339: contig of 5306 bp in length
* 37340 37440: gap of 100 bp
* 37440 42858: contig of 5419 bp in length
* 42859 42959: gap of 100 bp
* 42959 48810: contig of 5852 bp in length
* 48811 48910: gap of 100 bp
* 48911 56029: contig of 7119 bp in length
* 56030 56129: gap of 100 bp
* 56130 62189: contig of 6060 bp in length
* 62190 62289: gap of 100 bp
* 62290 82959: contig of 20670 bp in length
* 82960 83059: gap of 100 bp
* 83060 107059: contig of 24000 bp in length
* 107060 107159: gap of 100 bp
* 107160 154840: contig of 47681 bp in length.

FEATURES
source
1. 154840
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="17"
/map="17p"
/clone="RP11-141D15"
/clone_lib="RPC1-11 Human Male BAC"

ORIGIN

Alignment Scores:

Prod. No.: 2 666-31 length: 154840
Score: 37.00 Matches: 37
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 26.06% Indels: 0
DB: 2 Gaps: 0

US-09-690-825-34 (1-142) x AC032035 (1-154840)

OY 1 MetGlyAlaProThrLeuProProAlaTTPGlnProPhenLeuLYsAspHisArgIleSer 20

DB 31031 ATGGGGGCCCCGACGTTGGCCCTGCTGGCAGCCCTTTCTCAAGACACCGCATCTCT 31090

OY 21 ThrPheLYsAsnTyrProPheLeuGluGlyCysAlaCysThrProGluArg 37

DB 31091 ACATTCAAGAACTGGCCCTTTCTTGAAGGGCTGCGCTGCACCCCGGACGG 31141

RESULT 40

AC010532 229426 bp DNA linear HTG 05-SEP-2000

AC010532 Homo sapiens chromosome 17 clone RP11-219G17, LOW-PASS SEQUENCE

AC010532 229426 bp DNA linear HTG 05-SEP-2000

AC010532 229426 bp DNA linear HTG 05-SEP-2000

AC010532 229426 bp DNA linear HTG 05-SEP-2000

AC010532 229426 bp DNA linear HTG 05-SEP-2000

AC010532 229426 bp DNA linear HTG 05-SEP-2000

AC010532 229426 bp DNA linear HTG 05-SEP-2000

AC010532 229426 bp DNA linear HTG 05-SEP-2000

AC010532 229426 bp DNA linear HTG 05-SEP-2000

AC010532 229426 bp DNA linear HTG 05-SEP-2000

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
2 (bases 1 to 229426)
DOE Joint Genome Institute.
Direct Submission
Submitted (15-SEP-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jan 26, 2000 this sequence version replaced gi:5882406.
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: <http://www.jgi.doe.gov>

* NOTE: This record contains 99 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
1 563: contig of 563 bp in length
* 564 1436: gap of unknown length
* 1437 1649: gap of 213 bp in length
* 1650 2523: gap of unknown length
* 2524 3286: gap of 763 bp in length
* 3287 3613: gap of 327 bp in length
* 3614 5430: gap of unknown length
* 5431 6681: gap of 1251 bp in length
* 6682 7357: gap of 676 bp in length
* 7358 8117: gap of 760 bp in length
* 8118 8718: gap of 601 bp in length
* 8719 9464: gap of 746 bp in length
* 9465 9964: gap of 500 bp in length
* 9965 10959: gap of 995 bp in length
* 10960 11873: gap of 914 bp in length
* 11874 12656: gap of 783 bp in length
* 12657 13674: gap of 1018 bp in length
* 13675 14935: gap of 1261 bp in length
* 14936 16423: gap of unknown length
* 16424 17186: gap of 763 bp in length
* 17187 18079: gap of unknown length
* 18080 18813: gap of 734 bp in length
* 18814 19729: gap of 916 bp in length
* 19730 20675: gap of 946 bp in length
* 20676 21721: gap of unknown length
* 21722 23111: contig of 1390 bp in length

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*      23112      25188:      gap of unknown length
*      25189      26588:      contig of 1400 bp in length
*      26589      27644:      gap of unknown length
*      27645      29372:      contig of 1056 bp in length
*      29373      29495:      gap of unknown length
*      29496      30431:      contig of 123 bp in length
*      30432      31449:      gap of unknown length
*      31450      32983:      contig of 936 bp in length
*      32984      33162:      gap of unknown length
*      33163      33975:      contig of 179 bp in length
*      33976      35031:      gap of unknown length
*      35032      35709:      contig of 813 bp in length
*      35710      37308:      gap of unknown length
*      37309      38107:      contig of 1599 bp in length
*      38108      39102:      gap of unknown length
*      39103      39591:      contig of 799 bp in length
*      39592      41151:      gap of unknown length
*      41152      42842:      contig of 489 bp in length
*      42843      43828:      gap of unknown length
*      43829      44009:      contig of 1560 bp in length
*      44010      44874:      gap of unknown length
*      44875      45191:      contig of 181 bp in length
*      45192      46147:      gap of unknown length
*      46148      47504:      contig of 865 bp in length
*      47505      49091:      gap of unknown length
*      49092      50259:      contig of 1587 bp in length
*      50260      51361:      gap of unknown length
*      51362      52631:      contig of 1168 bp in length
*      52632      53607:      gap of unknown length
*      53608      54820:      contig of 1102 bp in length
*      54821      56600:      gap of unknown length
*      56601      58236:      contig of 1213 bp in length
*      58237      59716:      gap of unknown length
*      59717      62221:      contig of 1480 bp in length
*      62222      65085:      gap of unknown length
*      65086      66739:      contig of 2505 bp in length
*      66739      67399:      gap of unknown length

```

```

*      66740      68359:      gap of unknown length
*      68360      70014:      contig of 1620 bp in length
*      70015      71808:      gap of unknown length
*      71809      73581:      contig of 1655 bp in length
*      73582      75574:      gap of unknown length
*      75575      78468:      contig of 1794 bp in length
*      78469      79231:      gap of unknown length
*      79232      83240:      contig of 1773 bp in length
*      83241      86157:      gap of unknown length
*      86158      89150:      contig of 1993 bp in length
*      89151      92671:      gap of unknown length
*      92672      95442:      contig of 2894 bp in length
*      95443      98476:      gap of unknown length
*      98477      100815:      contig of 2993 bp in length
*      100816      103005:      gap of unknown length
*      103006      105514:      contig of 2339 bp in length
*      105515      108704:      gap of unknown length
*      108705      111097:      contig of 3150 bp in length
*      111098      114888:      gap of unknown length
*      114889      117423:      contig of 2393 bp in length
*      117423      119423:      gap of unknown length

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Alignment Scores:

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Pred. No.:      3,92e-31      Length:      229426
Score:          37.00         Matches:      37
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:      26.06%      Indels:      0
DB:               2          Gaps:      0

```

US-09-690-825-34 (1-142) x AC010532 (1-229426)

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QY      1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
Db      77692 ATGGAGTCCCGCGAGTGGCCCTGCTGCGACCCCTTCTCAGACACACCGCACTCT 77751
QY      21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArg 37
Db      77752 ACAATTGAGAACTGGCCCTCTTGAGAGGCTGGCTGCACCCCGAGCGG 77802

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```

RESULT 41
CRUCIRA      779 bp      DNA      linear      ROD 27-APR-1993
LOCUS        CRUCIRA
DEFINITION   Cricetus griseus carcinogen-induced rearranged DNA.
ACCESSION    M80243
VERSION      M80243.1 GI:191034
KEYWORDS
SOURCE
ORGANISM     Cricetus griseus (Chinese hamster)
              Cricetus griseus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
              Cricetulus.
REFERENCE    1 (bases 1 to 779)
AUTHORS     Barr,F.G., Davis,R.J., Eichenfield,L. and Emanuel,B.S.

```

TITLE Structural analysis of a carcinogen-induced genomic rearrangement
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 89 (3), 942-946 (1992)
MEDLINE 92141234
PUBMED 1736310
COMMENT Original source text: Cricetus griseus (library: Lambda Charon 35) DNA.

FEATURES
source
Location/Qualifiers
1..779
/organism="Cricetus griseus"
/mol_type="genomic DNA"
/db_xref="taxon:10029"
/haplotype="---"
/cell_line="RJK92 - V79 derivative"
/cell_type="fibroblast"
/tissue_id="Lambda Charon 35"

ORIGIN

Alignment Scores:
Pred. No.: 4,96e-30 Length: 779
Score: 34.00 Matches: 34
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 23.94% Indels: 0
DB: 10 Gaps: 0

US-09-690-825-34 (1-142) x CRUCIRA (1-779)

Qy 38 MetAlaGuaIaGlyPheIleHisCysProThrgluAsnGluProAspLeuAlaGlnCys 57
Db 581 ATGCCGAGAGCGGCTTCATCCATCCGAGAACGAGCTGATTTGGCCAGTGT 522

Qy 58 PhePheCysPheIleGluGlnGlyTTPGluProAspAsp 71
Db 521 TTTTCTGCTTTAAGAGCTGGAAGCTGGAGCCAGATGAC 480

RESULT 42
AF077351 9263 bp DNA linear ROD 20-DEC-2000
LOCUS Mus musculus inhibitor of apoptosis homolog gene, complete cds.
ACCESSION AF077351
VERSION AF077351.1 GI:11907561
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Uren,A.G., Wong,L., Pakusch,M., Fowler,K.J., Burrows,F.J., Vaux,D.L. and Choo,K.H.
TITLE Survivin and the inner centromere protein INCENP show similar cell-cycle localization and gene knockout phenotype
JOURNAL Curr. Biol. 10 (21), 1319-1326 (2000)
PUBMED 11084331
JOURNAL MEDLINE 20538917
REFERENCE 2 (bases 1 to 9263)
AUTHORS Uren,A.U. and Vaux,D.L.
TITLE Direct Submision
COMMENT Submitted (08-JUN-1998) Molecular Cancer Division, The Walter and Eliza Hall Institute, Royal Parade, Parkville, Vic 3052, Australia

FEATURES
source
Location/Qualifiers
1..9263
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="Black 6"
/db_xref="taxon:10090"
/join(1902..2027,2330..2429,5226..5343,7788..8300)
/product="inhibitor of apoptosis homolog"
/join(1917..2027,2320..2429,5226..5343,7788..7871)
/note="TAP"
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/product="inhibitor of apoptosis homolog"
/protein_id="AAG41214.1"

/db_xref="GI:11907562"
/translation="MGAPALPOLMOLYLNRYLATPKMWPLEDCACTPERMAAGFI
HCPTEHPDLACGFCFCFKEISGMBDDNDPIEHRKSGSCAFLLTVKXMEELTVSEFL
KIDRQRAKKIKIAETNNKKCFEETAKTTRQSTIEQLAA"

ORIGIN

Alignment Scores:
Pred. No.: 5,67e-29 Length: 9263
Score: 34.00 Matches: 34
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 23.94% Indels: 0
DB: 10 Gaps: 0

US-09-690-825-34 (1-142) x AF077351 (1-9263)

Qy 38 MetAlaGuaIaGlyPheIleHisCysProThrgluAsnGluProAspLeuAlaGlnCys 57
Db 2320 ATGCCGAGAGCTTCATCCATCCGAGAACGAGCTGATTTGGCCAGTGT 2379

Qy 58 PhePheCysPheIleGluGlnGlyTTPGluProAspAsp 71
Db 2380 TTTTCTGCTTTAAGAGATGGAAGCTGGAGAACCGATGAC 2421

RESULT 43
AB036741 10074 bp DNA linear ROD 22-DEC-2000
LOCUS Mus musculus gene for TAP, complete cds.
ACCESSION AB036741
VERSION AB036741.1 GI:11990425
KEYWORDS TAP.
SOURCE Mus musculus (house mouse)
ORGANISM
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Otake,M., Hatano,M., Kobayashi,K., Ogasawara,T., Kuriyama,T. and Tokuhisa,T.
TITLE Cell cycle dependent regulation of TAP/m-survivin expression
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 10074)
AUTHORS Otake,M., Hatano,M. and Tokuhisa,T.
TITLE Direct Submision
COMMENT Submitted (07-JAN-2000) Masayuki Otake, Chiba University Graduate School of Medicine, Department of Developmental Genetics, 1-8-1 Inohana Chuo-ku, Chiba, Chiba 260-8670, Japan
/E-mail:otake@devgenol.m.chiba-u.ac.jp/, Tel:81-43-226-2182, URL:http://devgenol.m.chiba-u.ac.jp/,
Fax:81-43-226-2183)

FEATURES
source
Location/Qualifiers
1..10074
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129/Sv"
/db_xref="taxon:10090"
/join(12824..2934,3227..3336,6134..6251,8694..8777)
/gene="TAP"
/join(2824..2934,3227..3336,6134..6251,8694..8777)
/gene="TAP"
/codon_start=1
/product="TAP"
/protein_id="BAB19787.1"
/translation="MGAPALPOLMOLYLNRYLATPKMWPLEDCACTPERMAAGFI
HCPTEHPDLACGFCFCFKEISGMBDDNDPIEHRKSGSCAFLLTVKXMEELTVSEFL
KIDRQRAKKIKIAETNNKKCFEETAKTTRQSTIEQLAA"

ORIGIN

Alignment Scores:
Pred. No.: 6,15e-29 Length: 10074
Score: 34.00 Matches: 34
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match:	23.94%	Indels:	0
DB:	10	Gaps:	0
US-09-690-825-34 (1-142) x AB036741 (1-10074)			
Oy	38	MetAlGluAlGlyPheIleHisCysProThrGlnuSncInuProAspIeuAaClnCys	57
Db	3227	ATGGCGAGAGCTGGCTTCATCCACGCCCCCTCCAGAGACAGAGCTGATTGGCCCGACGTG	3286
Oy	58	PhaepeCysPheIeuGlnuGlnuIyTrpAluProAspAsp	71
Db	3287	TTTTCTGCTTTAGCAATGGAAGGCTGGAGACCCCATGAC	3328
RESULT 44			
AF115517			
LOCUS	10919 bp	DNA	linear
DEFINITION	Mus musculus survivin40, survivin121, and survivin40 genes,		
ACCESSION	AF115517		
VERSION	AF115517.1		
KEYWORDS	GI:4588767		
ORGANISM	Mus musculus (house mouse)		
REFERENCE	1. Mus musculus		
AUTHORS	Ekaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scuriunathi; Muridae; Murinae; Mus.		
TITLE	1 (bases 1 to 10919)		
JOURNAL	Conway, E.M., Pollefeyle, S., Corneliussen, J., Debaere, I., Ong, K., Collien, D. and Schuh, A.C.		
REFERENCE	2 (bases 1 to 10919)		
AUTHORS	Conway, E.M., Pollefeyle, S., Corneliussen, J., Debaere, I., Ong, K., Collien, D. and Schuh, A.C.		
TITLE	Direct Submission		
JOURNAL	Submitted (21-DEC-1998) Center for Transgene Technology, University of Leuven, Herestraat 49, 9th floor, Leuven B-3000, Belgium		
FEATURES	location/Qualifiers		
Source	1..10919		
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	/chromosome="11"		
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Score: 34.00 Matches: 34
Percent Similarity: 100.00% Conservative: 0
Best local Similarity: 100.00% Mismatches: 0
Query Match: 23.94% Indels: 0
DB: 10 Gaps: 0

US-09-690-825-34 (1-142) x AF155517 (1-10919)
Oy 38 MetAlaGluAlaGlyPheIleHsCsGpProThGluAsnGluProAspMetAlaGlnCs 57
Db 3268 ATGGCGAGAGCGCGGCTTATCCATCGCCATCCGAGAACGAGCGCTCATTTGGCCAGTGT 3327
Oy 58 PhePheCysPheNlysGluLeuGluGlyTyrGluProAsp 71
Db 3328 TTTTCTGCTTTAAAGATTGGAAGGCTGGGAACCGGATGAC 3369

RESULT 45
LOCUS AL954690 197194 bp DNA linear HTG 15-NOV-2002
DEFINITION Mus musculus chromosome 11 clone RP23-386A4.
ACCESSION AL954690
VERSION AL954690.2 GI:25136861
HTG: HTG_PHASE2; HTGS_CANCELLED.
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 197194)
Tromans,A.
Direct Substitution
Submitted (13-NOV-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
On Nov 19, 2002 this sequence version replaced gi:25045706.
Sequence from the Mouse Genome Sequencing Consortium whole genome
shotgun may have been used to confirm this sequence. Sequence data
from the whole genome shotgun alone has only been used where it has
a phred quality of at least 30.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquerry@sanger.ac.uk
----- Project Information
Center project name: dm386A4
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 195990 bases at least Q40
Consensus quality: 196234 bases at least Q30
Consensus quality: 196338 bases at least Q20
Insert size: 197194; sum-of-contigs
Insert size: 189681; 3.6% error; agarose-fp
Quality coverage: 7,24x in Q20 bases; sum-of-contigs Quality
coverage: 7,53x in Q20 bases; agarose-fp
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 1 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and

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* the accession number will be preserved.
1 197194: contig of 197194 bp in length.
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/db_xref="taxon:10090"
/chromosome="11"
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clone_end:SP6
vector_side:left"

misc_feature

ORIGIN

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score:	1.15e-27	197194	34	0	0	0
Percent Similarity:	100.00%					
Best Local Similarity:	100.00%					
Query Match:	23.94%					

US-09-690-825-34 (1-142) x AL954690 (1-197194)

Qy 38 MetAlaGluAlaGlyPheHleHisCysProThrGluAsnGluProAspLeuAlaGlnCys 57

Db 67096 ATGGCGAGCGCTGGCTTCATCCACTGCCCTACCGAGAAAGAGCTGATTGGCCACGTGT 67155

Qy 58 PhePheCysPheIysGluLeuGluGlyTTPGluProAspAsp 71

Db 67156 TTTTCTGCTTTAAGGAATTGGAAAGCTCGGAACCCGATGAC 67197

RESULT 46

AL591433

LOCUS

DEFINITION

AL591433 203336 bp DNA linear ROD 21-DEC-2002
Mouse DNA sequence from clone RP23-268N22 on chromosome 11,
complete sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

JOURNAL

COMMENT

TITLE

ABSTRACT

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

JOURNAL

COMMENT

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Elhaj, C., Emerling, S., Escotto, M., Falls, T., Ferraruto, D.,
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Washington, C., Wallington, S., Williams, G., Williamson, A.,
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Zorilla, S., Zuchelapatti, R., Weinstein, G., and Gibbs, R.

Unpublished
3 (bases 1 to 143111)
Moriy, K.C.
Direct Submission
Submitted (09-APR-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

-- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web Site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Project Information
Center project name: LDDs
Center clone name: CH250-268D1
Summary Statistics
Chemistry: Dye-terminator Big Dye 3.1
Consensus quality: 21640 bases at least Q40
Consensus quality: 24831 bases at least Q20
Consensus quality: 28074 bases at least Q20

-- NOTE: Estimated insert size may differ from sequence length
-- (see http://www.hgsc.bcm.tmc.edu/docs/genbank_drift_data.html)
-- NOTE: The contigs are based on the application (NCBI build 31)
-- of the FGI method using the Human genome (NCBI build 31)
-- as the comparative genome.
-- NOTE: This is a 'working draft' sequence. It currently
-- consists of 1 contigs. Gaps between the contigs
-- are represented as runs of N. The order of the pieces
-- is believed to be correct as given, however the sizes
-- of the gaps between them are based on estimates that have
-- been provided by the submitter.
-- This sequence will be replaced
-- by the finished sequence as soon as it is available and
-- the accession number will be preserved.
1 143111: contig of 143111 bp in length.
Location/Qualifiers
1..143111
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/mol_type="genomic DNA"

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CONFIDENCE: 0.83"

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ALIGNMENT SCORES:

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Pred. No.: 2.52e-11 Length: 143111
Score: 20.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 14.08% Indels: 0
DB: 2 Gaps: 0

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US-09-690-825-34 (1-142) x AC143833 (1-143111)

QY 75 GUGUHUHSLYSLYSHLSERSEGLYCYSAJAPHLEUSERVALYSLYGLNPHGLU 94

DB 34047 GAGGAACATPAAAAAGCATTCATCCGGTTCCGCTTCTTCTGTCAAGACACATTGAA 34106

RESULT 48 AC142802 138875 bp DNA linear HTG 09-APR-2003

AC142802 Macaca mulatta clone CH250-268E5, *** SEQUENCING IN PROGRESS ***

DEFINITION AC142802.1 GI:29567441

ACCESSION AC142802.1 HTG: HTGS_PHASE2; HTGS_PGI

VERSION AC142802.1 HTG: HTGS_PHASE2; HTGS_PGI

KEYWORDS Macaca mulatta (rhesus monkey)

SOURCE Macaca mulatta

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

Cercopithecoidea; Macaca.

REFERENCE 1 (bases 1 to 138875)

Cueros, M. and Milosavljevic, A.

Pooled genomic indexing (PGI): mathematical analysis and experiment

design

(in) Guigo, R. and Gusfield, D. (Eds.);

ALGORITHMS IN BIOINFORMATICS, SECOND INTERNATIONAL WORKSHOP, MABI

2002, ROME, ITALY, SEPTEMBER 17-21, 2002, PROCEEDINGS, 10-28;

Springer (2002)

2 (bases 1 to 138875)

Milosavljevic, A., Sodergren, E., Cueros, M., Li, B., Jackson, A.R.,

Adams, C., Adio-Oduola, B., Ali-oshan, F.R., Allen, C., Alsbrooks, S.L.,

Amaratunga, H.C., Are, J.R., Ayale, M., Banks, T., Barbara, D.,

Benton, J., Binage, K., Brown, E., Brown, M., Bryant, N.P., Buhay, C.,

Bowle, S., Briviera, C., Burrell, K.L., Byrd, N.C., Carron, T.F.,

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Washington, C., Wallington, S., Williams, G., Williamson, A.,

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 Zorrilla, S., Zuchterlapati, R., Weinstein, G. and Gibbs, R.
 Direct Submission
 Title
 JOURNAL
 Unpublished
 3 (bases 1 to 138875)
 Worley, K.C.
 Direct Submission
 Submitted (05-APR-2003) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 4 (bases 1 to 138875)
 Worley, K.C.
 Direct Submission
 Submitted (09-APR-2003) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 COMMENT
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 Project Information
 Center project name: LDP0
 Center clone name: CH250-26885
 Summary Statistics
 Chemistry: Dye-Primer Bodypy: inf of reads
 Chemistry: Dye-Terminator Big Dye: inf of reads
 Consensus quality: 3324 bases at least Q40
 Consensus quality: 3942 bases at least Q30
 Consensus quality: 4602 bases at least Q20
 * NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)
 * NOTE: The contigs are based on the application
 * of the PGI method using the Human genome (NCBI build 31)
 * as the comparative genome.
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 1 contigs. Gaps between the contigs
 * are represented as runs of N. The order of the pieces
 * is believed to be correct as given, however the sizes
 * of the gaps between them are based on estimates that have
 * provided by the submitter.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.
 * 138875: contig of 138875 bp in length.
 Location/Qualifiers
 1. 138875
 /organism="Macaca mulatta"
 /mol type="genomic DNA"
 /db xref="taxon:9544"
 /clone="CH250-26885"
 1. 138875
 /note="assembly name: CH250-26885.1A
 CONFIDENCE: 0.67"
 misc_feature
 ORIGIN
 Alignment Scores:
 Pred. No.: 3.67e-10 Length: 138875
 Score: 19.00 Matches: 19
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 13.38% Indels: 0
 DB: 2 Gaps: 0

US-09-690-825-34 (1-142) x AC142802 (1-138875)
 Cy 114 AlalysGluThrMetAsnLysLysGluPheGluGluThrAlaLysLysValArg 132
 Db 104968 GCAAGAGGAAACCAACATTAAGAGAAAGATTGGAGAAATCGCAAGAGAGCGCC 105024
 RESULT 49
 AC142803 166874 bp DNA linear HTG 09-APR-2003
 LOCUS
 DEFINITION
 Macaca mulatta clone CH250-26886, *** SEQUENCING IN PROGRESS ***.
 AC142803.1 GI:29567442
 VERSION
 HTG: HTGS PHASE2; HTGS PGI.
 KEYWORDS
 Macaca mulatta (rhesus monkey)
 SOURCE
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 Cercopithecinae; Macaca.
 1 (bases 1 to 166874)
 Curoso, M., and Milosavljevic, A.
 Pooled genomic indexing (PGI): mathematical analysis and experiment
 design
 TITLE
 JOURNAL
 (in) Guigo, R. and Gusfield, D. (Eds.):
 ALGORITHMS IN BIOINFORMATICS, SECOND INTERNATIONAL WORKSHOP, WABI
 2002, ROME, ITALY, SEPTEMBER 17-21, 2002. PROCEEDINGS: 10-28,
 Springer (2002)
 2 (bases 1 to 166874)
 Milosavljevic, A., Sodergren, E., Curoso, M., Li, B., Jackson, A.R.,
 Adams, C., Adio-Ondolo, B., Ali-osman, F.R., Allen, C., Ashcocks, S.L.,
 Amaratunga, H.C., Are, J.R., Ayele, M., Banks, T., Barbara, J.,
 Benton, J., Biraghe, K., Blankenburg, K., Bonini, D., Bouck, U.,
 Bowles, S., Brileva, M., Brown, S., Brown, M., Bryant, N.P., Bulay, C.,
 Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F.,
 Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R.,
 Chen, Z., Chiu, D., Chowdhury, I., Christopoulos, C., Cleveland, C.D.,
 Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C.,
 Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O.,
 Dem, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H.,
 Dugan-Rocha, S., Durbin, K.J., Egan, A., Ehmhart, C., Edwards, C.C.,
 Elhaj, C., Emerling, S., Escotto, M., Falls, T., Ferriguto, D.,
 Flagg, N., Ford, J., Foster, P., Frantz, P., Gabris, A., Gao, J.,
 Garcia, A., Garner, T., Garza, N., Gill, R., Gorell, J.H., Guevara, M.,
 Gunaratne, P., Hale, S., Hamilton, K., Han, J., Harris, C., Harris, K.,
 Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O.,
 Hodson, A., Hughes, M., Holloway, C., Hollins, B., Homsl, F.,
 Howard, S., Huber, J., Hui, Y., Hui, S., Hume, J., Ioshikhes, I., Jackson, L.E.,
 Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,
 Karlsson, E., Kelly, S., Khan, U., King, L., Korvan, J., Kovar, C.,
 Kravovic, J., Kureshi, A., Landry, N., Leal, B., Lee, E., Lewis, L.C.,
 Lewis, L., Li, J., Li, Z., Lichtharge, O., Ilean, C., Liu, J., Liu, W.,
 Louisedge, H., Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R.,
 Ma, J., Maheshwari, M., Mapa, P., Marondei, I., Martin, R.,
 Martindale, A., Martinez, E., Massey, E., Mamhney, E., McLeod, M.P.,
 Medor, M., Mei, G., Merscher, S., Metzker, M., Miller, A., Miner, G.,
 Miner, Z., Mitchell, T., Mohabbat, K., Montgomery, K.T., Morgan, M.,
 Morris, S., Moser, M., Neal, D., Nelson, D., Newton, J., Newton, N.,
 Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokweto, S.,
 Oguh, M., Okomou, G., Oragunye, N., Oyedele, R., Pace, A., Payton, B.,
 Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.,
 Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojibokan, I., Rolfe, M.,
 Ruiz, S., Saverly, G., Scherer, S., Scott, G., Shen, H., Shim, C.,
 Shooshitari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A.,
 Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A.,
 Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B.,
 Thomas, N., Thomas, S., Usmami, K., Vasquez, L., Vera, V., Villalon, D.,
 Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R.,
 Washington, C., Wallington, S., Williams, G., Williamson, A.,
 Wleczky, R., Woodson, S., Worley, K., Wu, C., Wu, Y., Wu, Y. F., Zhou, J.,
 Zorrilla, S., Zuchterlapati, R., Weinstein, G. and Gibbs, R.
 Direct Submission
 Title
 JOURNAL
 Unpublished
 3 (bases 1 to 166874)


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* 18080 18813: contig of 734 bp in length
* 18814 19729: contig of 916 bp in length
* 19730 20675: contig of 946 bp in length
* 20676 21721: contig of 1046 bp in length
* 21722 23111: contig of 1390 bp in length
* 23112 25188: contig of 2077 bp in length
* 25189 26588: contig of 1400 bp in length
* 26589 27644: contig of 1056 bp in length
* 27645 29372: contig of 1728 bp in length
* 29373 29495: contig of 123 bp in length
* 29496 30431: contig of 936 bp in length
* 30432 31449: contig of 1018 bp in length
* 31450 32983: contig of 1534 bp in length
* 32984 33162: contig of 179 bp in length
* 33163 33975: contig of 813 bp in length
* 33976 35031: contig of 1056 bp in length
* 35032 35709: contig of 678 bp in length
* 35710 37308: contig of 1599 bp in length
* 37309 38107: contig of 799 bp in length
* 38108 39102: contig of 995 bp in length
* 39103 39591: contig of 489 bp in length
* 39592 41151: contig of 1560 bp in length
* 41152 42842: contig of 1691 bp in length
* 42843 43828: contig of 986 bp in length
* 43829 44009: contig of 181 bp in length
* 44010 44874: contig of 865 bp in length
* 44875 45191: contig of 317 bp in length
* 45192 46147: contig of 956 bp in length
* 46148 47504: contig of 1357 bp in length
* 47505 49091: contig of 1587 bp in length
* 49092 50259: contig of 1168 bp in length
* 50260 51361: contig of 1102 bp in length
* 51362 52631: contig of 1270 bp in length
* 52632 53607: contig of 976 bp in length
* 53608 54820: contig of 1213 bp in length
* 54821 56600: contig of 1780 bp in length
* 56601 58236: contig of 1636 bp in length

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* 58237 59716: gap of unknown length
* 59717 62221: gap of unknown length
* 62222 65085: gap of unknown length
* 65086 66739: gap of unknown length
* 66740 68359: gap of unknown length
* 68360 70014: gap of unknown length
* 70015 71808: gap of unknown length
* 71809 73581: gap of unknown length
* 73582 75574: gap of unknown length
* 75575 78468: gap of unknown length
* 78469 79231: gap of unknown length
* 79232 83240: gap of unknown length
* 83241 86157: gap of unknown length
* 86158 89150: gap of unknown length
* 89151 92671: gap of unknown length
* 92672 95442: gap of unknown length
* 95443 98476: gap of unknown length
* 98477 100815: gap of unknown length
* 100816 103005: gap of unknown length
* 103006 105514: gap of unknown length
* 105515 108704: gap of unknown length
* 108705 111097: gap of unknown length
* 111098 114888: gap of unknown length
* 114889 117423: gap of unknown length

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Alignment Scores:

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Pred. No.: 3,07e-05 Length: 229426
Score: 15.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 10.56% Indels: 0
DB: 2 Gaps: 0

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US-09-690-825-34 (1-142) x AC010532 (1-229426)

Qy 114 AAlaYsGluThrAsnAsnIySlySgluphegiuclurrrAla 128

Db 159273 GCAAGAGAACCAACATACAGAAAGAAATTTGAGAACTGCG 159229

RESULT 51

AY174765

LOCUS AY174765 772 bp mRNA linear VRT 15-JAN-2003

DEFINITION Xenopus laevis SIX mRNA, complete cds.

ACCESSION AY174765

VERSION AY174765.1 GI:27762628

KEYWORDS

SOURCE Xenopus laevis (African clawed frog)

ORGANISM Xenopus laevis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; Xenopodinae; Xenopus.
 1 (bases 1 to 772)
 Song, K.-H., Kim, T.-M., Kim, H.-J., Kim, J.W., Kim, H.-H., Kwon, H.-B., Kim, W.S. and Choi, H.-S.
 Molecular cloning and characterization of a novel inhibitor of apoptosis protein from *Xenopus laevis*
 Unpublished
 2 (bases 1 to 772)
 Song, K.-H., Kim, T.-M., Kim, H.-J., Kim, J.W., Kim, H.-H., Kwon, H.-B., Kim, W.S. and Choi, H.-S.
 Direct Submission
 Submitted (07-NOV-2002) Hormone Research Center, 300 Yongsong-dong Buk-gu, Kwangju 500-757, Korea
 Location/Qualifiers
 1. 772
 /organism="Xenopus laevis"
 /mol_type="mRNA"
 /db_xref="taxon:8355"
 6. 479
 /note="survivin in *Xenopus*"
 /codon_start=1
 /product="Six"
 /protein_id="AA020085.1"
 /db_xref="GI:27762628"
 /translation="WLSISPLRCDNEFSPDEWRLYNATRLRTFSNPFEDC
 ACPEPMAEGFACPTDNPVCKFCCKELEGQPEDPDEHKKSPSCFLAL
 KKRAEHLTSLFKLDELHTKIKWQKQNMHIERFQKANEVGHLEKADADPTQ"
 ORIGIN
 Alignment Scores:
 Pred. No.: 2.56e-05 Length: 772
 Score: 13.00 Matches: 13
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 9.15% Indels: 0
 Gaps: 0
 DB: 5
 US-09-690-825-34 (1-142) x AV174765 (1-772)
 Cy 31 CysAlaCysThrProGluArgMetAlaGluIaIyphye 43
 Db 135 TGGCGTTGTACCCAGAGCGATGCGAGAGCGTGATTT 173
 RESULT 52 AC141438 207347 bp DNA linear HTG 16-MAR-2003
 LOCUS AC141438 Mus musculus chromosome UNK clone RP23-212C9, WORKING DRAFT
 DEFINITION SEQUENCE, 8 unordered pieces.
 AC141438
 AC141438.2 GI:28975182
 HTG, HTGS_PHASE1, HTGS_DRAFT, HTGS_FULLTOP.
 KEYWORDS Mus musculus (house mouse)
 SOURCE
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 207347)
 McPherson, J.D. and Waterston, R.H.
 The sequence of Mus musculus clone
 Unpublished
 2 (bases 1 to 207347)
 McPherson, J.D. and Waterston, R.H.
 Direct Submission
 Submitted (15-MAR-2003) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
 3 (bases 1 to 207347)
 McPherson, J.D. and Waterston, R.H.
 Direct Submission
 Submitted (16-MAR-2003) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
 On Mar 16, 2003 this sequence version replaced gi:28973971.
 COMMENT

----- Genome Center -----
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: <http://genome.wustl.edu/gsc/index.shtml>
 Contact: submissions@watson.wustl.edu
 Project Information
 Center project name: M_BA0212C09
 ----- Summary Statistics -----
 Sequencing vector: M13; 0%
 Sequencing vector: plasmid; 100%
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 204828 bases at least Q40
 Consensus quality: 205544 bases at least Q30
 Consensus quality: 206016 bases at least Q20

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 8 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
 * 1
 * 1063 1062: contig of 1062 bp in length
 * 1163 1162: gap of unknown length
 * 1163 5221: contig of 4039 bp in length
 * 5222 5221: gap of unknown length
 * 5322 16616: contig of 11295 bp in length
 * 16617 16716: gap of unknown length
 * 16717 31077: contig of 14361 bp in length
 * 31078 31177: gap of unknown length
 * 31178 59093: contig of 27916 bp in length
 * 59094 59193: gap of unknown length
 * 59194 74865: contig of 15672 bp in length
 * 74866 74966: gap of unknown length
 * 74966 128601: contig of 53636 bp in length
 * 128602 128701: gap of unknown length
 * 128702 207347: contig of 78646 bp in length.
 * Location/Qualifiers
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 1. 207347
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 /chromosome="UNK"
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 1163. 5221
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 5322. 16616
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 16717. 31077
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 31178. 59093
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 59194. 74865
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 74966. 128601
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 128702. 207347
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 Alignment Scores:
 Pred. No.: 0.00628 Length: 207347
 Score: 13.00 Matches: 13
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 9.15% Indels: 0
 Gaps: 0
 DB: 2

US-09-690-825-34 (1-142) x AC141438 (1-207347)

Qy 108 ArgAlaIysAsnIysIleAlaIysGluThrAsnAsnIys 120
 |||||
 Db 27135 AGAGCCAGACAAATTCGAAAGAGACCAACACACAG 27173

RESULT 53

AF442492 483 bp mRNA linear VRT 03-DEC-2002
 LOCUS Xenopus laevis survivin mRNA, complete cds.
 DEFINITION AF442492
 ACCESSION AF442492
 VERSION AF442492.1 GI:25990776

KEYWORDS Xenopus laevis (African clawed frog)
 SOURCE Xenopus laevis
 ORGANISM Xenopus laevis

REFERENCE 1 (bases 1 to 483)
 AUTHORS Murphy, C.R., Sabel, J.L., Sandler, A.D. and Dagle, J.M.
 TITLE Survivin mRNA is down-regulated during early Xenopus laevis
 embryogenesis
 JOURNAL Dev. Dyn. 225 (4), 597-601 (2002)

REFERENCE 2 (bases 1 to 483)
 MEDLINE 22341152
 PUBMED 12454937

REFERENCE 2 (bases 1 to 483)
 AUTHORS Murphy, C.R., Sabel, J.L., Sandler, A.D. and Dagle, J.M.
 TITLE Direct Submission
 SUBMITTED (01-NOV-2001) Pediatrics, University of Iowa, 200 Hawkins
 Drive, Iowa City, IA 52242, USA
 JOURNAL Location/Qualifiers

FEATURES

source 1.483
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 /db_xref="taxon:8355"
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CDS

Alignment Scores:
 Pred. No.: 0.000243 Length: 483
 Score: 12.00 Matches: 12
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 8.45% Indels: 0
 DB: 5 Gaps: 0

ORIGIN

US-09-690-825-34 (1-142) x AF442492 (1-483)
 Qy 62 LysGluLeuGluGlyTrpGluProAspAspAspPro 73
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 Db 211 AAGGAGCTGGAGGCTGGAGCCAGATGATGACCT 246

RESULT 54
 LOCUS AY115553 483 bp mRNA linear VRT 17-JUL-2002
 DEFINITION Xenopus laevis survivin mRNA, complete cds.
 ACCESSION AY115553
 VERSION AY115553.1 GI:21898547

KEYWORDS Xenopus laevis (African clawed frog)
 SOURCE Xenopus laevis
 ORGANISM Xenopus laevis

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
 Xenopodinae; Xenopus.
 1 (bases 1 to 483)
 Bolton, M.A., Lan, W., Powers, S.E., McClelland, M.L., Kuang, J. and
 Stukenberg, P.T.
 Aurora B kinase exists in a complex with survivin and INCENP and
 its kinase activity is stimulated by survivin binding and
 phosphorylation
 Mol. Biol. Cell (2002) In press

TITLE

JOURNAL

REFERENCE 2 (bases 1 to 483)
 AUTHORS Bolton, M.A., Lan, W., Powers, S.E., McClelland, M.L., Kuang, J. and
 Stukenberg, P.T.
 TITLE Direct Submission
 SUBMITTED (28-MAY-2002) Biochemistry and Molecular Genetics,
 University of Virginia Medical School, Health Systems Box 800733,
 Charlottesville, VA 22908, USA
 JOURNAL Location/Qualifiers

FEATURES

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 /dev_stage="11.5-14"
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 associated with INCENP and aurora B kinase; mitotic
 regulator of the inner centromere"

CDS

Alignment Scores:
 Pred. No.: 0.000243 Length: 483
 Score: 12.00 Matches: 12
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 8.45% Indels: 0
 DB: 5 Gaps: 0

ORIGIN

US-09-690-825-34 (1-142) x AY115553 (1-483)
 Qy 62 LysGluLeuGluGlyTrpGluProAspAspAspPro 73
 |||||
 Db 211 AAGGAGCTGGAGGCTGGAGCCAGATGATGACCT 246

RESULT 55
 LOCUS AF322051 503 bp mRNA linear VRT 23-AUG-2002
 DEFINITION Gallus gallus survivin mRNA, complete cds.
 ACCESSION AF322051
 VERSION AF322051.1 GI:11992272

KEYWORDS Gallus gallus (chicken)
 SOURCE Gallus gallus
 ORGANISM Gallus gallus

REFERENCE 1 (bases 1 to 503)
 AUTHORS Johnson, A.L., Langer, J.S. and Brigham, J.T.
 TITLE Survivin as a Cell Cycle-Related and Antiapoptotic Protein in
 Granulosa Cells
 JOURNAL Endocrinology 143 (9), 3405-3413 (2002)

REFERENCE 2 (bases 1 to 503)
 PUBMED 12193553
 AUTHORS Langer, J.S., Johnson, A.L. and Brigham, J.T.
 TITLE Direct Submission
 SUBMITTED (17-NOV-2000) Department of Biology, University of Notre

FEATURES
Source Dame, P.O. Box 369, Notre Dame, IN 46556, USA
Location/Qualifiers
1..503
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9..437
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/db_xref="GI:11992273"
/translation="MAAYAEMLPKEMLVLYVSTRATFRNWPFTGCACTPERMAAG FVHCPSNSPDVACCFCLKEGEPDDDDLEHKKHSAGCAFAALQKDPNLTVOE FLTKDKRTKNVIRKKAISQKEDIDVAKGVRAIENMG"

ORIGIN
Alignment Scores:
Pred. No.: 0.000253 Length: 503
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.45% Indels: 0
DB: 5 Gaps: 0

US-09-690-825-34 (1-142) x AF322051 (1-503)

QY 62 lysglulengluglyttrgjuProaspaspapPro 73
Db 198 AAGGAGCTGGAGGCTGGAGCCGACGACGACCCG 233

RESULT 56 AF377323 555 bp mRNA linear VRT 23-AUG-2002
AF377323
LOCUS Gallus gallus survivin delta mRNA, complete cds, alternatively spliced.
DEFINITION
ACCESSION AF377323.1 GI:14194233
VERSION AF377323
KEYWORDS
SOURCE Gallus gallus (chicken)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 555)
AUTHORS Johnson,A.L., Langer,J.S. and Bridgham,J.T.
TITLE Survivin as a Cell Cycle-Related and Antiapoptotic Protein in Granulosa Cells
JOURNAL Endocrinology 143 (9), 3405-3413 (2002)
12193553
2 (bases 1 to 555)
REFERENCE Langer,J.S., Bridgham,J.T. and Johnson,A.L.
AUTHORS Direct Submission
TITLE Submitted (07-MAY-2001) Biology, University of Notre Dame, P.O. Box 369, Notre Dame, IN 46556, USA
JOURNAL
FEATURES
Source Location/Qualifiers
1..555
/organism="Gallus gallus"
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/db_xref="taxon:9031"
1..408
/note="splice variant containing insertion beyond BIR domain which changes C-terminal predicted survivin"

CDS

ORIGIN
/codon_start=1
/product="survivin delta"
/protein_id="AA05308.1"
/db_xref="GI:14194234"
/translation="MAAYAEMLPKEMLVLYVSTRATFRNWPFTGCACTPERMAAG FVHCPSNSPDVACCFCLKEGEPDDDDLEHKKHSAGCAFAALQKDPNLTVOE FLTKDKRTKNVIRKKAISQKEDIDVAKGVRAIENMG"

Alignment Scores:
Pred. No.: 0.000278 Length: 555
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.45% Indels: 0
DB: 5 Gaps: 0

US-09-690-825-34 (1-142) x AF377323 (1-555)

QY 62 lysglulengluglyttrgjuProaspaspapPro 73
Db 190 AAGGAGCTGGAGGCTGGAGCCGACGACGACCCG 225

RESULT 57 AY100639 773 bp mRNA linear VRT 06-DEC-2002
AY100639
LOCUS Xenopus laevis survivin/XlaR1 mRNA, complete cds.
DEFINITION
ACCESSION AY100639
VERSION AY100639.1 GI:22651694
KEYWORDS
SOURCE Xenopus laevis (African clawed frog)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae; Xenopodinae; Xenopus.
REFERENCE 1 (bases 1 to 773)
AUTHORS Losada,A., Hirano,M. and Hirano,T.
TITLE Cohesin release is required for sister chromatid resolution, but not for condensin-mediated compaction, at the onset of mitosis
JOURNAL Genes Dev. 16 (23), 3004-3016 (2002)
22352081
MEDLINE
PUBMED 12464631
REFERENCE 2 (bases 1 to 773)
AUTHORS Hirano,M. and Hirano,T.
TITLE Direct Submission
JOURNAL Submitted (30-APR-2002) Cold Spring Harbor Laboratory, One Bungtown Road, Cold Spring Harbor, NY 11724, USA
Location/Qualifiers

FEATURES
Source Location/Qualifiers
1..773
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
33..515
/note="regulatory subunit of kinase complex"

CDS

ORIGIN

Alignment Scores:
Pred. No.: 0.000386 Length: 773
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
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Query Match: 8.45% Indels: 0
DB: 5 Gaps: 0

US-09-690-825-34 (1-142) x AY100639 (1-773)

QY 62 lysglulengluglyttrgjuProaspaspapPro 73
Db 243 AAGGAGCTGGAGGCTGGAGCCGACGACGACCCG 278

RESULT 58 AL831742 230800 bp DNA linear ROD 20-AUG-2002
AL831742/c
LOCUS Mouse DNA sequence from clone RP23-11F9 on chromosome 2, complete
DEFINITION

sequence.
 ACCESSION AL831742 GI:22449823
 VERSION HTG.
 KEYWORDS
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 230800)
 REFERENCE
 AUTHORS Tracey, A.
 TITLE Direct Submission
 JOURNAL Submitted (20-AUG-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail emutlites: humquerry@sanger.ac.uk
 On Aug 22, 2002 this sequence version replaced gi:22265551.
 COMMENT
 ----- Genome Center
 Center: Wellcome Trust Sanger Institute
 Center code: SC
 Web site: <http://www.sanger.ac.uk>
 Contact: humquerry@sanger.ac.uk

 During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
 This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats: all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; Sw, SWISSPROT; Tr, TrEMBL; Wp, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-11F9 is from the RPI-23 Mouse PAC Library
 constructed by the group of Pieter de Jong.
 For further details see <http://www.chori.org/bacpac/home.htm>
 VECTOR: pBAC6.6.
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 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 /chromosome="2"
 /clone="RP23-11F9"
 /clone_1ib="RPI-23"
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 Pred. No.: 23.7 Length: 230800
 Score: 10.00 Matches: 10
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 7.04% Indels: 0
 DB: 10 Gaps: 0
 US-09-690-825-34 (1-142) x AL831742 (1-230800)
 QY 132 ArgAgaAaIegIuGInleuA1a1awet 141
 DB 57705 AGGAGAGCATGACAGCTGCGACCATG 57676
 RESULT 59
 AC109963/c AC109963 266342 bp DNA linear HTG 18-SEP-2002
 LOCUS Rattus norvegicus clone CH230-139E1, *** SEQUENCING IN PROGRESS
 DEFINITION
 *** 3 unordered pieces.
 ACCESSION AC109963

VERSION AC109963.4 GI:23101152
 KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT; HTGS ENRICHED.
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 1 (bases 1 to 266342)
 REFERENCE
 AUTHORS Muzny, D., Marier, M., Metzger, M., Lee, A., Abramson, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyanebech, V., Ayagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Behnke, F., Biswal, K., Blatt, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Bunay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M., Davis, C., Day-Carroll, L., De Andrade, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabi, A., Ganta, R., Garcia, A., Garner, T., Garza, W., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guayra, M., Gunaratne, P., Haaland, W., Hamli, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S., Hodgson, A., Hogue, M., Hollins, B., Howell, S., Huiyk, S., Hume, D., Idledit, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kows, C., Kraft, C.L., Labow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, M., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensen, L., Louisedge, H., Lozano, R., Lu, X., Ma, J., Maheshwari, N., Maindarte, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapa, P., Martin, K., Martin, R., Martinez, E., Manning, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Muntada, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwackelamen, O., Okunolu, G., Olampunsa, A., Pal, S., Parke, K., Pascherak, S., Paul, H., Perez, A., Perez, L., Plankoch, C., Plopper, F., Poindexter, A., Popovic, D., Prims, E., Pu, L., Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smaj, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steinle, M., Strong, R., Sutton, A., Svatek, A., Taber, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Umani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, O., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wiczak, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinsteinstock, G., and Gibbs, R.A.
 Direct Submission
 Unpublished
 2 (bases 1 to 266342)
 TITLE
 JOURNAL
 AUTHORS
 TITLE
 JOURNAL
 REFERENCES
 DIRECT SUBMISSION
 Submitted (09-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 266342)
 TITLE
 JOURNAL
 REFERENCES
 DIRECT SUBMISSION
 Submitted (18-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 On Sep 18, 2002 this sequence version replaced gi:21738204.
 The sequence in this assembly is a combination of BAC based reads

ORGANISM

Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.

REFERENCE
AUTHORS
TITLE
1 (bases 1 to 316)
Johnson, A.L., Langer, J.S. and Bridgman, J.T.
Survivin as a Cell Cycle-Related and Antipoptotic Protein in
Granulosa Cells

JOURNAL
PUBMED
12193553
2 (bases 1 to 316)
Langer, J.S., Bridgman, J.T. and Johnson, A.L.

REFERENCE
AUTHORS
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Submitted (07-MAY-2001) Biology, University of Notre Dame, P.O. Box
369, Notre Dame, IN 46556, USA

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12193553
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REFERENCE
AUTHORS
TITLE
Submitted (07-MAY-2001) Biology, University of Notre Dame, P.O. Box
369, Notre Dame, IN 46556, USA

CDS

/db_xref="taxon:9031"
1..180
/note="splice variant containing deletion within BIR
domain and insertion beyond BIR domain; deletion results
in early truncation of predicted survivin"

/codon_start=1
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/protein_id="AAK56309.1"
/db_xref="GI:14194236"

/translation="MAAYAEMLPKENLVYVSTRATFRMPFTEGCACTPERGCTOK
ALRGARFCSSRSRL"

ORIGIN

Alignment Scores:
Pred. No.: 0.761
Score: 9.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 6.34%

DB: 5
Matches: 445
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-09-690-825-34 (1-142) x AF377324 (1-445)

QY 29 GIUGIYCYGALACySThPrOGLuArg 37

Db 91 GAGGCTGCGCTGCACGCCGAGCGG 117

RESULT 64

LOCUS AY057058 489 bp mRNA linear VRT 29-OCT-2001

DEFINITION Danio rerio survivin 2 (birsb) mRNA, complete cds.

ACCESSION AY057058

VERSION AY057058.1 GI:16508147

KEYWORDS

SOURCE Danio rerio (zebrafish)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.

REFERENCE 1 (bases 1 to 489)
Inohara, N. and Nunez, G.

TITLE Genes with homology to mammalian apoptosis regulators identified in
zebrafish

JOURNAL Cell Death Differ. 7 (5), 509-510 (2000)

PUBMED 10917738

REFERENCE 2 (bases 1 to 489)
Inohara, N. and Nunez, G.

TITLE Direct Submission

JOURNAL Submitted (24-SEP-2001) Department of Pathology, University of
Michigan Medical Center, 1500 E. Medical Center Dr., Ann Arbor, MI
48109, USA

FEATURES

source 1..489
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"

gene 1..489
/gene="birsb"

CDS 27..413
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/db_xref="GI:16508148"

ORIGIN

Alignment Scores:
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Score: 9.00
Length: 489
Matches: 9

Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 6.34%
 DB: 5
 Gaps: 0

US-09-690-825-34 (1-142) x AY057058 (1-489)

QY 63 GluLeuGluGlyTyrGluProAspAsp 71
 Db 180 GAACCTGAGGCGCTGGAGAACGATGAC 206

RESULT 65
 AC107911/c 88863 bp DNA linear PRI 25-FEB-2003
 LOCUS Homo sapiens chromosome 17, clone CTD-2507J6, complete sequence.
 AC107911
 AC107911.21 GI:28557953
 HTG.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 Birren,B., Nussbaum,C. and Lander,E.
 1 (bases 1 to 88863)
 2 (bases 1 to 88863)
 Homo sapiens chromosome 17, clone CTD-2507J6
 Unpublished

REFERENCE
 AUTHORS
 JOURNAL
 TITLE
 REFERENCE
 AUTHORS

Birren,B., Linton,L., Nussbaum,C., Lander,E., Ali,A., Allen,N.,
 Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Boukhgalter,B.,
 Brown,A., Camarata,J., Campopiano,A., Chang,U., Chazaro,B.,
 Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
 Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
 Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S.,
 Glade,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
 Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
 Kamat,A., Karatas,A., Kells,C., Lacroque,K., Lamazares,R.,
 Landers,T., Lehoczy,J., Levine,R., Liu,G., Maclean,C.,
 MacDonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M.,
 McMan,P., McKernan,K., Meldrum,J., Meneus,L., Mihova,T.,
 Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C.,
 Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,T.,
 Peterson,K., Phunhngang,P., Pierre,N., Pollara,V., Raymond,C.,
 Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,U.,
 Rosetti,M., Roy,A., Santos,R., Schauer,S., Schnupack,R., Seaman,S.,
 Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
 Straus,N., Subramanian,A., Talamas,J., Testfaye,S., Theodore,J.,
 Topham,K., Travers,M., Travis,N., Trigglio,J., Vassiliev,H.,
 Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
 Zainoun,J., Zemdek,L., Zimmer,A. and Zody,M.

TITLE
 JOURNAL
 REFERENCE
 AUTHORS

Submitted (24-JAN-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 88863)
 Direct Submission
 Birren,B., Nussbaum,C., Lander,E., Abouelleil,A., Allen,N.,
 Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
 Boguslavsky,L., Boukhgalter,B., Camarata,U., Chang,U., Choepel,Y.,
 Collymore,A., Cook,A., Cooke,P., Corum,B., Dearellano,K.,
 Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,
 Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S.,
 Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B.,
 Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
 Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
 Lindblad-Toh,K., Liu,G., Lui,A., Mabbitt,R., Maclean,C.,
 MacDonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,
 Meldrum,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J.,
 Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,
 O'Neil,D., Oliver,T., Peterson,K., Phunhngang,P., Pierre,N.,
 Rachupka,A., Ramsamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,
 Roman,U., Schauer,S., Schnupack,R., Seaman,S., Severy,P., Smith,C.,
 Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,
 Talamas,J., Testfaye,S., Theodore,J., Topham,K., Travers,M.,
 Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
 Wyman,D., Young,G., Zainoun,J., Zemdek,L., Zimmer,A. and Zody,M.

TITLE
 JOURNAL
 REFERENCE
 AUTHORS

Direct Submission
 Submitted (22-JAN-2003) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 4 (bases 1 to 88863)
 Birren,B., Nussbaum,C., Lander,E., Abouelleil,A., Allen,N.,
 Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
 Boguslavsky,L., Boukhgalter,B., Camarata,U., Chang,U., Choepel,Y.,
 Collymore,A., Cook,A., Cooke,P., Corum,B., Dearellano,K.,
 Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,
 Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S.,
 Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B.,
 Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
 Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
 Lindblad-Toh,K., Liu,G., Lui,A., Mabbitt,R., Maclean,C.,
 MacDonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,
 Meldrum,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J.,
 Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,
 O'Neil,D., Oliver,T., Peterson,K., Phunhngang,P., Pierre,N.,
 Rachupka,A., Ramsamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,
 Roman,U., Schauer,S., Schnupack,R., Seaman,S., Severy,P., Smith,C.,
 Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,
 Talamas,J., Testfaye,S., Theodore,J., Topham,K., Travers,M.,
 Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
 Wyman,D., Young,G., Zainoun,J., Zemdek,L., Zimmer,A. and Zody,M.

TITLE
 JOURNAL
 REFERENCE
 AUTHORS

Submitted (25-FEB-2003) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Feb 25, 2003 this sequence version replaced gi:27819569.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: MIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence.submissions@genome.wi.mit.edu
 Project information
 Center project name: L23028
 Center clone name: 2507_J_6

FEATURES
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repeat_region
 1..107
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 112..404
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 /rpt_family="AluSx"
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 2306..2361
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repeat_region 18601, .18839
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/rpt_family="L1MC4a"
repeat_region 19640, .19773
/rpt_family="AlusG/x"
repeat_region 19774, .20064
/rpt_family="AlusX"
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repeat_region 21235, .21532
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Alignment Scores:

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Score:	9.00	Matches:	9
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Best Local Similarity:	100.00%	Mismatches:	0

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Query Match: 6.34% Indels: 0
DB: 9 Gaps: 0
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Cy 130 LysValArgAlaGlnGluGlnLeu 138
Db 60477 AAGGTAGAGAGACTATTGACGACTC 60451

RESULT 66
AC016292 104435 bp DNA linear pri 19-MAR-2003
LOCUS Homo sapiens chromosome 17, clone RP11-22G12, complete sequence.
DEFINITION AC016292
AC016292.26 GI:29124200
VERSION AC016292.26
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 104435)
Biren,B., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 17, clone RP11-22G12
Unpublished
2 (bases 1 to 104435)
Biren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baldwin,J., Barna,A., Beckert,L., Boguslavsky,L., Boukhgalter,B.,
Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
Cooke,P., DeRubeis,A., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
Ferreira,P., Fitzhugh,W., Forrest,C., Funke,R., Gage,D.,
Galligan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howard,J., Johnson,R., Jones,C., Kamm,L., Karatas,A., Klein,J.,
Lehoczky,J., Lieu,C., Locke,K., MacDonald,P., Marquis,N.,
McGowan,P., McGurk,A., McKernan,C., McLaughlin,J., Meldrum,J.,
Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
Stange,Thomann,N., Stojanovic,N., Sudarmanian,A., Talamas,J.,
Testa,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (24-NOV-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 104435)
Biren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
Boguslavsky,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y.,
Collymore,A., Cook,A., Cooke,P., Corum,B., DeRubeis,A.,
Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,
Ferreira,P., Fitzgerald,M., Gage,D., Galligan,J., Gardyna,S.,
Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B.,
Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamm,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
Lindblad-Toh,K., Liu,G., Lui,A., Mabbitt,R., Maclean,C.,
Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,
Meldrum,J., Menus,L., Mihova,T., Menga,V., Murphy,T., Naylor,J.,
Nguyen,C., Nicot,R., Norbu,C., O'Connor,T., O'Donnell,P.,
O'Neill,D., Oliver,J., Peterson,K., Phukhang,P., Pierre,N.,
Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Riese,C., Rogov,P.,
Roman,V., Schauer,S., Schupbach,R., Seaman,S., Severy,P., Smith,C.,
Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,
Talamas,J., Testa,S., Theodore,J., Topham,K., Travers,M.,
Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (31-JAN-2003) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
4 (bases 1 to 104435)
Biren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
Boguslavsky,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y.,
Collymore,A., Cook,A., Cooke,P., Corum,B., DeRubeis,A.,
Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,
Ferreira,P., Fitzgerald,M., Gage,D., Galligan,J., Gardyna,S.,

```

TITLE
JOURNAL

COMMENT
All repeats were identified using RepeatMasker:
Smit, A.P.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information
Center project name: L4116
Center clone name: 22_G_12

Only the first 104,4 Kilobases of this clone are being submitted.
The remainder overlaps accession number AC015884 [WIGR project L731].

FEATURES

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/clone_lib="RPC1-11 Human Male BAC"
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complement (1745. .1925)
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/note="probably C; possibly T"
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3831. 4079
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4912. .4980
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repeat_region	complement (6705. .6997)
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repeat_region	complement (12613. .12910)
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repeat_region	complement (14173. .14226)
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repeat_region	complement (14256. .14414)
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repeat_region	complement (15128. .15200)
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repeat_region	complement (15302. .15360)
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Alignment Scores:
Pred. No.: 163
Score: 9.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 6.34%
DB: 9
Gaps: 0

US-09-690-825-34 (1-142) x AC016292 (1-104435)

QY 130 LysValArgArgAlaIleGlnGlnLeu 138
 DB 47584 AAGGTAGAGAGAGCTATTGACGAGCTC 47610

RESULT 67
 AC145222

LOCUS AC145222 136470 bp DNA linear HTG 04-DEC-2003
 DEFINITION Medicago truncatula clone mth2-29a15, WORKING DRAFT SEQUENCE, 7
 unorderded pieces.
 AC145222
 AC145222.7 GI:38678560
 HTG: HTGS PHASE1; HTGS DRAFT.
 SOURCE Medicago truncatula (barrel medic)
 ORGANISM Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eustosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
 Medicago.

REFERENCE
 AUTHORS 1 (bases 1 to 136470)
 Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
 Cook,D., Kim,D. and Roe,B.A.
 TITLE Medicago truncatula BAC Clone mth2-29a15
 JOURNAL Unpublished
 2 (bases 1 to 136470)
 Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
 Cook,D., Kim,D. and Roe,B.A.
 TITLE Direct Submission
 JOURNAL Submitted (17-JUN-2003) Department Of Chemistry And Biochemistry,
 The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
 OK 73019, USA
 3 (bases 1 to 136470)
 Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
 Cook,D., Kim,D. and Roe,B.A.
 TITLE Direct Submission
 JOURNAL Submitted (04-DEC-2003) Department Of Chemistry And Biochemistry,
 The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
 OK 73019, USA

COMMENT
 ----- Genome Center
 Center: Department Of Chemistry And Biochemistry
 The University Of Oklahoma
 Center code:UOKNOR

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 7 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1
 3445 3444: contig of 3444 bp in length
 3545 3544: gap of unknown length
 10199: contig of 6655 bp in length
 10200 10299: gap of unknown length
 10300 10299: gap of unknown length
 22748: contig of 12449 bp in length
 22848: gap of unknown length
 39691: contig of 16843 bp in length
 39791: gap of unknown length
 39792 65273: contig of 25482 bp in length
 65274 65373: gap of unknown length
 65374 92085: contig of 26712 bp in length
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 /mol_type="genomic DNA"
 /db_xref="taxon:3880"
 /clone="mth2-29a15"

ORIGIN /clone_lib="Medicago truncatula BAC library H2"

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 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 6.34% Indels: 0
 DB: 2 Gaps: 0

US-09-690-825-34 (1-142) x AC145222 (1-136470)

QY 115 LysGluThrAspAsnLysLysGlu 123
 DB 130497 AAGAGACTAATTAACAGAGAAAGAA 130523

RESULT 68
 AC146981/c

LOCUS AC146981 146515 bp DNA linear HTG 30-OCT-2003
 DEFINITION Homo sapiens chromosome 17 clone RP13-856H21 map 17, WORKING DRAFT
 SEQUENCE, 22 unorderded pieces.
 AC146981
 AC146981.1 GI:38044233
 HTG: HTGS PHASE1; HTGS DRAFT; HTGS FULLTOP.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 AUTHORS 1 (bases 1 to 146515)
 Birren,B., Nusbaum,C. and Lander,E.
 TITLE Homo sapiens chromosome 17, clone RP13-856H21
 JOURNAL Unpublished
 2 (bases 1 to 146515)
 Birren,B., Nusbaum,C., Lander,E., Aboueleil,A., Allen,N.,
 Anderson,N., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
 Boguslavsky,L., Boukhgalter,B., Camarata,J., Chang,Y., Choepel,Y.,
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 Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,
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 Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,
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 O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
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 Roman,Y., Schauer,S., Schnupack,R., Seaman,S., Severy,P., Smith,C.,
 Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,
 Talamas,J., Testaye,S., Theodore,J., Topham,K., Travers,M.,
 Vasilev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
 Wymann,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
 Direct Submission
 JOURNAL Submitted (30-OCT-2003) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html
 ----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WPIR
 Web site: http://www-seg.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: U30056
 Center clone name: 856.H.21
 ----- Summary Statistics
 Sequencing vector: M13; M77815; 50% of reads
 Sequencing: n/a; 50% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731

Consensus quality: 118962 bases at least Q40
 Consensus quality: 141529 bases at least Q30
 Consensus quality: 142778 bases at least Q20
 Insert size: 197000; agarose-fp
 Insert size: 144415; sum-of-coverage
 Quality coverage: 8.7 in Q20 bases; agarose-fp
 Quality coverage: 11.8 in Q20.
 NOTE: This is a 'working draft' sequence. It currently
 consists of 22 contigs. The true order of the pieces
 is not known and their order in this sequence record is
 arbitrary. Gaps between the contigs are represented as
 runs of N, but the exact sizes of the gaps are unknown.
 This record will be updated with the finished sequence
 as soon as it is available and the accession number will
 be preserved.

1 16866: contig of 16866 bp in length
 16867 16966: gap of 100 bp
 16967 17387: contig of 421 bp in length
 17388 17487: gap of 100 bp
 17488 17552: contig of 65 bp in length
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 19369 19669: gap of 100 bp
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 21564 22396: contig of 834 bp in length
 22397 22496: gap of 100 bp
 22497 22855: contig of 359 bp in length
 22856 22956: gap of 100 bp
 22957 24036: contig of 1081 bp in length
 24037 24136: gap of 100 bp
 24137 26011: contig of 1875 bp in length
 26012 26111: gap of 100 bp
 26112 28326: contig of 2215 bp in length
 28327 28426: gap of 100 bp
 28427 30147: contig of 1721 bp in length
 30148 30247: gap of 100 bp
 30248 31844: contig of 1597 bp in length
 31845 31944: gap of 100 bp
 31945 34909: contig of 2965 bp in length
 34910 35009: gap of 100 bp
 35010 36835: contig of 1826 bp in length
 36836 36935: gap of 100 bp
 36936 48373: contig of 11438 bp in length
 48374 48473: gap of 100 bp
 48474 61952: contig of 13479 bp in length
 61953 76344: gap of 100 bp
 76345 76444: gap of 100 bp
 76445 91535: contig of 15091 bp in length
 91536 91635: gap of 100 bp
 91636 109845: contig of 18210 bp in length
 109846 109945: gap of 100 bp
 109946 146515: contig of 36570 bp in length.

FEATURES

Source

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ORIGIN

Alignment Scores:

Pred. No.: 228 Length: 146515
 Score: 9.00 Matches: 9
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 6.34% Indels: 0
 DB: 2 Gaps: 0

US-09-690-825-34 (1-142) x AC146981 (1-146515)

Qy 130 lvsValARGATGAlleGUGInleu 138

Db 110664 AAGGTGAGGAGCTATTGACGAGCTC 110638

RESULT 69

LOCUS BX649590

DEFINITION Danio rerio clone CH211-14316, WORKING DRAFT SEQUENCE, 3 unordered pieces.

ACCESSION BX649590

VERSION BX649590.3 GI:37606081

KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT; HTGS FULLTOP.

SOURCE Danio rerio (zebrafish)

ORGANISM Danio rerio

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostraciophysi;

Cypriniformes; Cyprinidae; Danio.

AUTHORS McLaren,S.

TITLE 1 (bases 1 to 180849)

JOURNAL Submitted (30-OCT-2003) Wellcome Trust Sanger Institute, Hinxton,

Cambridgehire, CB10 1SA, UK. E-mail enquiries:
zfish-hel@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Oct 9, 2003 this sequence version replaced g1:37496403.

----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: zfish-hel@sanger.ac.uk
----- Project Information

Center project name: zc14316
----- Summary Statistics

Assembly program: XGAP4; version 4.5
Chemistry: dye-terminator; 100% of reads
Consensus quality: 180245 bases at least Q40
Consensus quality: 180416 bases at least Q20
Consensus quality: 180499 bases at least Q20
Insert size: 180643; sum-of-contigs
Insert size: 179152; 5.1% error; agarose-fp
Quality coverage: 9.17x in Q20 bases; sum-of-contigs quality
coverage: 9.40x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 3075: contig of 3075 bp in length
* 3076 3175: gap of 100 bp
* 3176 93133: contig of 89958 bp in length
* 93134 93234: gap of 100 bp
* 93234 180849: contig of 87616 bp in length.
Location/Qualifiers

FEATURES

source

1. 180849
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="CH211-14316"
/clone_id="CHORI-211"
1. 3075
/note="assembly fragment:01583
fragment chain:1
clone_end:r7
vector_side:left"

misc_feature

3176..93133
/note="assembly fragment:00359
fragment chain:1"

misc_feature

93234..180849
/note="assembly fragment:01693
fragment chain:1
clone_end:sp6
vector_side:right"

ORIGIN

Alignment Scores:

Pred. No.: 280 Length: 180849
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 6.34% Indels: 0
DB: 2 Gaps: 0

US-09-690-825-34 (1-142) x BK645590 (1-180849)

QY 115 LysGIUTrAsrAsnLyLyLyGlu 123

DB 20152 AAAGAAACAAATTAATAAAAAGAAAGA 20178

RESULT 70

AC015532/C

LOCUS AC015532 184592 bp DNA

linear

HTG 26-MAY-2001

DEFINITION

Homo sapiens chromosome 18 clone RP11-497J22 map 18, WORKING DRAFT

SEQUENCE, 24 unordered pieces.

ACCESSION

AC015532.4 GI:14209776

VERSION

HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.

KEYWORDS

Homo sapiens (human)

SOURCE

Homo sapiens

ORGANISM

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 184592)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.

AUTHORS

2 (bases 1 to 184592)
Unpublished

TITLE

Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,
Baldwin, J., Barna, N., Beckerly, R., Boguslavsky, L., Boukhalter, B.,
Brown, A., Castle, A., Colangelo, M., Collins, S., Collamore, A.,
Cooke, P., DeRellano, K., Dewar, K., Dominko, M., Donelan, L., Doyle, M.,
Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D.,
Gaisgan, J., Gardyna, S., Grant, G., Hagos, B., Heath, A., Horton, L.,
Howland, J., Johnson, R., Jones, C., Kahn, L., Karatas, A., Klein, J.,
Lehoczy, J., Lieu, C., Locke, K., Macdonald, P., Margulis, N.,
McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meidrim, T.,
Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,
Peterson, K., Pollard, V., Riley, R., Roy, A., Santos, R., Severy, P.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, U.,
Testaye, S., Threll, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,
Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.

REFERENCE

Submitted (16-NOV-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On May 26, 2001 this sequence version replaced g1:13449485.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

TITLE

Direct Submission

COMMENT

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: MIBS
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information

Center project name: 497_J_22
Center clone name: 14304
----- Summary Statistics
Sequencing vector: Plasmid; N/A; 99% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 173769 bases at least Q40
Consensus quality: 179123 bases at least Q20
Consensus quality: 181017 bases at least Q20
Insert size: 168000; agarose-fp
Insert size: 182292; sum-of-contigs
Quality coverage: 11.4 in Q20 bases; agarose-fp
Quality coverage: 10.5 in Q20.

* NOTE: This is a 'working draft' sequence. It currently
* consists of 24 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 118291: contig of 118291 bp in length
* 118292 118391: gap of 100 bp
* 118392 119283: contig of 892 bp in length
* 119284 119383: gap of 100 bp in length
* 119384 120009: contig of 626 bp in length
* 120010 120109: gap of 100 bp in length
* 120110 120974: contig of 865 bp in length
* 120975 121074: gap of 100 bp in length
* 121075 122027: contig of 953 bp in length
* 122028 122127: gap of 100 bp

JOURNAL
Submitted (28-AUG-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE
3 (bases 1 to 184717)
AUTHORS
Britten, B., Linton, L., Nussbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L.,
Boukhalter, B., Brown, A., Camarata, J., Campobasso, A., Chang, J.,
Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A.,
Cook, A., Cooke, P., Dekrellano, K., Dewar, K., Diaz, J., Dodge, S.,
Faro, S., Ferrel, P., Fitzhugh, W., Gage, D., Galagan, J., Galdyna, S.,
Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Kells, C., Lacroque, K., Lamazares, R.,
Landers, T., Lehoczy, J., Levine, R., Lindblad-Toh, K., Liu, G.,
Maclean, C., Macdonald, P., Major, J., Marcus, N., Matthews, C.,
McCarthy, M., McKernan, P., McKernan, K., Meldrum, J., Meneus, L.,
Minova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R.,
Norbu, C., Norman, C., O'Connor, T., O'Donnell, P., O'Neil, D.,
Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupbach, R.,
Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talama, J., Testfaye, S., Theodore, J.,
Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE
JOURNAL
Submitted (10-APR-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE
4 (bases 1 to 184717)
AUTHORS
Britten, B., Linton, L., Nussbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L.,
Boukhalter, B., Brown, A., Camarata, J., Campobasso, A., Chang, J.,
Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A.,
Cook, A., Cooke, P., Dekrellano, K., Dewar, K., Diaz, J., Dodge, S.,
Faro, S., Ferreira, P., Fitzgerald, M., Fitzhugh, W., Gage, D.,
Galagan, J., Galdyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I.,
Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Lacroque, K.,
Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lindblad-Toh, K.,
Liu, G., Maclean, C., Macdonald, P., Major, J., Margulis, N.,
Matthews, C., McCarthy, M., McKernan, P., McKernan, K., Meldrum, J.,
Meneus, L., Minova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C.,
Nicol, R., Norbu, C., Norman, C., O'Connor, T., O'Donnell, P.,
O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,
Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C.,
Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S.,
Schupbach, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N.,
Stojanovic, N., Strauss, N., Subramanian, A., Talama, J., Testfaye, S.,
Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., J.,
Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE
JOURNAL
Submitted (15-JUN-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT
On Jun 15, 2002 this sequence version replaced g1:20128507.
All repeats were identified using RepeatMasker:
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: W1BR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Project Information
Center project name: L2462
Center clone name: 534_N_16
Location/Qualifiers
1. 184717
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="18"

/map="18"
/clone="RP11-534N16"
/clone_id="RP11-534N16 Human Male BAC"
98.1129
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repeat_region
complement(1847..2078)
/rpt_family="MLTID"
repeat_region
complement(2190..2369)
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/rpt_family="L1ME"
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                    /rpt_family="Musc"
repeat_region      32854. .32915
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repeat_region      33359. .33594
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                    /rpt_family="AluSq"
repeat_region      34590. .34615
                    /rpt_family="AT_rich"
repeat_region      complement(34952. .35106)
                    /rpt_family="T1MC/D"
repeat_region      35119. .35262
                    /rpt_family="U2"
repeat_region      complement(35384. .35559)
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repeat_region      36614. .36924
                    /rpt_family="AluSx"
repeat_region      38297. .38326
                    /rpt_family="(TATRA)n"
repeat_region      38615. .38662
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Alignment Scores:

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Pred. No.:      286      Length:      184717
Score:          9.00      Matches:      9
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      6.34%      Indels:      0
DB:              9      Gaps:      0

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US-09-690-825-34 (1-142) X AC009717 (1-184717)

QY 96 leuhtlenglygluphelaulylen 104

Db 161494 TTAACATTAGGTGAATCTTAAACCTT 161520

RESULT 72

AC122238

LOCUS AC122238 188476 bp DNA linear ROD 25-NOV-2003

DEFINITION Mus musculus BAC clone RP23-143D4 from chromosome 10, complete

ACCESSION AC122238

VERSION AC122238.4 GI:37361064

KEYWORDS HTG.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 188476)

REFERENCE Swearingen-Shahid,S. and Bielicki,L.

TITLE The sequence of Mus musculus BAC clone RP23-143D4

JOURNAL Unpublished (2001)

REFERENCE 2 (bases 1 to 188476)

AUTHORS Wilson,R.

TITLE Sequencing of Mus musculus

JOURNAL Unpublished (2001)

REFERENCE 3 (bases 1 to 188476)

AUTHORS McPherson,J.D. and Waterston,R.H.

TITLE Direct Submission

JOURNAL Direct Submission

REFERENCE Submitted (23-MAY-2002) Genome Sequencing Center, 4444 Forest Park

AUTHORS Parkway, St. Louis, MO 63108, USA

REFERENCE 4 (bases 1 to 188476)

AUTHORS McPherson,J.D. and Waterston,R.H.

TITLE Direct Submission

JOURNAL Submitted (19-MAR-2003) Genome Sequencing Center, 4444 Forest Park

REFERENCE Parkway, St. Louis, MO 63108, USA

AUTHORS Wilson,R.K.

TITLE Direct Submission

JOURNAL Submitted (02-OCT-2003) Genome Sequencing Center, 4444 Forest Park

REFERENCE Parkway, St. Louis, MO 63108, USA
6 (bases 1 to 188476)
AUTHORS Wilson,R.
TITLE Direct Submission
JOURNAL Submitted (25-NOV-2003) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Oct 2, 2003 this sequence version replaced gi:29124323.
COMMENT ----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu
Contact: submissions@watson.wustl.edu
----- Summary Statistics
Center project name: M_BA0143D04

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu>

SOURCE INFORMATION:
The RP23-23 BAC library has been constructed by Kazutoyo Osegawa and Minako Tateo in the laboratory of Pieter de Jong (<http://www.chori.org>) from female C57BL/6J mouse kidney and/or brain genomic DNA. The clone and detailed information can be obtained from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>

NEIGHBORING SEQUENCE INFORMATION:
This sequence is the entire insert of the clone. This clone is overlapped by AC122239.

FEATURES

source

1. 188476

/organism="Mus musculus"

/mol_type="genomic DNA"

/db_xref="taxon:10090"

/chromosome="10"

/map="10"

/clone="RP23-143D4"

/clone_1lb="RP23-23"

1854..2004

/rpt_family="MaltR"

2049..2197

/rpt_family="Alu"

2244..2391

/rpt_family="MaltR"

3040..3222

/rpt_family="B2"

3236..3404

/rpt_family="Alu"

3452..3615

/rpt_family="B4"

4689..4855

/rpt_family="B4"

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/rpt_family="L1"

5661..5767

/rpt_family="Alu"

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repeat_region      8204..8266
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repeat_region      8411..8661
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repeat_region      8662..8856
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                    complement(8778..8950)
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                    /note="Likely pseudogene (MM Sc=38.89 / Sec struct
                    Sc=-12.60)"
repeat_region      9012..9089
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repeat_region      9267..9417
                    /rpt_family="Alu"
repeat_region      10811..10955
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repeat_region      11986..12120
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repeat_region      13709..14011
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repeat_region      14351..14407
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repeat_region      24265..24399
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repeat_region      24400..24669
                    /rpt_family="B4"
repeat_region      24670..24828
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repeat_region      26212..26318
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unsure             28600..28626
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repeat_region      /rpt_family="L1"
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                    31585..31631
repeat_region      /rpt_family="ERV1"
                    31709..31791
repeat_region      /rpt_family="B4"
                    32334..32483
repeat_region      /rpt_family="Alu"
                    32610..32756
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                    33052..33360
repeat_region      /rpt_family="L1"
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                    35091..35172
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Alignment Scores:

Pred. No.:	292	Length:	188476
Score:	9.00	Matches:	9
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	6.34%	Indels:	0
DB:	10	Gaps:	0

US-09-690-825-34 (1-142) x AC122238 (1-188476)

QY 82 SerGlyCysAlaPheLeuSerVallys 90

DB 37686 TCTGGGTGCGCCTCTCTCAGTAAAG 37712

RESULT 73

AL607066

LOCUS

DEFINITION

Mouse DNA sequence from clone RP23-406N5 on chromosome 4, complete

sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

COMMENT

COMMENT

COMMENT

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AL607066 194837 bp DNA linear ROD 12-AUG-2002

Mouse DNA sequence from clone RP23-406N5 on chromosome 4, complete

sequence.

AL607066

AL607066.23 GI:22213654

HTG.

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 194837)

Direct Submission

Submitted (09-AUG-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Aug 13, 2002 this sequence version replaced gi:21953272.

----- Genome Center

Center: Wellcome Trust Sanger Institute

Center code: SC

Web site: <http://www.sanger.ac.uk>

Contact: humquerry@sanger.ac.uk

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least

FEATURES	source
location/Qualifiers	1..194837
organism="Mus musculus"	
mol_type="genomic DNA"	
db_xref="taxon:10090"	
chromosome="4"	
clone="NPJ-506N5"	
clone_1b="Pc1-23"	

US-09-690-825-34 (1-142) X AL607066 (1-194837)

QY 133 ArgAlaIleGluGlnLeuAlaIaMet 141
 |||||
Db 131454 AGAGCAATTGAGCAACTGACACAAATG 131480

RESULT	74
AC109161/c	
LOCUS	
DEFINITION	Mus musculus clone RP24-112H1, WORKING DRAFT SEQUENCE, 20 ordered pieces.
ACCESSION	AC109161
VERSION	AC109161.4 GI:314425C9
KEYWORDS	HTG; HTGS PHASE2; HTGS_DRAFT; HTGS_FULUTOP.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 195590)
TITLE	Birren,B., Nusbaum,C. and Lander,E.
JOURNAL	Mus musculus, clone RP24-112H1
REFERENCE	Unpublished
REFERENCE	2 (bases 1 to 195590)
AUTHORS	Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., ...

Brown, A., Camarata, J., Campoliano, A., Chang, Y., Charato, B., Choesel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeCarliano, K., Dewar, K., Diaz, J. S., Dodge, S., Fero, S., Ferreira, P., Fitzhugh, W., Gage, D., Galasso, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Haggø, B., Horton, I., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kama, A., Karakas, A., Kelle, C., Lacroque, K., Lamaras, R., Lenders, T., Lekočský, J., Levine, R., Liu, G., Maclean, C., MacDonald, P., Major, V., Margus, N., Matthews, C., McCarthy, M., McKenna, P., Melidoni, V., Menus, L., Mihova, T., Mišna, V., Murphy, T., Naylor, J., Nguyen, C., Nicot, R., Noidy, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Punnkhang, P., Plerre, N., Pollara, V., Raymond, C., Retta, R., Rebeck, M., Riley, R., Rise, C., Rogov, F., Roman, U., Rosell, M., Roy, A., Santos, R., Schauer, S., Schnupack, R., Seaman, S., Severy, P., Spencer, B., Stange, Thomann, N., Stojanovic, N., Stratus, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tophan, K., Travers, M., Travs, N., Trigglio, J., Vassiliou, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.

Bognuslavsky, L., Boukhvalter, B., Canazata, J., Chang, J., Choepeli, Y.,
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 Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, W.
 Direct Submission
 TITLE
 JOURNAL
 COMMENT
 Submitted (06-JUN-2003) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Jun 6, 2003 this sequence version replaced gi:20303722.

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http://ftp.genome.washington.edu/RM/RepeatMasker.html
Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Project Information
Center project name: L18917
Center clone name: 112 H.1

----- Summary Statistics -----
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 194243 bases at least Q40
Consensus quality: 196079 bases at least Q30
Consensus quality: 197024 bases at least Q20
Insert size: 183000; agarose-fp
Insert size: 197690; sum-of-contigs
Quality coverage: 12.2 in Q20 bases; agarose-fp
Quality coverage: 11.3 in Q20 bases; sum-of-contigs

-----
NOTE: This is a 'working draft' sequence. It currently
consists of 20 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces
is believed to be correct as given, however the sizes
of the gaps between them are based on estimates that have
provided by the submittor.
This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.

1
18112: contig of 18112 bp in length
18213: gap of 100 bp
18213: contig of 41 bp in length
18623: gap of 100 bp
18724: contig of 766 bp in length
18724: gap of 100 bp
19490: contig of 582 bp in length
19589: gap of 100 bp
19590: contig of 582 bp in length
20172: gap of 100 bp
20271: contig of 706 bp in length
20272: gap of 100 bp
20978: contig of 665 bp in length
21078: gap of 100 bp
21078: contig of 100 bp
21562: gap of 100 bp
21562: contig of 100 bp

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*	22649	22748:	gap of 100 bp	
*	22749	23615:	contig of 867 bp	in length
*	23615	23715:	gap of 100 bp	
*	23716	24867:	contig of 1152 bp	in length
*	24868	24967:	gap of 100 bp	
*	24968	26657:	contig of 1690 bp	in length
*	26658	26757:	gap of 100 bp	
*	26758	28082:	contig of 1325 bp	in length
*	28083	28182:	gap of 100 bp	
*	28183	29563:	contig of 1381 bp	in length
*	29564	29663:	gap of 100 bp	
*	29664	31551:	contig of 1888 bp	in length
*	31552	31651:	gap of 100 bp	
*	31652	34091:	contig of 2440 bp	in length
*	34092	34191:	gap of 100 bp	
*	34192	39340:	contig of 5145 bp	in length
*	39341	39440:	gap of 100 bp	
*	39441	44766:	contig of 5326 bp	in length
*	44767	44866:	gap of 100 bp	
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*	71941	72040:	gap of 100 bp	
*	72041	98326:	contig of 26286 bp	in length
*	98327	98426:	gap of 100 bp	
*	98427	168712:	contig of 71286 bp	in length
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vector_side:left"				
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vector_side:right"

ORIGIN
Alignment Scores:
Pred. No.: 309 Length: 199590
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 6.34% Indels: 0
Gaps: 2

US-09-690-825-34 (1-142) x AC109161 (1-199590)
Ox 118 AaTAsTLySLySLyGluPhGluGlu 126
Db 47550 AACAAATPAAAGAAAGAGATTGAAGAG 47524

RESULT 75
LOCUS AL805939 202366 bp DNA linear HTG 06-JUL--2002
DEFINITION Mus musculus chromosome 4 clone RP23-327K19, 8 unordered pieces.
ACCESSION AL805939
VERSION AL805939.8 GI:21711913
KEYWORDS HTG; HTGS PHASE1; HTGS CANCELLED.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Plumb,B.
Direct Submission
Submitted (04-JUL-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humgery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jul 8, 2002 this sequence version replaced GI:21684715.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humgery@sanger.ac.uk
----- Project Information
Center project name: BM327K19
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 200675 bases at least Q40
Consensus quality: 201042 bases at least Q30
Consensus quality: 201317 bases at least Q20
Insert size: 201666; sum-of-contigs
Insert size: 202485; 5.9% error; agarose-fp
Quality coverage: 7.92x in Q20 bases; sum-of-coverage
Quality coverage: 8.00x in Q20 bases; agarose-fp
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 31397: contig of 31397 bp in length
* 31398 31497: gap of 100 bp
* 31498 37803: contig of 6306 bp in length
* 37804 37903: gap of 100 bp
* 37904 95452: contig of 57549 bp in length
* 95453 95552: gap of 100 bp
* 95553 100802: contig of 5250 bp in length
* 100803 100902: gap of 100 bp

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* 100903 114281: contig of 13379 bp in length
* 114382 114381: gap of 100 bp
* 114382 183917: contig of 69536 bp in length
* 183918 184017: gap of 100 bp
* 184018 188034: contig of 4017 bp in length
* 188035 188134: gap of 100 bp
* 188135 202366: contig of 14232 bp in length.
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            fragment_chain:1"
            100903..114281
              /note="assembly_fragment:01472
              fragment_chain:1"
              114382..183917
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                fragment_chain:1"
                184018..188034
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                    vector_side:right"

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misc_feature
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  clone_end:T7
  vector_side:left"
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        fragment_chain:1"
        100903..114281
          /note="assembly_fragment:01472
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              fragment_chain:1"
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                fragment_chain:1
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                vector_side:right"

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ORIGIN

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Alignment Scores:
Pred. No.: 313 Length: 202366
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 6.34% Indels: 0
DB: 2 Gaps: 0

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US-09-690-825-34 (1-142) X AL805939 (1-202366)

QY 133 ArgAlaIleGInLeuAlaIaMet 141
 DB 158009 AGAGCAATTGACAACTAGCAGCATG 158035

Search completed: August 16, 2004, 02:46:59
 Job time : 4302 secs

Tue Aug 17 05:54:54 2004

us-09-690-825-34.oligo.rst

Page 1

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 16, 2004, 01:12:49 / Search time 2761 Seconds

(without alignments)
1535.831 Million cell updates/sec

Title: US-09-690-825-34
Perfect score: 142
Sequence: 1 MGAPLPPAWOPFLKDHRS.....EFETAKKVRRAIEQLAAMD 142

Scoring table:
OLIGO
Xgapop 60.0, Xgapext 60.0
Ygapop 60.0, Ygapext 60.0
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 27513289 segs, 14931090276 residues

Word size: 1

Total number of hits satisfying chosen parameters: 55025471

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: listing first 100 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgm2_1/USPRO.spool/US09690825/runat_11082004_141015_13804/app_query.fasta_1.327
-DB=EST -OPMT=fastap -SUPPLX=oligo.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdt -LIST=100
-DOCALLIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=75 -MODE=LOCAL -OUTFMT=ptc
-NORM=ext -HEAPSITE=500 -MUTLEN=0 -MAXLEN=2000000000
-USER=US09690825 @CGN_1_1_3437 @runat_11082004_141015_13804 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -Fgapop=6
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Database :

EST: *
1: em_estdb: *
2: em_esthum: *
3: em_estlin: *
4: em_estmu: *
5: em_estov: *
6: em_estpl: *
7: em_estro: *
8: em_hnc: *
9: gb_est1: *
10: gb_est2: *
11: gb_hnc: *
12: gb_est3: *
13: gb_est4: *
14: gb_est5: *
15: gb_estfun: *
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18: em_gss_inv: *
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20: em_gss_vrt: *
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22: em_gss_mam: *
23: em_gss_mus: *
24: em_gss_pro: *
25: em_gss_rnd: *
26: em_gss_phg: *
27: em_gss_vrl: *
28: gb_gest: *

29: gb_gss2: *
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
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2	142	100.0	478	9	AW710957
3	142	100.0	517	10	AW411195
4	142	100.0	552	12	BG258128
5	142	100.0	552	12	BG258128
6	142	100.0	553	14	BH839824
7	142	100.0	553	14	CH138359
8	142	100.0	563	12	BH835829
9	142	100.0	574	14	CH111125
10	142	100.0	580	10	AM409701
11	142	100.0	584	14	CH128010
12	142	100.0	585	12	BG776624
13	142	100.0	602	9	AL603004
14	142	100.0	605	12	BH841904
15	142	100.0	613	10	AM409816
16	142	100.0	624	14	CH135918
17	142	100.0	629	10	BE297733
18	142	100.0	644	12	BE788077
19	142	100.0	646	12	B1252508
20	142	100.0	682	10	BE796084
21	142	100.0	698	10	BE796061
22	142	100.0	703	10	BE796061
23	142	100.0	707	12	BE115707
24	142	100.0	718	12	BE827836
25	142	100.0	726	13	BH421971
26	142	100.0	742	10	BE907403
27	142	100.0	760	12	BE020628
28	142	100.0	766	12	BG682887
29	142	100.0	772	12	BE750227
30	142	100.0	785	13	BE600185
31	142	100.0	815	12	BG335442
32	142	100.0	815	12	BG744230
33	142	100.0	821	12	BW542207
34	142	100.0	822	9	AU130493
35	142	100.0	826	13	BH171608
36	142	100.0	828	13	BH600854
37	142	100.0	836	9	AU126048
38	142	100.0	861	13	BQ438198
39	142	100.0	868	13	BQ882604
40	142	100.0	874	10	BE883968
41	142	100.0	875	10	BE898710
42	142	100.0	875	12	BG528273
43	142	100.0	880	12	BH450871
44	142	100.0	883	13	BQ650551
45	142	100.0	888	13	BQ227378
46	142	100.0	889	12	BG250436
47	142	100.0	896	13	BK425472
48	142	100.0	908	10	BF972840
49	142	100.0	915	12	BG110508
50	142	100.0	924	12	B1760504
51	142	100.0	933	13	BQ959492
52	142	100.0	934	10	BF982118
53	142	100.0	935	10	BE883927
54	142	100.0	943	10	BF981768
55	142	100.0	943	13	BQ929774
56	142	100.0	962	13	BH649501
57	142	100.0	963	12	B1114304
58	142	100.0	965	13	BH501647
59	142	100.0	974	12	BH463502
60	142	100.0	976	13	BQ064557
61	142	100.0	985	12	BH802009
62	142	100.0	990	13	BQ958253

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63 142 100.0 993 12 BM564739 BM564739 AGENCOURT
64 142 100.0 995 12 BM471181 BM471181 AGENCOURT
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70 142 100.0 1052 12 B1518504 B1518504
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72 142 100.0 1073 13 BG394560 BG394560
73 142 100.0 1114 12 BM551159 BM551159 AGENCOURT
74 142 100.0 1115 9 BQ053391 BQ053391 AGENCOURT
75 142 100.0 1138 2 AL549362 AL549362
76 142 100.0 1201 9 AL515837 AL515837
77 142 100.0 1201 9 AL553525 AL553525
78 142 100.0 1201 13 BX416171 BX416171
79 142 100.0 1201 13 BX422525 BX422525
80 141 99.3 459 12 BG472824 BG472824
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82 141 99.3 1124 10 BE794850 BE794850
83 140 98.6 712 12 BG830958 BG830958
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86 139 97.9 1055 12 BQ890576 BQ890576 AGENCOURT
87 139 97.9 1139 12 BM549522 BM549522 AGENCOURT
88 138 97.2 532 10 BE892608 BE892608
89 138 97.2 535 13 BU659089 BU659089
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91 138 97.2 584 10 BE269775 BE269775
92 133 93.7 757 12 B1334392 B1334392
93 131 92.3 1156 12 BM465375 BM465375 AGENCOURT
94 130 91.5 599 10 BE615441 BE615441
95 129 90.8 718 10 BF219949 BF219949
96 129 90.8 882 12 B1114918 B1114918
97 129 90.8 923 12 BG748549 BG748549
98 129 90.8 1056 10 BF686145 BF686145
99 128 90.1 557 12 BM838065 BM838065
100 128 90.1 788 12 BG254935 BG254935

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ALIGNMENTS

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RESULT 1
LOCUS BM54864
DEFINITION K-EST0032467 SL1SNUI Homo sapiens cDNA clone SL1SNUI-12-C02 5',
          mRNA sequence.
ACCESSION BM754864
VERSION BM754864
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 472)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.

```

```

TITLE Z1C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr

```

```

FEATURES
source 1..472
location/Qualifiers
1..472
/organism="Homo sapiens"
/mol_type="mRNA"

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/db xref="taxon:9606"
/clone="SL1SNUI-12-C02"
/sex="M"
/tissue_type="Stomach"
/cell_type="Lymphoblast-like"
/cell_line="SNU-1"
/lab host="Top10F"
/clone lib="SL1SNUI"
/note="Organ: Stomach; Vector: pME18-PJ3; Site 1: XhoI;
Site 2: XhoI; The poly (A) + RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then deacapped
with tabacco acid pyrophosphatase (TAP). The deacapped
intraet mRNA was ligated with DNA-RNA linker including SfiI
site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized with Superscript II using SfiI
oligo-dT primer. After first strand synthesis, RNA was
degraded by NaOH treatment and cDNA was amplified by PCR
reaction. The PCR products were digested with SfiI and
cloned into DraIII- digested pME18-PJ3 vector. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

```

ORIGIN

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Alignment Scores:
Pred. No.: 7,37e-149 Length: 472
Score: 142.00 Consesive: 142
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 12 Gaps: 0

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US-09-690-825-34 (1-142) x BM754864 (1-472)

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Cy 1 MetGLYALPProThrLeuProAlaTrpGlnProPheLeuYAspHisArgIleSer 20
Db 45 ATGGGCGCCCAACGTCGTCCTGCGACGCTTTCACAGACACCGCATCTCT 104
Cy 21 ThrPheLeuAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
Db 105 ACATTCAAAAGACTGGCCCTTCTTGAGAGGCTGCGCTTCACCCCGAGCGGATGCGCAG 164
Cy 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlyCysPheCys 60
Db 165 GCTGGCTTATCATCACTGCCCCCTGAGACAGCCAGACTGGCCAGCTTCTTCTGCG 224
Cy 61 PheLeuGluLeuGluGlyTrpGluProAspAspProIleGluGluHisIleCys 80
Db 225 TTCAAGAGAGCTGAAAGGCTGGAGCGAGTACGACCCCATAGAGCAATATAAAGCAT 284
Cy 81 SerSerGlyCysAlaPheLeuSerValIleGlyGlnPheGluLeuThrLeuGlyGlu 100
Db 285 TCGTCGGTTGCGCTTCTTCTTCTGCAAGAGCGAGTTGAGAAATTAACCTTGCTGAA 344
Cy 101 PheLeuLeuLeuAspArgGluArgAlaIleAsnIleAlaIleGlyThrAsnAsnIle 120
Db 345 TTTTGAAGACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 404
Cy 121 LysGlyGluPheGluGluThrAlaIleGlyValAlaGAGAGAlaIleGluGlnLeuAla 140
Db 405 AAGAAAGAAATTGAGAGAACTCGAAGAAAGTGGCCCGTCATGACAGCTGGCTGCC 464
Cy 141 MetAsp 142
Db 465 ATTCAT 470

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RESULT 2
LOCUS AL710957
DEFINITION DKFZ0686A0177.r1 686 (synonym: h1ccc3) Homo sapiens cDNA clone
ACCESSION AL710957

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VERSION      AT1710957.1  GI:19694312
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mamalia; Eutheria; Primates; Carnivora; Homnidae; Homo.
TITLE        1 (bases 1 to 478)
JOURNAL      Wamburt,R., Heubner,D., Wewes,W., Weill,B. and Wiemann,S.
COMMENT      EST (Wamburt,R., Heubner,D., Wewes,H.W., Weill,B. and Wiemann,S.)
              Unpublished (1999)
              Contact: MIPS
              MIPS
              Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
              This is the 5' sequence of the clone insert
              Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
              Research Center (DKFZ), Email: s.wiemann@dkfz-heidelberg.de;
              sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
              consortium of the German Genome Project.
              No s1 sequence available.
              This clone (DKFZp686A0177) is available at the RZPD in Berlin.
              Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
              Berlin-Charlottenburg, GERMANY; Email: clonesrzd.de.

FEATURES
  source
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        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="DKFZp686A0177"
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        /lab_host="DH10B"
        /clone_lib="686 (synonym: hicc3)"
        /note="Vector: pTRIPlex2; Site_1: sf11A; site_2: sf11B;
        cDNA-collection"

ORIGIN
Alignment Scores:
Pred. No.:      7,45e-149      Length:      478
Score:          142.00         Matches:      142
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    100.00%       Indels: 0
DB:             9             Gaps: 0

US-09-690-825-34 (1-142) x AL710957 (1-478)
QY      1 MetGlyAaProThrLeuProProAlaTrpGlnProPheLeuYsaPshIaArgIleSer 20
Db      22 ATGGGTGCCCCGACGTTGCCCTGCGAGCCCTTCTCAAGACCAACCGATCTCT 81
QY      21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
Db      82 ACATTCAGAACTGCGCCCTTCTGAGGGCTGCGCCGACCCCGAGCGGATGCGCGAG 141
QY      41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
Db      142 GCTGGCTTCACTGACCTGCCCCACAGACGACCACTTGGCCCGATGTTCTTCTGCG 201
QY      61 PheLysGluLeuGluGlyTrpGluProAspAspAspProIleGluGluHis 80
Db      202 TTCAGAGAGCTGAGAGCTGAGACCGACGATGACACCCCATAGAGGAACATAAAAGCAT 261
QY      81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlu 100
Db      262 TCGTCCGCTGCGCTTCTTCTCTGTCAGAGAGAGATTGAAGATTAAACCTTGGTGA 321
QY      101 PheLeuYsaLeuAspArgIuArgAlaLysAsnLysIleAlaLysGluTrpAsnAsnLys 120
Db      322 TTTTGAAGACTGACAGAGAAAGAGCAAGCAAAATTGCAAGAAAGAAACCAATTAAG 381
QY      121 LysLysGluPheGluGluGluThrAlaLysLysValArgArgAlaIleGluGluAla 140
Db      382 AAGAAAGATTGAGAAATGCGAAGAAAGTGGCGGTCGATGAGCAGCTGGCTGCC 441

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QY      141 MetAsp 142
Db      442 ATGGAT 447

RESULT 3
AM411195
LOCUS      517 bp      mRNA      linear      EST 29-JUN-2000
DEFINITION fthob09.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2964713 5',
            mRNA sequence.
ACCESSION  AM411195
VERSION    AM411195.1  GI:6536736
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mamalia; Eutheria; Primates; Carnivora; Homnidae; Homo.
REFERENCE  NIH-MGC http://mgs.nci.nih.gov/.
AUTHORS    1 (bases 1 to 517)
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
            Email: cgs@bs-remail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNLI)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC)
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/ILNLI at:
            www-bio.lnli.gov/btrp/image/image.html
            Plate: LHC64 row: 0 column: 18
            Seg primer: -21M13 forward primer (ABI).

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        /db_xref="taxon:9606"
        /clone="IMAGE:2964713"
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        /lab_host="DH10B (phage-resistant)"
        /clone_lib="NIH MGC 17"
        /note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
        Site_2: XhoI; cDNA made by clico-dt priming.
        Directionally cloned into EcoRI/XhoI sites using the
        following 5' adaptor: GGCACGAG(G). Size-selected >500bp
        for average insert size 1.8kb. Library constructed by
        Ling Hong in the laboratory of Gerald M. Rubin (University
        of California, Berkeley) using ZAP-cDNA synthesis kit
        (Stratagene) and Superscript II RT (Life Technologies). "

ORIGIN
Alignment Scores:
Pred. No.:      7,96e-149      Length:      517
Score:          142.00         Matches:      142
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    100.00%       Indels: 0
DB:             10             Gaps: 0

US-09-690-825-34 (1-142) x AM411195 (1-517)
QY      1 MetGlyAaProThrLeuProProAlaTrpGlnProPheLeuYsaPshIaArgIleSer 20
Db      44 ATGGGTGCCCCGACGTTGCCCTGCGAGCCCTTCTCAAGACCAACCGATCTCT 103
QY      21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
Db      104 ACATTCAGAACTGCGCCCTTCTGAGGGCTGCGCCCTCAACCCCGAGCGGATGCGCGAG 163
QY      41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
Db      164 GCTGGCTTCACTGACCTGCCCCACAGACGACCACTTGGCCCGATGTTCTTCTGCG 223

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QY 61 PheLysGluLeuGluGlyTyrGluProAspAspProIleGluGluHis 80
 DB 224 TTCAAGAGAGCTGAGAGCTGGAGCCAGATGACGACCCCATAGAGAAACATAAATCAT 283
 QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
 DB 284 TCGTCGGGTGGCTTCTCTTCTGTCAGAGAGCGATTGAGAAATTAACCTTGCGAA 343
 QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
 DB 344 TTTTGAACCTGACAGAGAAAGAGCCAGAAACAAATTCAGAGAGAAACCAACATAG 403
 QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGluLeuAlaAla 140
 DB 404 AAGAAGAAATTGAGAGAACTCGAGAGAAAGTCCCTGCTGCATCGAGCACTGCTGCC 463
 QY 141 MetAsp 142
 DB 464 ATGGAT 469

RESULT 4
 BG258128 552 bp mRNA linear EST 13-FEB-2001
 LOCUS 602379226F1 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:4510014 5'
 DEFINITION mRNA sequence.
 ACCESSION BG258128
 VERSION BG258128.1 GI:12767944
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 552)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LHAM10391 row: C column: 07
 High quality sequence stop: 552.
 Location/Qualifiers

FEATURES
 source 1..552
 Location/Qualifiers

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4510014"
 /tissue_type="embryonal carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 92"
 /note="Organ: testis; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
 Average insert size 2.5 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 8-42e-149 Length: 552
 Score: 142.00 Matches: 142
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Gaps: 0
 DB: 12

US-09-690-825-34 (1-142) x BG258128 (1-552)

QY 1 MetGlyAlaProThrLeuProAlaIleGlnProPheLeuAspHisArgIleSer 20
 DB 32 ATGGAGGCCCGACAGTGGCCCCCTGCGACGCCCTTCTCAAGAGACACCGCATCTCT 91
 QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
 DB 92 ACATTCAAACTGAGCTGCTTCTTGAAGGCTGCGCTGACCCCGAGCGAGTGGCCAG 151
 QY 41 AlaGlyPheIleHisCysProThrGluGlnGluProAspLeuAlaGlnCysPhePheCys 60
 DB 152 GCTGCTTATCATCACTGCCCTGAGAGAGAGCCAGACTTGCCAGTGTCTTCTGCG 211
 QY 61 PheLysGluLeuGluGlyTyrGluProAspAspAspProIleGluGluHisLysLysHis 80
 DB 212 TTCAAGAGAGCTGAGAGCTGGAGGAGCAGATGACGCCCATAGAGAGAACTAAAAAGAT 271
 QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
 DB 272 TCGTCGGGTGGCTTCTCTTCTGTCAGAGAGCGATTGAGAAATTAACCTTGCTGAA 331
 QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
 DB 332 TTTTGAACCTGACAGAGAAAGAGCCAGAAACAAATTCAGAGAGAAACCAACATAG 391
 QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGluLeuAlaAla 140
 DB 392 AAGAAGAAATTGAGAGAACTCGAGAGAAAGTCCCTGCTGCATCGAGCACTGCTGCC 451
 QY 141 MetAsp 142
 DB 452 ATGGAT 457

RESULT 5
 BM839824 552 bp mRNA linear EST 06-MAR-2002
 LOCUS BM839824
 DEFINITION K-EST0116794 S13KMS5 Homo sapiens cDNA clone S13KMS5-32-F06 5',
 mRNA sequence.
 ACCESSION BM839824
 VERSION BM839824.1 GI:19196233
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 552)
 Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.
 21C Frontier Korean EST Project 2001
 Unpublished (2002)
 CONTACT: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Beon-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Place: 32 row: F column: 06
 High quality sequence stop: 552.
 Location/Qualifiers

FEATURES
 source 1..552
 Location/Qualifiers

TITLE
 JOURNAL
 COMMENT

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="S13KMS5-32-F06"
 /tissue_type="myeloma"
 /cell_line="KMS-5"
 /lab_host="Top10P"
 /clone_lib="S13KMS5"
 /note="Vector: pCNS; Site 1: EcoRI; Site 2: NotI; The poly
 (A) + RNA was dephosphorylated with bacterial alkaline
 phosphatase (BAP) and then decapped with tobacco acid
 pyrophosphatase (TAP). The decapped intact mRNA was

ligated with DNA-RNA linker including Ecor I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-tailed mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10⁺ by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Alignment Scores:

Pred. No.:	8,42e-149	Length:	552
Score:	142.00	Matches:	142
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	12	Gaps:	0

US-09-690-825-34 (1-142) x BM839824 (1-552)

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Qy      1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
Db      78 ATGGGTGCCCCGAGCTGGCCCCCTGGCGAGCCCTTCTCAAGGACCCGCACTCTCT 137
Qy      21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
Db      138 ACATTCAAGAACTGCGCCCTTCTTGAGAGGCTGCGCCCTGCAACCCGAGCGGAGCGGAG 137
Qy      41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
Db      198 GCTGCGCTTCACTCCCTCCCACTGAGACGAGCAGACACTTGCGCCCTTCTTCTTCTGC 257
Qy      61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHis 80
Db      258 TTCAAGAGAGCTGGAGGCTGGAGCCGAGATGACACCCCTAGAGAACTATAAAGCAT 317
Qy      81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluLeuThrLeuGlyGlu 100
Db      318 TCGCCGAGTTCGCTTCTTCTTCTGTCAGAGAGAGTTTGAAGATTAACCTTGCTGAA 377
Qy      101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
Db      378 TTTTGAAGACTGACAGAGAAAGCCAGAAACAAATTGCAAGAGAAACCAACAAATAG 437
Qy      121 LysLysGluPheGluGluThrAlaLysValArgArgAlaIleGluGlnLeuAlaAla 140
Db      438 AAGAAAGATTTTGAAGAACTGCGAAGAAAGTGGCGGTCGATCGAGCAGCTGGCTGCC 437
Qy      141 MetAsp 142
Db      498 ATGGAT 503

RESULT 6
CB138359      553 bp      mRNA      linear      EST 29-JAN-2003
DEFINITION   K-EST0191218 LSHUK1 Homo sapiens cDNA clone LSHUK1-23-G07 5', mRNA
ACCESSION    CB138359
VERSION      CB138359.1 GI:28109974
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE    1 (bases 1 to 553)
AUTHORS     Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE       21C Frontier Korean EST Project 2001

```

JOURNAL COMMENT

Unpublished (2002)
 Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 23 row: G column: 07
 High quality sequence stop: 553.
 Location/Qualifiers

FEATURES

source

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1..553
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="LSHUK1-23-G07"
/sex="M"
/cell_line="HLK-1"
/lab_host="Top10+"
/clone_lib="LSHUK1"
/note="Organ: Liver; Vector: pcNS-D2; Site:1: EcoRI; Site:2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then deacapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10+ by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."
```

ORIGIN

Alignment Scores:

Pred. No.:	8,43e-149	Length:	553
Score:	142.00	Matches:	142
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	14	Gaps:	0

US-09-690-825-34 (1-142) x CB138359 (1-553)

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Qy      1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
Db      40 ATGGGTGCCCCGAGCTGGCCCCCTGGCGAGCCCTTCTCAAGAGACCAAGCATCTCT 99
Qy      21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
Db      100 ACATTCAAGAACTGCGCCCTTCTTGAGAGGCTGCGCCCTGCAACCCGAGCGGAGTGCAG 159
Qy      41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
Db      160 GCTGCGCTTCACTCCCTTCTTCTGTCAGAGAGAGCTGAGCAAGCTTGCCCAAGTTCCTGC 219
Qy      61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHisLysLysHis 80
Db      220 TTCAAGAGAGCTGAGAGGCTGGAGCGGATGACGACCCCATAGAGAAACATATAAAGCAT 279
Qy      81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluThrLeuGlyGlu 100
Db      280 TCGTCGAGTTCGCTTCTTCTTCTGTCAGAGAGAGCTTGAAGATTAACCTTGCTGAA 339
Qy      101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
Db      340 TTTTGAAGACTGACAGAGAAAGCCAGAAACAAATTGCAAGAGAAACCAACAAATAG 399
Qy      121 LysLysGluPheGluGluThrAlaLysValArgArgAlaIleGluGlnLeuAlaAla 140

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Db      400 AAGAAAGATTGGAAGAACTGCGAAGAACTGCGCTGCCTGCGAGCTGCTGCC 459
QY      141 Metasp 142
Db      460 ATGGAT 465

RESULT 7
LOCUS   BM835829
DEFINITION K-EST0111069 S11SNU1 Homo sapiens cDNA clone S11SNU1-73-H09 5',
            mRNA sequence.
ACCESSION BM835829
VERSION   BM835829.1 GI:19192238
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 563)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
COMMENT  Contact: Kim YS
        Genome Research Center
        Korea Research Institute of Bioscience & Biotechnology
        52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
        Tel: +82-42-860-4470
        Fax: +82-42-860-4409
        Email: yongsung@mail.kribb.re.kr
        Plate: 73 row: H column: 09
        High quality sequence stop: 563.
        Location/Qualifiers
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                /clone_lib="S11SNU1"
                /note="Organ: Stomach; Vector: pME18-FL3; Site_1: XhoI;
                Site_2: XhoI; The poly (A) + RNA was dephosphorylated with
                bacterial alkaline phosphatase (BAP) and then decapped
                with tobacco acid pyrophosphatase (TAP). The decapped
                intact mRNA was ligated with DNA-RNA linker including SfiI
                site by treatment of T4 RNA ligase and the first strand
                cDNA was synthesized with Superscript II using SfiI
                oligo-dT primer. After first strand synthesis, RNA was
                degraded by NaOH treatment and cDNA was amplified by PCR
                reaction. The PCR products were digested with SfiI and
                cloned into DraIII-digested pME18S-FL3 vector. The
                obtained cDNA vectors were used for transformation of
                competent cells E. coli Top10F by electroporation method.
                The cDNA libraries constructed by this method are
                full-length enriched cDNA library."

ORIGIN
Alignment Scores:
Pred. No.:      8,566-149      Length:      563
Score:          142.00         Matches:      142
Percent Similarity: 100.00%     Conservative: 0
Best Local Similarity: 100.00%  Mismatches:  0
Query Match:    100.00%        Indels:      0
DB:             12             Gaps:        0

US-09-690-825-34 (1-142) x BM835829 (1-563)

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QY      1 MetGlyAlaProThrLeuProProAlaIatPglInProPheLeuYasPHisArgIleSer 20
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QY      21 ThrPheLeuAsnTTPProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
Db      105 ACATTCAAAAGCTGAGCCCTCTTGGAGGAGCTGGCCCTGACCCCGAGCGAGATGGCCAG 164
QY      41 AlaGlyPheIleHisCysAsPProThrGluAsnGluProAsPLeuAlaGlnCysPhePheCys 60
Db      165 GCTGGCTTATCATCATCGCCCGCCACTGAGAACGAGCCAGACTGGCCCACTGTTCTTCG 224
QY      61 PheLeuGluLeuGluGlyTTPGluProAsPAspAsPProIleGluGluHisLeuHis 80
Db      225 TTCAGAGAGCTGAGAGGCTGGAGGACAGATGACGCCCAATGAGAGAACATAAAAAGCAT 284
QY      81 SerSerGlyCysAlaPheLeuSerValIysIysGlnPheGluGluLeuThrLeuGlyGlu 100
Db      285 TGCTCCGGTGGCGCTTCTTCTCTCAAGAGCAGTGGAGATTAACCTTGTCGAA 344
QY      101 PheLeuYLeuAspArgGluArgAlaIysAsnIysIleAlaIysGluThrAsnAsnIys 120
Db      345 TTTTGAAACTGACAGAGAAAGACCAAGAACAAATTTGAAAGAGAAACCAACATTAAG 404
QY      121 LysIysGluPheGluGluThrAlaIysIysValArgArgAlaIleGluGluLeuAlaIa 140
Db      405 AAGAAAGATTGAGAGAACTGCGAAGAAAGTGGCCGCTGCATGACGACTGCTGCC 464
QY      141 Metasp 142
Db      465 ATGGAT 470

RESULT 8
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DEFINITION K-EST0152661 LSHK1 Homo sapiens cDNA clone LSHK1-8-G05 5', mRNA
            sequence.
ACCESSION CB111125
VERSION   CB111125
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 574)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
COMMENT  Contact: Kim YS
        Genome Research Center
        Korea Research Institute of Bioscience & Biotechnology
        52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
        Tel: +82-42-860-4470
        Fax: +82-42-860-4409
        Email: yongsung@mail.kribb.re.kr
        Plate: 8 row: G column: 05
        High quality sequence stop: 574.
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                Site_2: NotI; The poly (A) + RNA was dephosphorylated with
                bacterial alkaline phosphatase (BAP) and then decapped
                with tobacco acid pyrophosphatase (TAP). The decapped

```

intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10[®] by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Alignment Scores:

Pred. No.:	8,71e-149	Length:	574
Score:	142.00	Matches:	142
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	14	Gaps:	0

US-09-690-825-34 (1-142) x CB111125 (1-574)

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OY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
DB 55 ATGGGTCCCCCGAGCTTGGCCCTTCTTGAAGGAGCCCTTCTCAAGACACCGCATCTCT 114
OY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 115 ACATTCAGAGACTGGCCCTTCTTGAAGGAGCTGGCCCTGCAACCCCGAGCGGATGGCCGAG 174
OY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
DB 175 GCTGGCTTCATCCACTGCCCCACAGAGACGAGCACTGGCCCGCATCTTCTTCTGCG 234
OY 61 PheLysGluLeuGluGlyTrpGlnProAspAspAspProIleGluGluHisLysLysHis 80
DB 235 TTCAGAGAGCTGAGAGCTGGAGCCAGATGACACCCCTTAGAGACATTAAAGCAT 234
OY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
DB 295 TCGCCCGGTGGCTTCTTCTTCTGTCAGAGAGAGTTGAAGAATTAAACCTTGTGTGA 354
OY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
DB 355 TTTTGAACCTGACACAGAAAGAGCCAGACCAAAATTGCANAGGAAACCAACAAATAAG 414
OY 121 LysLysGluPheGluGluGluThrAlaLysLysValArgArgAlaIleGluGluLeuAlaIa 140
DB 415 AAGAAAGAAATTGAGAAACTGCGAAGAAAGTGGCCGTCATCGACGAGCTGGTGGC 474
OY 141 MetAsp 142
DB 475 ATGGAT 480
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RESULT 9
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LOCUS f010e02.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2961099 5',
DEFINITION mRNA sequence.
ACCESSION AM409701
VERSION AM409701.1 GI:6935175
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 580)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.

FEATURES

source

Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www-bio.lnl.nih.gov/bbrp/image/image.html
Plate: LNCM55 row: I column: 3
Seq primer: 21M3 forward primer (ABI).
Location/Qualifiers
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/clone_lib="NIH_MGC_17"
/note="Organ: muscle; Vector: pOTB7, Site 1: EcoRI,
Site 2: XhoI; cDNA made by oligo-dt priming.
directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Alignment Scores:

Pred. No.:	8,78e-149	Length:	580
Score:	142.00	Matches:	142
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-09-690-825-34 (1-142) x AM409701 (1-580)

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OY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 113 ACATTCAGAGACTGGCCCTTCTTGAAGGAGCTGGCCCTGCAACCCCGAGCGATGGCCGAG 172
OY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
DB 173 GCTGGCTTCATCCACTGCCCCACAGAGACGAGCACTGGCCCGCATGTTCTTCTGCG 232
OY 61 PheLysGluLeuGluGlyTrpGlnProAspAspAspProIleGluGluHisLysLysHis 80
DB 233 TTCAGAGAGCTGAGAGCTGGAGCCAGATGACGACCCCATAGAGAAACATPAAAAAGCAT 292
OY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
DB 293 TCGTCGGGTGGCTTCTTCTTCTGTCAGAGAGAGCTTGAAGATTAACTTGTGTGA 352
OY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
DB 355 TTTTGAACCTGACACAGAAAGAGCCAGACCAAAATTGCAAGAGAAACCAACAAATAAG 412
OY 121 LysLysGluPheGluGluGluThrAlaLysLysValArgArgAlaIleGluGluLeuAlaIa 140
DB 413 AAGAAAGAAATTGAGAGAACTGCGAAGAAAGTGGCCCGTCATCGACGAGCTGGTGGC 472
OY 141 MetAsp 142
DB 473 ATGGAT 478
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RESULT 10

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 LOCUS K-EST0177364 C1SNUI7 Homo sapiens cDNA clone C1SNUI7-12-G02 5',
 DEFINITION mRNA sequence.
 CB128010
 ACCESSION CB128010.1 GI:28090807
 VERSION EST.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 584)
 Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.
 21C Frontier Korean EST Project 2001
 JOURNAL Unpublished (2002)
 COMMENT Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Eosun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 12 row: G column: 02
 High quality sequence stop: 584.
 Location/Qualifiers
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 /mol_type="mRNA"
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 /clone="C1SNUI7-12-G02"
 /sex="F"
 /tissue_type="uterine"
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 /clone_11b="C1SNUI7"
 /note="Organ: Cervix; Vector: pCNS-D2; Site: 1: EcoRI;
 Site 2: NotI; The poly (A) + RNA was dephosphorylated with
 bacterial alkaline phosphatase (BAP) and then decapped
 with tobacco acid pyrophosphatase (TAP). The decapped
 intact mRNA was ligated with DNA-RNA linker including
 EcoRI site by treatment of T4 RNA ligase and the first
 strand cDNA was synthesized from oligo dt-selected mRNA by
 priming with dt-tailed vector. The dt-tailed vector was
 adjusted to have about 60nt. The cDNA vector was
 circularized with E. coli DNA ligase after digestion of
 EcoRI which site is also included in vector. An RNA strand
 converted to a DNA strand by Okayama-Berg method. The
 obtained cDNA vectors were used for transformation of
 competent cells E. coli Top10F by electroporation method.
 The cDNA libraries constructed by this method are
 full-length enriched cDNA library."

ORIGIN
 Alignment Scores: 8.84e-149 Length: 584
 Pred. No.: 142.00 Matches: 142
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 Percent Similarity: 100.00% Mismatches: 0
 Best Local Similarity: 100.00% Indels: 0
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 DB: 14
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 DB 55 ATGGGAGCCCGACGTCGCGCCCTCTGCGAGCCCTTCTCAAGAGACACCGCATCTCT 114
 QY 21 ThrPheLysAsnTyrProPheLeuGlnGlyCysAlaCysThrProGluArgMetAlaGlu 40
 DB 115 ACATTCAAGAACTGGCCCTTCTTGAGAGGCGCTGCGCTGACCCCGAGCGGATGCGCGAG 174

QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
 DB 175 GCTGGCTTCATCATCGATGCCCACTGAGAACAGCCAGCACTTGCCCACTGCTTCGCG 234
 QY 61 PheLysGluLeuGlnGlyTyrGluProAspAspPheProIleGluGluHisLysHis 80
 DB 235 TTCAGAGAGCTGAGAGCGCTGGAGCGACATGACGCCCATAGAGAAACATAAAGCAT 294
 QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGlnGluLeuThrLeuGlyGlu 100
 DB 295 TCGTCGGGTGGCTTCCTTCCTTCCTCAAGAGCGATTGTAAGATTACCTTGGTGAA 354
 QY 101 PheLeuLysLeuAspArgGluAlaGlyAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
 DB 355 TTTTGAAGAACTGACAGAGAGAAAGACCAAGAACAAATTCGAAAGAAACCAACATAG 414
 QY 121 LysLysGluPheGlnGluThrAlaLysLysValAlaGalaIleGluGlnLeuAla 140
 DB 415 AAGAAAGAAATTGAGAGAACTGCGAAGAAAGTGCCTGCTCATGAGCACTGGCTGCC 474
 QY 141 MetAsp 142
 DB 475 ATCGAT 480

RESULT 11
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 DEFINITION mRNA sequence.
 ACCESSION BG776624
 VERSION BG776624.1 GI:14046941
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 585)
 NIH-MGC http://mgi.mc.man.ac.uk/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cga@nsi.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNLI)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILNLI at:
 http://image.llnl.gov
 Plate: LLCML662 row: d column: 19
 High quality sequence stop: 585.
 Location/Qualifiers
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 /clone_11b="NIH-MGC_59"
 /note="Organ: lung; Vector: pDNR-11B (Clontech); Site: 1:
 SfiI (ggcgccctcgcc); Site 2: SfiI (ggcgccatggcc);
 Double-stranded cDNA was prepared from cell line RNA. 5'
 and 3' adaptors were used in cloning as follows: 5'
 adaptor sequence: 5'-ATTCTAGAGCGCGCGCGCGCGATG-dt(30)-BN-3'
 (where B = A, C, or G and N = A, C, G, or T). Average
 insert size 1.65 kb (range 0.9-4.0 kb). 15/15 clones
 contained inserts by PCR. This library was enriched for
 full-length clones and was constructed by Clontech
 Laboratories (Palo Alto, CA). Note: this is a NIH-MGC
 library."

FEATURES
 source

ORIGIN

Alignment Scores:
 Pred. No.: 8.85e-149 Length: 585
 Score: 142.00 Matches: 142
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 12 Gaps: 0

US-09-690-825-34 (1-142) x BG776624 (1-585)

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 QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
 Db 106 ACATTCAAGAACTGGCCCTCTTGGAGGCTGCGCTGCAAGCCCGGAGCGGATGGCCGAG 165
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 Db 166 GCTGGCTTCACTCCATCCCTCCACAGAGAGAGCAAGCCAGCTTGGCCAGCTTTCTCTGCG 225
 QY 61 PheLysGluLeuGluGlyTTPGlnProAspAspAspProIleGluGluHisIleLysLysHis 80
 Db 226 TTCAAGAGAGCTGGAGAGCTGGAGCCAGATGACCAAGCCATAGAGGAACTTAAAGCAT 285
 QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGluGlu 100
 Db 286 TCGTCCGCTTCCGCTTCTTCTTCTGTCAGAGAGAGCTTGAAGATTAACCTTGTGGA 345
 QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
 Db 346 TTTTGAAGACTGGACAGAGAAAGAGCCAGAACTTGCAGAAAGCAACCAATTAAG 405
 QY 121 LysLysGluPheGluGluGluThrAlaLysLysValaArgArgAlaIleGluGluLeuAlaAla 140
 Db 406 AAGAAAGAAATTGGAGAACTGCGAAGAAAGTGGCCGCTCATGAGCAAGCTGGCTGCC 465
 QY 141 MetAsp 142
 Db 466 ATGGAT 471

RESULT 12

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 DEFINITION DKFZP686K1620.5', mRNA sequence.

ACCESSION AL603004
 VERSION AL603004.1 GI:15166510
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 602)
 AUTHORS Wandut, R., Heubner, D., Mewes, W., Weil, B. and Wiemann, S.
 TITLE EST (Wandut, R., Heubner, D., Mewes, W., Weil, B. and Wiemann, S.)
 JOURNAL Unpublished (1999)
 COMMENT Contact: MIPS

FEATURES
 location/Qualifiers
 Insoleader Landstr. 1, D-85764 Neuherberg, Germany
 This is the 5' sequence of the clone insert
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ), Email: s.wiemann@dkfz-heidelberg.de;
 sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing consortium of the German Genome Project.
 No sl sequence available.
 This clone (DKFZP686K1620) is available at the RZPD in Berlin.
 Please contact the RZPD: Resourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

source

1..602
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 /clone_lib="686 (synonym: hicc3)"
 /note="Vector: pTRIPLEX2; Site_1: SfiIA; Site_2: SfiIB;
 cDNA-collection"

ORIGIN

Alignment Scores:
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 Score: 142.00 Matches: 142
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-690-825-34 (1-142) x AL603004 (1-602)

QY 1 MetGlyAlaProThrLeuProProAlaTTPGlnProPheLeuLysAspHisArgIleSer 20
 Db 45 ATGGGTGCCCCGAGCGTTGCCCTGCTGGCAGCCCTTCTCAAGGACCAAGCATCTCT 104
 QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
 Db 105 ACATTCAAGAACTGGCCCTCTTGGAGGCTGCGCTGACCCCGGAGCGGATGGCCGAG 164
 QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
 Db 165 GCTGGCTTCACTCCATCCCTCCACAGAGAGAGCAAGCCAGCTTGGCCAGCTTTCTCTGCG 224
 QY 61 PheLysGluLeuGluGlyTTPGlnProAspAspAspProIleGluGluHisIleLysLysHis 80
 Db 225 TTCAAGAGAGCTGGAGAGCTGGAGCCAGATGACCAAGCCATAGAGGAACTTAAAGCAT 284
 QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGluGlu 100
 Db 285 TCGTCCGCTTCCGCTTCTTCTTCTGTCAGAGAGAGCTTGAAGATTAACCTTGTGGA 344
 QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
 Db 345 TTTTGAAGACTGGACAGAGAAAGAGCCAGAACTTGCAGAAAGCAACCAATTAAG 404
 QY 121 LysLysGluPheGluGluGluThrAlaLysLysValaArgArgAlaIleGluGluLeuAlaAla 140
 Db 405 AAGAAAGAAATTGGAGAACTGCGAAGAAAGTGGCCGCTCATGAGCAAGCTGGCTGCC 464
 QY 141 MetAsp 142
 Db 465 ATGGAT 470

RESULT 13

BM841904 605 bp mRNA linear EST 06-MAR-2002
 LOCUS K-EST0119223.S13KMS Homo sapiens cDNA clone S13KMS-34-A12.5',
 DEFINITION mRNA sequence.

ACCESSION BM841904
 VERSION BM841904.1 GI:19198313
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 605)
 AUTHORS Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Kim, Y.S., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.
 TITLE 21C Frontier Korean EST Project 2001
 JOURNAL Unpublished (2002)
 COMMENT Contact: Kim YS

Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52, Boseun-dong, Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 34 row: A column: 12
High quality sequence stop: 605.
Location/Qualifiers

1. 605
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/lab_host="Top10F"
/clone_lib="S13KMS5"
/note="Vector: pcms; Site 1: EcoRI; Site 2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then deccapped with tobacco acid pyrophosphatase (TAP). The deccapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Alignment Scores:
Pred. No.: 9, 116-149 Length: 605
Score: 142.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-690-825-34 (1-142) x BK841904 (1-605)

QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
DB 78 ATGGTATGCCCGAGCGTTCCTGCGAGCGCTTCTCAAGAGCAACCGCATCTCT 137
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 138 ACATTCAAGAACTGGCCCTCTCTTGAGGGCTGCCCTGCACCCCGAGCGGATGGCCGAG 197
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
DB 198 GGTGGCTTCATCCACTGCCCCCACTGAGAACGAGCCAGCTGGCCCACTGTTCTTCTGCG 257
QY 61 PheLysGluLeuGluGlyTyrGluProAspAspPhePheIleGluGluHis 80
DB 258 TTCAAGAGAGCTGAGAGCTGGAGCCAGATGACGCCCAAGAGGAACATAAAGACAT 317
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGluGlu 100
DB 318 TCGTCCGGTGGCTTCTCTTCTCTCTCAAGAGCACTTGAAGAAATTAACCTTGGTGA 377
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
DB 378 TTTTGAAGCTGAGCAGAGAAAGAGCCAAAGAAATTTGCAAGGAACCAACATTAAG 437
QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGluLeuAlaAla 140
DB 438 AAGAAAGAAATTTGAGAAACTGCGAAGAAAGTGGCGCTGCCATCGAGCGACTGGCTGCC 497

QY 141 MetAsp 142
DB 498 ATGCAT 503
RESULT 14
AM409816
LOCUS
DEFINITION
AM409816 613 bp mRNA linear EST 29-JUN-2000
fb02e10.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:296115 5',
mRNA sequence.
AM409816
AM409816
VERSION
AM409816.1 GI:6935357
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
NIH-MGC http://mhc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ULNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ULNL at:
www.bio.lim.gov/bbtp/image/image.html
Plate: LHCW55 row: I column: 20
Seq primer: -21M3 forward primer (ABI).

FEATURES

source

1. 613
/organism="Homo sapiens"
/mol_type="rRNA"
/db_xref="taxon:9606"
/clone="IMAGE:296115"
/tissue_type="Thadomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 17"
/note="Organ: muscle; Vector: pOT87; Site 1: EcoRI;
Site 2: XhoI; cDNA made by oligo-dt priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Alignment Scores:
Pred. No.: 9, 216-149 Length: 613
Score: 142.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-690-825-34 (1-142) x AM409816 (1-613)

QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
DB 53 ATGGGATGCCCGACGTTGCGCCCTGCGAGCGCTTCTCAAGAGCAACCGCATCTCT 112
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 113 ACATTCAAGAACTGGCCCTCTCTTGAGGGCTGCCCTGCACCCCGAGCGGATGGCCGAG 172
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
DB 173 GCTGGCTTCATCCACTGCCCCCACTGAGAACGAGCCAGACTTGGCCCATGTTCTTCTGCG 232

QY 61 PhelysGluLeuGluGlyTTPGluProAspAspProIleGluGluHis 80
Db 233 TTCAGAGAGCTGGAAAGCTGGAGCCAGATGACGCCATTAAGAACTAAAGCAT 292
QY 81 SerSerGlyCysAlaPheLeuSerValIleGluGluGluLeuThrLeuGlyGlu 100
Db 293 TCGTCCGCTGCGCTTCTTCTTCTGTCAGAGAGATTGAAGATTAACCTTGTGA 352
QY 101 PheLeuIleuAspArgIleArgAlaIleAsnIleAlaIleGluGluThrAsnAsn 120
Db 353 TTTTGAAGCTGACAGAGAAAGCCAGAACCAATTCAGAGAAACCAATTAAG 412
QY 121 LysIleGluPheGluGluGluThrAlaIleValArgArgAlaIleGluGluGluAla 140
Db 413 AAGAAAGAAATTGGAGAACTGCGAAGAAAGTGGCCGCTCCATCGAGCAGTGGCTGCC 472
QY 141 MetAsp 142
Db 473 ATGGAT 478
RESULT 15
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LOCUS K-EST0188232 LSHLK1 Homo sapiens cDNA clone LSHLK1-27-C08 5', mRNA
DEFINITION sequence.
ACCESSION CB135918
VERSION CB135918.1 GI:28103005
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.W., Park, H.S., Kim, S. and
Kim, Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
CONTACT: Kim YS
Genome Research Center
Korea Research Institute of BioScience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsun@mail.krdb.re.kr
Plate: 27 row: C column: 08
High quality sequence stop: 624.
Location/Qualifiers
1..624
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="LSHLK1-27-C08"
/sex="M"
/cell_line="HK-1"
/lab_host="TOP10"
/clone_id="LSHLK1"
/note="Organ: Liver; Vector: pCNS-D2; Site: 1: EcoRI;
Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then deacapped
with tobacco acid pyrophosphatase (TAP). The deacapped
intact mRNA was ligated with DNA-RNA linker including
EcoRI site by treatment of T4 RNA ligase and the first
strand cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli TOP10 by electroporation method.
The cDNA libraries constructed by this method are

ORIGIN full-length enriched cDNA library."
Alignment Scores:
Pred. No.: 9.35e-149 Length: 624
Score: 142.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0
US-09-690-825-34 (1-142) x CB135918 (1-624)
QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuIleAspHisArgIleSer 20
Db 25 ATGGGTGCCGACGACCTGCGCCCTGCTGCGAGCCCTTTTCAGAGACACCGCATCTCT 84
QY 21 ThrPheIleAsnTrpProPheLeuGluGlyCysAlaCysTrpProGluArgMetAlaGlu 40
Db 85 ACATTCAGAACTGGCCCTTCTTGGAGGCTGCGCTCCACCCCGAGCGATGGCCGAG 144
QY 41 AlaGlyPheIleHisCysPProThrGluGluGluProAspIleAlaGluCysPhePheCys 60
Db 145 GGTGCTTCATCTCACTGCGCCCTGAGAACGAGCCAGCTTGGCCAGTGTCTTCTGCG 204
QY 61 PheIleGluLeuGluGlyTTPGluProAspAspProIleGluGluHis 80
Db 205 TTCAGAGAGCTGGAGAGCTGGAGCCAGATGACGCCATAGAGAACTAAAGCAT 264
QY 81 SerSerGlyCysAlaPheLeuSerValIleGluGluGluLeuThrLeuGlyGlu 100
Db 265 TCGTCCGCTGCGCTTCTTCTTCTGTCAGAGAGATTGAAGATTAACCTTGTGA 324
QY 101 PheLeuIleuAspArgIleArgAlaIleAsnIleAlaIleGluGluGluThrAsnAsn 120
Db 325 TTTTGAAGCTGACAGAGAAAGCCAGAACCAATTCAGAGAAACCAATTAAG 384
QY 121 LysIleGluPheGluGluGluThrAlaIleValArgArgAlaIleGluGluGluAla 140
Db 385 AAGAAAGAAATTGGAGAACTGCGAAGAAAGTGGCCGCTCCATCGAGCAGTGGCTGCC 444
QY 141 MetAsp 142
Db 445 ATGGAT 450
RESULT 16
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LOCUS BE292733
DEFINITION 601105764P1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2988543 5',
mRNA sequence.
ACCESSION BE292733
VERSION BE292733.1 GI:9175339
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE NIH-MGC http://mgi.nci.nih.gov/
NATIONAL INSTITUTES OF HEALTH, Mammalian Gene Collection (MGC)
Unpublished (1999)
CONTACT: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNL at: image.llnl.gov
Plate: LINC77 row: P column: 16
High quality sequence stop: 629.
Location/Qualifiers
1..629
source

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2988543"
/tissue_type="adenocarcinoma cell line"
/lab_host="RDH108 (phage-resistant)"
/clone_lib="NIM MGC_15"
/notes="Organ: colon; Vector: pOT87; Site 1: XhoI; Site 2:
EcoRI; CDNA made by oligo-dt priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAC(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"

```

ORIGIN

Alignment Scores:

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Pred. No.: 9,41e-149 Length: 629
Score: 142.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

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US-09-690-825-34 (1-142) x BE292733 (1-629)

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QY 1 MetGlyAlaProThleuProProAlaTrpGlnProPheLeuYsaPHisArgIleSer 20
DB 6 ATGGGTGCCCCGACGCTTCCCTGCTGCGAGCCCTTTCAGAGACCAACCGCATCTCT 65
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 66 ACATTCAGAGACTGCGCCCTTCTTGAGGGCGCGGCTTCACCCGGAGCGGATGCCGAG 125
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
DB 126 GGTGGCTTCATCTCACTGCCCCACGAGAACGAGCCAGCTGGCCAGTGTCTTCTTGC 185
QY 61 PheLysGluLeuGluGlyTrpGlnProAspAspProlIegIleGluHisIleLysLysHis 80
DB 186 TTCAGAGAGCTGAGAGGCTGGAGGCGCAGATGACGCCCATAGAGAACATMAAACAT 245
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
DB 246 TCGTCGCGGTGGCTTCTTCTTCTGTCAGAGACGATTGAAGATTAAACCTTGCTGAA 305
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAspAspLys 120
DB 306 TTTTGAAGACTGACAGAGAAAGAGCCAGAACCAAAATTGCAAGAGAAACCAACATPAG 365
QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAlaAla 140
DB 366 AAGAAAGATTGAGAGAAAGCTGCGAAGAAAGTGCGCGCTGCATCGAGAGCTGCTGCC 425
QY 141 MetAsp 142
DB 426 ATGGAT 431

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RESULT 17

BM788077

LOCUS

K-BST0067173 S10SNUI Homo sapiens cDNA clone S10SNUI-21-E12 5',

BM788077

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

644 bp mRNA linear EST 05-MAR-2002

mRNA sequence.

BM788077.1 GI:19136309

EST.

Homo sapiens (human)

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 644)

Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,

TITLE

JOURNAL

COMMENT

Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.

21C Frontier Korean EST Project 2001

Unpublished (2002)

Contact: Kim YS

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Eoen-dong, Yuseong-gu, Daejeon 305-353, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 21 row: E column: 12

High quality sequence stop: 644.

Location/Qualifiers

FEATURES

source

1..644

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="S10SNUI-21-E12"

/sex="M"

/tissue_type="Stomach"

/cell_type="Lymphoblast-like"

/cell_line="SNU-1"

/lab_host="Top10F"

/clone_lib="S10SNUI"

/note="Organ: Stomach; Vector: pME18-FL3; Site 1: XhoI; Site 2: XhoI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then deapped with tobacco acid pyrophosphatase (TAP). The deapped intact mRNA was ligated with DNA-RNA linker including SfiI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized with Superscript II using SfiI oligo-dT primer. After first strand synthesis, RNA was degraded by NaOH treatment and cDNA was amplified by PCR reaction. The PCR products were digested with SfiI and cloned into DraIII- digested pME18-FL3 vector. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Alignment Scores:

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Pred. No.: 9,61e-149 Length: 644
Score: 142.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

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US-09-690-825-34 (1-142) x BM788077 (1-644)

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QY 1 MetGlyAlaProThleuProProAlaTrpGlnProPheLeuYsaPHisArgIleSer 20
DB 45 ATGGGTGCCCCGACGCTTCCCTGCTGCGAGCCCTTTCAGAGACCAACCGCATCTCT 104
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 105 ACATTCAGAGACTGCGCCCTTCTTGAGGGCGCGGCTTCACCCGGAGCGGATGCCGAG 164
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
DB 165 GGTGGCTTCATCTCACTGCCCCACGAGAACGAGCCAGCTGGCCAGTGTCTTCTGCG 224
QY 61 PheLysGluLeuGluGlyTrpGlnProAspAspProlIegIleGluHisIleLysLysHis 80
DB 225 TTCAGAGAGCTGGAAGGCTGGAGGCGCAGATGACGCCCATAGAGAGAAACAAAAAGCAT 284
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
DB 285 TCGTCGCGGTGGCTTCTTCTTCTGTCAGAGACGATTGAAGATTAAACCTTGCTGAA 344
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAspAspLys 120

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Db      345 TTTTGAACCTGACAGAGAAAGCCAGACAACTTGGACAGAAACCAATTAAG 404
Qy      121 LysylsGluPheGluGluThrAlaIlysIysValArgaTgaIarIegIuInLeuAla 140
Db      405 AAGAAAGATTGAGAAACTGACAGAAAGTGGCCGTGCATCGACAGCTGGTGGC 464
Qy      141 MetAsp 142
Db      465 ATGGAT 470

RESULT 18
B1252508      646 bp      mRNA      linear      EST 17-JUN-2001
LOCUS      602952974.F1 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:5087178 5',
DEFINITION      mRNA sequence.
ACCESSION      B1252508
VERSION      B1252508.1 GI:14803034
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      NIH-MGC http://mgs.nci.nih.gov/.
AUTHORS      National Institutes of Health, Mammalian Gene Collection (MGC)
TITLES      Unpublished (1999)
JOURNAL
COMMENT      Contact: Robert Strausberg, Ph.D.
      Email: cgabs-remail.nih.gov
      Tissue Procurement: CGAP (Stanford)
      CDNA Library Preparation: Ling Hong/Rubin Laboratory
      DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
      DNA Sequencing by: Incyte Genomics, Inc.
      Clone distribution: MGC clone distribution information can be
      found through the I.M.A.G.E. Consortium/LNL at:
      http://image.llnl.gov
      Plate: LNCM1844 row: c column: 19
      High quality sequence stop: 644.
      Location/Qualifiers
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              /mol_type="mRNA"
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              /clone="IMAGE:5087178"
              /tissue_type="hepatocellular carcinoma, cell line"
              /lab_host="DH10B (phage-resistant)"
              /clone_1lb="NIH MGC 100"
              /note="Organ: liver; Vector: pOTB7; Site 1: XhoI; Site 2:
              EcoRI; cDNA made by oligo-dT priming. Directionally cloned
              into EcoRI/XhoI sites using the following 5' adaptor:
              GGACGAG(G). Size-selected >500bp for average insert size
              1.8kb. Library constructed by Ling Hong in the laboratory
              of Gerald M. Rubin (University of California, Berkeley)
              using ZAP-cDNA synthesis kit (Stratagene) and Superscript
              II RT (Life Technologies). Note: this is a NIH_MGC
              Library."

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Db      116 ACATTCANAACTGGCCCTCTTGTAGAGGCTCGCTGCACCCCGAGGGATGGCCAG 175
Qy      41 AlaGluPheIleHisCysProThrGluAenGluProAspLeuAlaGlnCysPheCys 60
Db      176 GCTGCGTTTATCATCATGCCCCCACTGAGAACGACCAAGACTTGGCCAGTCTTCTTCC 235
Qy      61 PheIysGluLeuGluGlyTTPGluProAspAspProIleGluGluHisIysIysHis 80
Db      236 TTCAGAGAGCTGGAAGGCTGGAGCCAGATGACGACCCCATAGAGAAACATAAAAGCAT 295
Qy      81 SerSerGlyCysAlaPheLeuSerValIysIysGluIlePheGluLeuThrIleuGlyIu 100
Db      296 TCGTCCGTTGGCGCTTCTTCTGTCAAGAAAGCTTTGAAGAAATTAACCTTGCTGA 355
Qy      101 PheLeuIysLeuAspArgGluArgAlaIysAsnIysIleAlaIysGluThrAsnAsnIys 120
Db      356 TTTTGAACCTGACAGAGAAAGACCAAGAACAAATTTGCAAGAAACCAACATTAAG 415
Qy      121 LysIysGluPheGluGluThrAlaIysIysValArgaTgaIarIegIuInLeuAla 140
Db      416 AAGAAAGATTGAGAGAACTGCGAAGAAAGTGGCCGTGCATCGACAGCTGGCTGCC 475
Qy      141 MetAsp 142
Db      476 ATGGAT 481

RESULT 19
B2796084      682 bp      mRNA      linear      EST 20-SEP-2000
LOCUS      601591091.F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945214 5',
DEFINITION      mRNA sequence.
ACCESSION      B2796084
VERSION      B2796084.1 GI:10217282
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      NIH-MGC http://mgs.nci.nih.gov/.
AUTHORS      National Institutes of Health, Mammalian Gene Collection (MGC)
TITLES      Unpublished (1999)
JOURNAL
COMMENT      Contact: Robert Strausberg, Ph.D.
      Email: cgabs-remail.nih.gov
      Tissue Procurement: DCTD/DRP
      CDNA Library Preparation: Ling Hong/Rubin Laboratory
      CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
      DNA Sequencing by: Incyte Genomics, Inc.
      Clone distribution: MGC clone distribution information can be
      found through the I.M.A.G.E. Consortium/LNL at: image.llnl.gov
      Plate: LNCM803 row: e column: 23
      High quality sequence start: 3
      High quality sequence stop: 681.
      Location/Qualifiers
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              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone="IMAGE:3945214"
              /tissue_type="small cell carcinoma"
              /cell_line="MGC3"
              /lab_host="DH10B (phage-resistant)"
              /clone_1lb="NIH MGC 7"
              /note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
              EcoRI; cDNA made by oligo-dT priming. Directionally
              cloned into EcoRI/XhoI sites using the following 5'
              adaptor: GGACGAG(G). Size-selected >500bp for average
              insert size 1.8kb. Library constructed by Ling Hong in
              the laboratory of Gerald M. Rubin (University of
              California, Berkeley) using ZAP-cDNA synthesis kit
              (Stratagene) and Superscript II RT (Life Technologies)."

```

ORIGIN

Alignment Scores:

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Pred. No.:      9.63e-149      Length:      646
Score:          142.00      Matches:      142
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:            12      Gaps:      0

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US-09-690-825-34 (1-142) x B1252508 (1-646)

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Qy      1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuIysAspHisArgIleSer 20
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Qy      21 ThrPheIysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40

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ORIGIN

Alignment Scores:

Pred. No.: 1,03e-148 Length: 698
Score: 142.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-690-825-34 (1-142) x BE796084 (1-682)

QY 1 MetGlyAlaProThrLeuProAlaTyrGlnProPheLeuLysAspHisArgIleSer 20
DB 23 ATGGGTGCCCCGAGCTTGCCTCCCTGGCAGCCCTTTCTCAAGACCCACCACTCTCT 82
QY 21 ThrPheLysAsnTyrProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 83 ACATTCAAGAACTGGCCCTTCTTGGAGGGCTGCCCTGCACCCCGGAGCGATGGCCGAG 142
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
DB 143 GCTGCTTCATCCATCCCTGCCCCAGACGAGCCCAAGCTTGGCCCGAGTCTTCTCTGC 202
QY 61 PheLysGluLeuGluGlyTyrGluProAspAspProIleGluGluHisIleLysHis 80
DB 203 TTCAAGAGAGCTGGAAGCTGGAGCCAGATGACGCCCATAGAGAACTAAAGCAT 262
QY 81 SerSerGlyCysAlaPheLeuSerValIleLysGlnPheGluLeuThrLeuGluGlu 100
DB 263 TCGTCCGGTTCGCTTCTTCTTCTGTCAGAGAGAGATTGAAGATTAACCTTGGTGA 322
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120
DB 323 TTTTGAACCTGAGACAGAGAAAGAGCCAGAAACAAATTGCAAGAGAACCAACATAG 382
QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAla 140
DB 383 AAGAAAGAAATTGAGAAACTGCGAAGAAAGTGGCCGCTGCCATGAGCAGCTGGCTCC 442
QY 141 MetAsp 142
DB 443 ATGGAT 448

RESULT 20
BE796061 698 bp mRNA linear EST 20-SEP-2000
LOCUS 601591059F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945206 5',
DEFINITION
MRNA sequence.
ACCESSION BE796061
VERSION BE796061.1 GI:10217259
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 698)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCM/DRP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed By: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at: image.jhmi.gov
plate: LNC803 row: e column: 15
High quality sequence start: 2
High quality sequence stop: 698.
Location/Qualifiers
1..698
/organism="Homo sapiens"

FEATURES

source
1..698
/organism="Homo sapiens"

ORIGIN

Alignment Scores:
Pred. No.: 1.03e-148 Length: 698
Score: 142.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-690-825-34 (1-142) x BE796061 (1-698)

QY 1 MetGlyAlaProThrLeuProAlaTyrGlnProPheLeuLysAspHisArgIleSer 20
DB 22 ATGGGTGCCCCGAGCTTGCCTCCCTGGCAGCCCTTTCAAGACCCACCACTCTCT 81
QY 21 ThrPheLysAsnTyrProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 82 ACATTCAAGAACTGGCCCTTCTTGGAGGGCTGCCCTGCACCCCGAGCGATGGCCGAG 141
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
DB 142 GCTGCTTCATCCATCCCTGCCCCAGACGAGCCCAAGCTTGGCCCGAGTCTTCTCTGC 201
QY 61 PheLysGluLeuGluGlyTyrGluProAspAspProIleGluGluHisIleLysHis 80
DB 202 TTCAAGAGAGCTGGAAGCTGGAGCCAGATGACGCCCATAGAGAACTAAAGCAT 261
QY 81 SerSerGlyCysAlaPheLeuSerValIleLysGlnPheGluLeuThrLeuGluGlu 100
DB 262 TCGTCCGGTTCGCTTCTTCTTCTGTCAGAGAGAGCTTGAAGATTAACCTTGGTGA 321
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120
DB 322 TTTTGAACCTGAGACAGAGAAAGAGCCCAAGAAACAAATTGCAAGAGAACCAACATAG 381
QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAla 140
DB 382 AAGAAAGAAATTGAGAAACTGCGAAGAAAGTGGCCGCTGCCATGAGCAGCTGGCTCC 441
QY 141 MetAsp 142
DB 442 ATGGAT 447

RESULT 21
BF219993 703 bp mRNA linear EST 08-NOV-2000
LOCUS 601296980F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2964713 5',
DEFINITION
MRNA sequence.
ACCESSION BF219993
VERSION BF219993.1 GI:11126087
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 703)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

Tue Aug 17 05:54:54 2004

us-09-690-825-34.oligo.rst

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TITLE
JOURNAL
COMMENT
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-rc@mail.nih.gov
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: IRALI row: p column: 19
High quality sequence stop: 656.

FEATURES
source
1. 703
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2964713"
/tissue_type="thymodysplasia"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 17"
/note="Organ: muscle, Vector: pOTB7, Site_1: EcoRI;
Site_2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN
Alignment Scores:
Pred. No.: 1.04e-148 Length: 703
Score: 142.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
US-09-690-825-34 (1-142) x BF219993 (1-703)

QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
DB 16 ATGGGTGCCCCGAGAGTGGCCCCCTGCTGGAGCCCTTCTCAAGACCAACCGCATCTCT 75
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 76 ACATTCAAGAACTGACCTCTTCTTGAAGGCTGCGCTGACCCCGAGCGGATGCGCGAG 135
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
DB 136 GCTGGCTTCATCCACTGCCCCACGAGACGACCACTGGCCCCAGGTTCTTCTCTGCT 195
QY 61 PheLysGluLeuGluGlyTrpGluProAspAspAspProIleGluLysIleLysLysHis 80
DB 196 TTCAAGAGCTGGAAGGCTGGAGCCAGATGACACCCCTAGAGGACATATAAAGCAT 255
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGluGlu 100
DB 256 TCGTCCGGTTGCGCTTCTTCTTCTGTCAGAGAGAGTTGAAGATTAAACCTGTGTGA 315
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120
DB 316 TTTTGAACCTGCAAGAGAGCCAAAGCAAAATTGCAAGAGAAACCAACATTAAG 375
QY 121 LysLysGluPheGluGluGluThrAlaLysLysValArgArgAlaIleGluGluLeuAla 140
DB 376 AAGAAAGATTTGAGGAAATCTGCAAGAGAGTGGCGCTGCATCGAGCAGCTGCTGCC 435
QY 141 MetAsp 142
DB 436 ATGGAT 441
RESULT 22

BG115707
LOCUS 707 bp mRNA linear EST 30-JAN-2001
DEFINITION 602317179F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:4417722 5',
mRNA sequence.
ACCESSION BG115707
VERSION BG115707.1 GI:12609213
KEYWORDS EST.
ORGANISM Homo sapiens (human)
SOURCE Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE NIH-MGC http://mgc.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-rc@mail.nih.gov
Tissue Procurement: ATCC
DNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL).
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LHAM10150 row: m column: 19
High quality sequence stop: 689.

FEATURES
source
1. 707
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4417722"
/tissue_type="duodenal adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 88"
/note="Organ: small intestine; Vector: pCMV-Sport6;
Site_1: NotI, Site_2: SalI; Cloned unidirectionally;
oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH-MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 1.04e-148 Length: 707
Score: 142.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0
US-09-690-825-34 (1-142) x BG115707 (1-707)

QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
DB 27 ATGGGTGCCCCGAGAGTGGCCCCCTGCTGGAGCCCTTCTCAAGACCAACCGCATCTCT 86
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 87 ACATTCAAGAACTGACCTCTTCTTGAAGGCTGCGCTGACCCCGAGCGGATGCGCGAG 146
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
DB 147 GCTGGCTTCATCCACTGCCCCACGAGACGACCACTGGCCCCAGGTTCTTCTGCT 206
QY 61 PheLysGluLeuGluGlyTrpGluProAspAspAspProIleGluLysIleLysLysHis 80
DB 207 TTCAAGAGCTGGAAGGCTGGAGCCAGATGACACCCCTAGAGGACATATAAAGCAT 266
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGluGlu 100
DB 267 TCGTCCGGTTGCGCTTCTTCTTCTGTCAGAGAGAGTTGAAGATTAAACCTGTGTGA 326
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120

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1..726
/organism="Homo sapiens"
/mol_type="mrna"
/db_xref="taxon:9606"
/clone="CS0DH006104"
/tissue="CYPB="T CELLS (URKAT CELL LINE)"
/cell_line="JURKAT CELL LINE"
/clone_lib="Homo sapiens T CELLS (URKAT CELL LINE)"
```

/note=vector: pcwvSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pcwvSPORT 6 vector. Library was not normalized.

ORIGIN

Alignment Scores:

Pred. No.:	1.08e-148	Length:	726
Score:	142.00	Matches:	142
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	13	Gaps:	0

US-09-690-825-34 (1-142) x BX421971 (1-726)

QY 1 MetGlyAlaProThrLeuProProAlaATrGlnProPheLeuLysAspHisArgIleSer 20
 DB 127 ATGGGTGCCCCGACGCTTGGCCCCCTGCGACGCCCTTTCTCAAGAACACCGCATCTCT 186
 QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
 DB 187 ACATTCAAGAACTGGCCCTTCTTGAGAGGCTGCCCTTCAACCCGGAGCGGATGCCGAG 246
 QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
 DB 247 GCTGGCTTCATCCACTGCCACCTAGAGACGACGACTTGCGCCCTGTTCTTCTTCTGC 306
 QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHisIleLysHis 80
 DB 307 TTCAAGAGCTGGAAGGCTGGAGCCAGATGACGCCCATAGAGAACATTAAGCAT 366
 QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
 DB 367 TCGTCCGTTGGGCTTCTTCTTCTCAAGAAAGCTTGAAGAAATTAACCTTGCTGAA 426
 QY 101 PheLeuLysLeuAspArgGluArgAlaLysValLysValLysGluThrAsnAsnLys 120
 DB 427 TTTTGAACCTGAGAGAAAGAGCCCAAGAAATTTGCAAGAAACCAACCAATTAAG 486
 QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAla 140
 DB 487 AAGAAAGAAATTTGAGAGAACTGCCAGAAAGATGCCCTGTCATCGACCACTGGCTGCC 546
 QY 141 MetAsp 142
 DB 547 ATGGAT 552

RESULT 25
 BE907403 742 bp mRNA linear EST 20-OCT-2000
 LOCUS 601500136F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901880 5',
 DEFINITION mRNA sequence.
 BE907403
 VERSION BE907403.1 GI:10400927
 ACCESSION
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens (human)
 Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:

http://image.llnl.gov
 Plate: LLM9703 row: h column: 09
 High quality sequence stop: 707.
 Location/Qualifiers
 1..742
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3901880"
 /tissue_type="epithelioid carcinoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_70"
 /note="Organ: pancreas; Vector: pcwv-SPORT6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.1 kb. Library constructed by Life
 Technologies."

FEATURES

Source

ORIGIN

Alignment Scores:

Pred. No.:	1.08e-148	Length:	742
Score:	142.00	Matches:	142
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-09-690-825-34 (1-142) x BE907403 (1-742)

QY 1 MetGlyAlaProThrLeuProProAlaATrGlnProPheLeuLysAspHisArgIleSer 20
 DB 30 ATGGGTGCCCCGACGCTTGGCCCCCTGCGACGCCCTTTCTCAAGAACACCGCATCTCT 89
 QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
 DB 90 ACATTCAAGAACTGGCCCTTCTTGAGAGGCTGCCCTTCAACCCGGAGCGGATGCCGAG 149
 QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
 DB 150 GCTGGCTTCATCCACTGCCACCTAGAGACGACGACTTGCGCCCTGTTCTTCTTCTGC 209
 QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHisIleLysLysHis 80
 DB 210 TTCAAGAGCTGGAAGGCTGGAGCCAGATGACGCCCATAGAGAAATTAAGCAT 269
 QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
 DB 270 TCGTCCGTTGGGCTTCTTCTTCTTCAAGAAAGCTTGAAGAAATTAACCTTGCTGAA 329
 QY 101 PheLeuLysLeuAspArgGluArgAlaLysValLysValLysGluThrAsnAsnLys 120
 DB 330 TTTTGAACCTGAGAGAGAAAGAGCCCAAGAAATTTGCAAGAAACCAACCAATTAAG 389
 QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAla 140
 DB 390 AAGAAAGAAATTTGAGAGAACTGCCAGAAAGATGCCCTGTCATCGACGACTGGCTGCC 449
 QY 141 MetAsp 142
 DB 450 ATGGAT 455

RESULT 26
 BM020628 760 bp mRNA linear EST 30-OCT-2001
 LOCUS 603643029F1 NIH_MGC_98 Homo sapiens cDNA clone IMAGE:5419087 5',
 DEFINITION mRNA sequence.
 BM020628
 VERSION BM020628.1 GI:16534982
 ACCESSION
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens (human)
 Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 (bases 1 to 760)

AUTHORS NIH-MGC <http://imgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: c9abbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: L1CM1871 row: 1 column: 08
 High quality sequence stop: 722.

FEATURES

Location/Qualifiers
 1..760
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5419087"
 /tissue_type="astrocytoma grade IV, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_1ib="NIH_MGC_98"
 /note="Organ: brain; Vector: pORF7, Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	1..11e-148	Length:	760
Score:	142.00	Matches:	142
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	12	Gaps:	0

US-09-690-825-34 (1-142) x BM020628 (1-760)

QY 1 MetG|A|A|P|ro|th|re|u|p|ro|f|a|a|t|p|g|n|p|ro|p|he|u|l|y|a|s|p|h|s|a|r|g|l|e|s|e|r 20
 Db 33 A|T|G|G|G|G|C|C|C|G|G|G|G|C|C|C|T|G|G|G|G|C|C|C|T|T|C|T|C|A|A|G|A|C|C|C|G|C|A|T|C|T|C|T 92
 QY 21 T|h|P|h|e|l|y|a|s|n|t|p|p|ro|p|he|u|g|l|y|C|y|s|a|l|a|C|y|s|T|h|P|ro|G|l|u|a|r|g|e|t|a|g|u 40
 Db 93 A|C|A|T|T|C|A|A|G|A|C|T|G|G|C|C|T|T|C|T|G|G|G|G|C|C|T|G|C|A|C|C|C|G|G|A|G|G|A|T|G|G|C|C|G|A|G 152
 QY 41 A|l|e|g|l|P|h|e|l|l|e|h|s|C|y|s|P|ro|T|h|r|g|l|u|a|e|n|g|l|u|P|ro|A|s|P|e|u|A|l|e|g|l|n|C|y|P|h|e|p|h|e|C|y|s 60
 Db 153 G|C|T|G|G|C|T|T|C|A|T|C|A|C|G|C|C|C|C|C|A|T|G|A|A|C|G|A|C|G|A|C|T|T|G|G|C|C|A|G|T|T|C|T|T|C|T|G|C 212
 QY 61 P|h|e|l|y|e|g|l|u|e|n|g|l|y|T|P|G|l|u|P|ro|A|s|P|a|s|P|P|ro|l|e|g|l|u|h|s|l|y|s|l|y|s|s|s 80
 Db 213 T|h|P|h|e|l|y|a|s|n|t|p|p|ro|p|he|u|g|l|y|C|y|s|a|l|a|C|y|s|T|h|P|ro|G|l|u|a|r|g|e|t|a|g|u 272
 QY 81 S|e|S|e|G|l|y|C|y|s|A|l|a|P|h|e|u|s|e|r|A|l|y|s|l|y|e|n|g|l|u|P|h|e|l|l|e|h|s|l|y|s|l|y|s|s|s 100
 Db 273 T|C|G|T|C|G|G|T|G|G|C|C|T|T|C|T|T|C|T|G|T|C|A|A|G|A|G|C|A|G|T|T|G|A|A|G|A|T|T|A|A|C|C|T|T|G|T|G|A|A 332
 QY 101 P|h|e|l|l|y|e|n|s|p|a|s|P|ro|G|l|u|a|r|g|e|t|a|g|u|A|l|y|s|a|s|l|y|s|l|e|a|l|y|e|n|g|l|u|P|h|e|l|l|y|e|n|s|l|y|s 120
 Db 333 T|T|T|T|G|A|A|C|T|G|A|C|A|G|A|A|G|C|C|A|A|G|C|A|A|A|T|T|G|C|A|A|A|G|A|A|C|C|A|C|A|T|A|A|G 392
 QY 121 L|y|e|l|y|e|g|l|u|P|h|e|l|l|y|e|n|g|l|u|P|h|e|l|l|y|e|n|g|l|u|P|h|e|l|l|y|e|n|g|l|u|P|h|e|l|l|y|e|n|g|l|u|P|h|e|l|l|y|e|n|g|l|u 140
 Db 393 A|A|A|A|A|A|A|T|C|A|G|A|A|A|A|C|T|G|A|A|A|A|G|T|G|C|G|C|G|C|A|T|G|A|G|A|G|T|G|C|T|G|C|C 452
 QY 141 M|e|t|A|s|P 142
 |||||

Db 453 ATGAT 458

RESULT 27
 BG682887 766 bp mRNA linear EST 01-MAY-2001
 LOCUS 602651082F1 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:4761932 5',
 DEFINITION mRNA sequence.
 ACCESSION BG682887
 VERSION BG682887.1 GI:13914271
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 766)
 REFERENCE NIH-MGC <http://imgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: c9abbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: L1CM1615 row: c column: 21
 High quality sequence stop: 763.
 Location/Qualifiers
 1..766
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4761932"
 /tissue_type="neuroblastoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_1ib="NIH_MGC_47"
 /note="Organ: brain; Vector: pORF7, Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

FEATURES

Location/Qualifiers
 1..766
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4761932"
 /tissue_type="neuroblastoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_1ib="NIH_MGC_47"
 /note="Organ: brain; Vector: pORF7, Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	1..11e-148	Length:	766
Score:	142.00	Matches:	142
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	12	Gaps:	0

US-09-690-825-34 (1-142) x BG682887 (1-766)

QY 1 MetG|A|A|P|ro|th|re|u|p|ro|f|a|a|t|p|g|n|p|ro|p|he|u|l|y|a|s|p|h|s|a|r|g|l|e|s|e|r 20
 Db 56 A|T|G|G|G|G|C|C|C|G|G|G|G|C|C|C|T|G|G|G|G|C|C|C|T|T|C|T|C|A|A|G|A|C|C|C|G|C|A|T|C|T|C|T 115
 QY 21 T|h|P|h|e|l|y|a|s|n|t|p|p|ro|p|he|u|g|l|y|C|y|s|a|l|a|C|y|s|T|h|P|ro|G|l|u|a|r|g|e|t|a|g|u 40
 Db 116 A|C|A|T|T|C|A|A|G|A|C|T|G|G|C|C|T|T|C|T|G|G|G|G|C|C|T|G|C|A|C|C|C|G|G|A|G|G|A|T|G|G|C|C|G|A|G 175
 QY 41 A|l|e|g|l|P|h|e|l|l|e|h|s|C|y|s|P|ro|T|h|r|g|l|u|a|e|n|g|l|u|P|ro|A|s|P|e|u|A|l|e|g|l|n|C|y|P|h|e|p|h|e|C|y|s 60
 Db 176 G|C|T|G|G|C|T|T|C|A|T|C|A|C|G|C|C|C|C|C|A|T|G|A|A|C|G|A|C|G|A|C|T|T|G|C|C|C|A|G|T|T|C|T|T|C|T|G|C 235
 QY 61 P|h|e|l|y|e|n|g|l|u|e|n|g|l|y|T|P|G|l|u|P|ro|A|s|P|a|s|P|P|ro|l|e|g|l|u|h|s|l|y|s|l|y|s|s|s 80
 |||||

Db 236 TTCAAGAGCTGGAAGCTGGAGCCAGATGACGACCCCATAGAGAACTAAAAAGCAT 295

Qy 81 SerSerGIYCySAIAPheLeuSerValIysIysGIuPheGIuLeuThrLeuGIYGIu 100

Db 296 TCGTCCGGTTCGCTTTCTTCTGTCTCAAGAAAGCACTTTGAAGAAATTAACTCTGTGA 355

Qy 101 PheLeuIysLeuAspArgGIuArgAlaIysAsnIysIleAlaIysGIuThrAsnAsnIys 120

Db 356 TTTTGAACCTGACAGACAGAAAGAGCCCAAGAAATTCAGAAAGAAACCAACATTAAG 415

Qy 121 LysIysGIuPheGIuLeuThrAlaIysIysValArgArgAlaIleGIuLeuAlaAla 140

Db 416 AAGAAAGAAATTGAGAAACTGCGAAGAAAGTGCCTGCGCATGAGAGCTGCTGCC 475

Qy 141 MetAsp 142

Db 476 ATGGAT 481

RESULT 28

Bi771953 768 bp mRNA linear EST 25-SEP-2001

LOCUS 603058976F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5208259 5'

DEFINITION mRNA sequence.

ACCESSION Bi771953

VERSION Bi771953.1 GI:15763531

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 768)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>

Plate: LHM1522 row: h column: 20

High quality sequence stop: 757.

Location/Qualifiers

1..768

FEATURES

source

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5208259"

/lab_host="DH10B"

/clone_lib="NIH_MGC_122"

/note="Organ: pooled lung and spleen; Vector: pCMV-SPORTS; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dT primed and directionally cloned (pcory site is destroyed upon cloning). Average insert size 1.4 kb. insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Prod. No.: 1,12e-148 Length: 768

Score: 142.00 Matches: 142

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 12 Gaps: 0

US-09-690-825-34 (1-142) x Bi771953 (1-768)

Qy 1 MetGIYAlaProThrLeuProProAlaATrGIuPheLeuIysAspHisArgIleSer 20

Db 48 ATGGAGGCCCCCAGCAGCTGCCCTGCTGCGAGCCCTTCTCAAGACACACCGCATCT 107

Qy 21 ThrPheIysAsnTrpProPheLeuGIuGIYCySAIaCysThrProGIuArgMetAlaGIu 40

Db 108 ACATTCAAGAACTGAGCGCTTCTTGGAGGGCTGCGCTGACCCCGAGCGGAGTGGCCGAG 167

Qy 41 AlaGIYPhelIleHisCysProThrArgIuAsnGIuProAspLeuAlaGIuCysPhePheCys 60

Db 168 GCTGGCTTCATCCACAGCCCTGACAGACAGCCAGACTTGGCCCAAGTTCCTTCTGC 227

Qy 61 PheIysGIuLeuGIuGIYTrpGIuProAspAspProIleGIuLeuHisIysIysHis 80

Db 228 TTCAAGAGCTGGAAGCTGGAGCCAGATGACGACCCCATAGAGAACTAAAAAGCAT 287

Qy 81 SerSerGIYCySAIAPheLeuSerValIysIysGIuPheGIuLeuThrLeuGIYGIu 100

Db 288 TCGTCCGGTTCGCTTTCTTCTGTCTCAAGAAAGCACTTTGAAGAAATTAACTCTGTGA 347

Qy 101 PheLeuIysLeuAspArgGIuArgAlaIysAsnIysIleAlaIysGIuThrAsnAsnIys 120

Db 348 TTTTGAACCTGACAGACAGAAAGAGCCCAAGAAATTCAGAAAGAAACCAACATTAAG 407

Qy 121 LysIysGIuPheGIuLeuThrAlaIysIysValArgArgAlaIleGIuLeuAlaAla 140

Db 408 AAGAAAGAAATTGAGAAACTGCGAAGAAAGTGCCTGCGCATGAGAGCTGCTGCC 467

Qy 141 MetAsp 142

Db 468 ATGGAT 473

RESULT 29

BG750227 772 bp mRNA linear EST 15-MAY-2001

LOCUS 602709025F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4845582 5'

DEFINITION mRNA sequence.

ACCESSION BG750227

VERSION BG750227.1 GI:14060880

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 772)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>

Plate: LHM1685 row: a column: 07

High quality sequence stop: 765.

Location/Qualifiers

1..772

FEATURES

source

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4845582"

/tissue_type="normal pigmented retinal epithelium"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_43"

/note="Organ: eye; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5'

ORIGIN

adaptor: GGCAAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

Alignment Scores:

Pred. No.:	1,12e-148	Length:	772
Score:	142.00	Matches:	142
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
	12	Gaps:	0

US-09-690-825-34 (1-142) x BG750227 (1-772)

QY 1 MetGlyAlaProThrLeuProProAlaTTPGlnProPheLeuLysAspHisArgIleSer 20
 Db 16 ATGGGAGGCGCCGACGTTGCCCTGCTGCGAGCCCTTCTCAAGACACCGCATCTCT 75
 QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
 Db 76 ACATTCAAGACTGGCCCTTCTTGAGAGGCTGCGCTGCAACCCGAGCGATGGCCAG 135
 QY 41 AlaGlyPheIleHisCysPProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
 Db 136 GCTGCTTCATCAGCTGCGCCCACTGAGAACGAGCCAGACTTGGCCAGTGTCTTCTG 195
 QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGlnHisIleLysLysHis 80
 Db 196 TTCAAGAGCTGGAGAGCTGGAGGCGCATGACGACCCCATGAGAAACATPAAAAAGAT 255
 QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluLeuThrLeuGlyGlu 100
 Db 256 TCGTCGGTTGGCGCTTCTTCTGTCAGAAAGCACTTGAAGATTAACTTGTGTGA 315
 QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120
 Db 316 TTTTGAAGACTGACAGAGAAAGAGCAAAATTGCAAGAAACCAACATATAG 375
 QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAla 140
 Db 376 AAGAAAGATTGAGGAAACTGGAAGAAAGTGGCCCGTCATGACAGCTGCTGCC 435
 QY 141 MetAsp 142
 Db 436 ATGGAT 441

RESULT 30
 BUE00185 785 bp mRNA linear EST 20-SEP-2002
 LOCUS AGENCOURT_8870047 NIH_MGC_142 Homo sapiens cDNA clone IMAGE:6463579
 DEFINITION 5', mRNA sequence.
 ACCESSION BUE00185
 VERSION BUE00185.1 GI:23251944
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 785)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-rc@mail.nih.gov
 Tissue Procurement: NCI
 cDNA Library Preparation: Michael Brownstein Laboratory
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LMNL at:

FEATURES

source

<http://image.lmnl.gov>
 plate: LICM655 row: e column: 20
 High quality sequence stop: 550.
 Location/Qualifiers

1..785
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6463579"
 /tissue_type="mixed (pool of 40 RNAs)"
 /lab_host="DH10B (T1-phage-resistant)"
 /clone_lib="NIH_MGC_142"
 /note="Vector: pDNR-LIB; Site 1: SfiI (ggccatcagcc); Site 2: SfiI (ggccgcctcgcc); Double-stranded cDNA was prepared from a pool of 40 cell line polyA+ RNAs (bladder - 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon - 4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%, kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%, ovary - 1.3%, and skin - 2.3%). 5' and 3' adaptors were used in cloning as follows:
 5'-AAGCAGTGGTATCAACGACGAGCGCCATTCAGCGCGG-3' and
 5'-ATTCTAGAGCGGAGCGGCGGCGCATG-AT(30)NN-3'. Full-length cDNA library was constructed using the clonech Creator SMART kit and size-selected to contain the >0.5 kb size fraction (other fractions present in NIH_MGC_141). Library created in the laboratory of M. Brownstein (NIH). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	1,14e-148	Length:	785
Score:	142.00	Matches:	142
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
	13	Gaps:	0

US-09-690-825-34 (1-142) x BUE00185 (1-785)

QY 1 MetGlyAlaProThrLeuProProAlaTTPGlnProPheLeuLysAspHisArgIleSer 20
 Db 58 ATGGGAGGCGCCGACGTTGCCCTGCTGCGAGCCCTTCTCAAGACACCGCATCTCT 117
 QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
 Db 118 ACATTCAAGACTGGCCCTTCTTGAGAGGCTGCGCTGCAACCCGAGCGATGGCCAG 177
 QY 41 AlaGlyPheIleHisCysPProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
 Db 178 GCTGCTTCATCAGCTGCGCCCACTGAGAACGAGCCAGACTTGGCCAGTGTCTTCTG 237
 QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGlnHisIleLysLysHis 80
 Db 238 TTCAAGAGCTGGAGAGCTGGAGGCGCATGACGACCCCATGAGAAACATPAAAAAGAT 297
 QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluLeuThrLeuGlyGlu 100
 Db 298 TCGTCGGTTGGCGCTTCTTCTGTCAGAAAGCACTTGAAGATTAACTTGTGTGA 357
 QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120
 Db 358 TTTTGAAGACTGACAGAGAAAGAGCAAAATTGCAAGAAACCAACATATAG 417
 QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAla 140
 Db 418 AAGAAAGATTGAGGAAACTGGAAGAAAGTGGCCCGTCATGACAGCTGCTGCC 477
 QY 141 MetAsp 142
 Db 478 ATGGAT 483

RESULT 31

```

BG335442      815 bp      mRNA      linear      EST 27-FEB-2001
LOCUS         602403907F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:4541737 5',
DEFINITION    mRNA sequence.
ACCESSION     BG335442
VERSION       BG335442.1 GI:13141880
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NIH-MGC http://mgc.nci.nih.gov/
1 (bases 1 to 815)
Unpublished (1999)
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1220 row: m column: 02
High quality sequence stop: 708.
Location/Qualifiers
1. 815
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4541737"
/tissue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_21"
/note="Organ: placenta; Vector: pOTB7, Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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ORIGIN

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Alignment Scores:
Pred. No.:      1,17e-148      Length:      815
Score:          142.00         Matches:      142
Percent Similarity: 100.00%     Conservative: 0
Best Local Similarity: 100.00%   Mismatches:  0
Query Match:    100.00%         Indels:       0
DB:             12             Gaps:         0

US-09-690-825-34 (1-142) x BG335442 (1-815)

QY      1 MetGtAlaProThrlEuProAlaTlPglNProPhleuLysaPhisArgIleSer 20
DB      13 ATGGGGGCCCGACGTTGGCCCTGGCTGGACCCCTTTCTCAAGACACCGCATCTCT 72
QY      21 ThrPhelVAsnTrpProPhleuGluGlyCyseAlaCyseThrProGluArgMetAlaGlu 40
DB      73 ACATTCAAAAGCTGCGCTTCTTGGAGGCTCGCTGACCCCGAGCGATGGCCGAG 132
QY      41 AlaGlyPheIleHisCyseProThrlGluAengluProAspLeuAlaGlnCysePheCys 60
DB      133 GCGGGCTTCATCCACTGCCCACTGAGACGAGCCGACGATTTGGCCGAGGTTCTTCTG 192
QY      61 PheLysGluLeuGluGlyTlPglNProAspAspAspProIleGluGlnHisLysLysHis 80
DB      193 TTCAAGAGAGCTGGAGGCTGGAGCGACATGACGACCCCATGAGGAACTAAAGCAT 252
QY      81 SetSerGlyCyseAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
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DB      253 TCGTCCGCTTGGCGCTTCTCTCTGTCAGAGACGAGTTTGAAAGATTAACCTGTGTGA 312
QY      101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrSerAsnLys 120
DB      313 TTTTGAACCTGACAGAGAAAGAGCCAGAACTTGCAAGAGAAACCAACATTAAG 372
QY      121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAlaIle 140
DB      373 AAGAAAGAAATTGAGGAACTCGAAGAAAGTGGCCCTGCTCCATCGACGAGCTGGCTGCC 432
QY      141 MetAsp 142
DB      433 ATGAT 438

RESULT 32
BG744230      815 bp      mRNA      linear      EST 15-MAY-2001
LOCUS         602723337F1 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:4849640 5',
DEFINITION    mRNA sequence.
ACCESSION     BG744230
VERSION       BG744230.1 GI:14054883
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NIH-MGC http://mgc.nci.nih.gov/
1 (bases 1 to 815)
Unpublished (1999)
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1689 row: j column: 09
High quality sequence stop: 752.
Location/Qualifiers
1. 815
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4849640"
/tissue_type="natural killer cells, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_106"
/note="Organ: blood; Vector: pOTB7, Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC library."
```

ORIGIN

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Alignment Scores:
Pred. No.:      1,17e-148      Length:      815
Score:          142.00         Matches:      142
Percent Similarity: 100.00%     Conservative: 0
Best Local Similarity: 100.00%   Mismatches:  0
Query Match:    100.00%         Indels:       0
DB:             12             Gaps:         0

US-09-690-825-34 (1-142) x BG744230 (1-815)

QY      1 MetGtAlaProThrlEuProProAlaTlPglNProPhleuLysaPhisArgIleSer 20
DB      33 ATGGGTGCGCCGACGTTGCCCTGGCTGGACCCCTTTCTCAAGACACCGCATCTCT 92
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Qy 21 ThPhelysantTppPropheluugluGlyCysAlaCysThrProgluThrMetAlaGlu 40
 Db 93 ACATTCAAGAACTGGCCCTTCTTGAGGGCTGGCTGACCCCGAGCGGATGCGCCGAG 152
 Qy 41 AlAGlYpHeIleHisCysProthrGluasngluProaspLeuAlaGlnCysPhepHeCys 60
 Db 153 GCTGGCTTCATCCACTGCCCCCTGAGAAAGAGCCAGACTTGCCCCAGTGTCTTCTG 212
 Qy 61 PhelysGluLeuGluGlyTTPGluProaspPaspProIleGluGluHis 80
 Db 213 TTCAGAGAGCTGAGAGGCTGGAGCAGATGAGACCCCATAGAGAACTATAAAGCAT 272
 Qy 81 SerSerGlyCysAlaPheLeuSerValIysGlnPheGluGluLeuThrGluGlu 100
 Db 273 TCGTCGGGTGGCCCTTCTTCTGTCAGAGCACTTGAGAAATTAACCTTGCTGAA 332
 Qy 101 PhelysLeuAspArgGluArgAlaIysAsnIysIleAlaIysGluThrAsnAsnIys 120
 Db 333 TTTTGAACCTGACAGAGAAAGAGCCAGAACAAATTGCAAGAGAAACCAACATAG 392
 Qy 121 LysLysGluPheGluGluThrAlaIysValIysValArgAlaIleGluGluLeuAlaIa 140
 Db 393 AAGAAAGAAATTGAGAGAACTGGAGAGAAAGTGGCCGTCATGAGCAGCTGGCTGCC 452
 Qy 141 MetAsp 142
 Db 453 ATGGAT 458

RESULT 33
 BMS42207 821 bp mRNA linear EST 20-FEB-2002
 LOCUS AGENCOURT 6436722 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5539841
 DEFINITION 5', mRNA sequence.
 ACCESSION BMS42207
 VERSION BMS42207.1 GI:18771512
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS NIH-MGC http://www.ncbi.nlm.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: ATCC/DCMD/DTF
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing By: The I.M.A.G.E. Consortium (LNL)
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LLNL2234 row: P column: 18
 High quality sequence stop: 448.

FEATURES
 source
 1..821
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5539841"
 /tissue_type="melanotic melanoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC_72"
 /note="Organ: skin; Vector: PCMV-SF0RT6; Site: 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 2 kb. Library constructed by Life
 Technologies."

ORIGIN
 Alignment Scores:
 Pred. No.: 1.18e-148 Length: 821

Score: 142.00 Matches: 142
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 12 Gaps: 0

US-09-690-825-34 (1-142) x BMS42207 (1-821)

Qy 1 MetGlyAlaProThrIleuProProAlaTTPGlnPropheluYsAspHisArgIleSer 20
 Db 8 ATGGGTGCCCGAGAGCTGGCCCTGCTGCTGAGACCCCTTCTCAAGAGACCCCATCTCT 67
 Qy 21 ThPhelysantTppPropheluugluGlyCysAlaCysThrProgluThrMetAlaGlu 40
 Db 68 ACATTCAAGAACTGGCCCTTCTTGAGGGCTGGCTGACCCCGAGCGGATGCGCCGAG 127
 Qy 41 AlAGlYpHeIleHisCysProthrGluasngluProaspLeuAlaGlnCysPhepHeCys 60
 Db 128 GCTGGCTTCATCCACTGCCCCCTGAGAAAGAGCCAGACTTGCCCCAGTGTCTTCTG 187
 Qy 61 PhelysGluLeuGluGlyTTPGluProaspPaspProIleGluGluHis 80
 Db 188 TTCAGAGAGCTGAGAGGCTGGAGCAGATGAGACCCCATAGAGAACTATAAAGCAT 247
 Qy 81 SerSerGlyCysAlaPheLeuSerValIysGlnPheGluGluLeuThrGluGlu 100
 Db 248 TCGTCGGGTGGCCCTTCTTCTGTCAGAGCACTTGAGAAATTAACCTTGCTGAA 307
 Qy 101 PhelysLeuAspArgGluArgAlaIysAsnIysIleAlaIysGluThrAsnAsnIys 120
 Db 308 TTTTGAACCTGACAGAGAAAGAGCCAGAACAAATTGCAAGAGAAACCAACATAG 367
 Qy 121 LysLysGluPheGluGluThrAlaIysValIysValArgAlaIleGluGluLeuAlaIa 140
 Db 368 AAGAAAGAAATTGAGAGAACTGGAGAGAAAGTGGCCGTCATGAGCAGCTGGCTGCC 427
 Qy 141 MetAsp 142
 Db 428 ATGGAT 433

RESULT 34
 LOCUS AUI30493 822 bp mRNA linear EST 01-ANG-2002
 DEFINITION AUI30493 NT2RP3 Homo sapiens cDNA clone NT2RP3000936 5', mRNA
 sequence.
 ACCESSION AUI30493
 VERSION AUI30493.1 GI:10990847
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 822)
 Oca.T., Nishikawa.T., Suzuki.Y., Ishii.S., Saito.K., Kawai.Y.,
 Yamamoto.J., Wakamatsu.A., Nakamura.Y., Nagai.T., Sugano.S. and
 ItoGai.T.

FEATURES
 source
 1..822
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"

TITLE
 JOURNAL
 COMMENT
 Unpublished (2000)
 Contact: Takao ItoGai
 Genomics Laboratory
 Helix Research Institute
 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3966
 Email: genomics@hri.co.jp
 HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
 Research Institute; cDNA library construction: Department of
 Virology, Institute of Medical Science, University of Tokyo, and
 Helix Research Institute

/db_xref="taxon:9606"
 /clone="NT2RP3000936"
 /cell_type="retalocarcinoma"
 /cell_line="NT2"
 /clone_1ib="NT2RP3"
 /note="Vector: pME18SFL3; mRNA from NT2 neuronal precursor
 cells after 2-weeks retinoic acid (RA) induction"

ORIGIN

Alignment Scores:

Pred. No.:	1.18e-148	Length:	822
Score:	142.00	Matches:	142
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-690-825-34 (1-142) x AU130493 (1-822)

QY 1 MetGlyAlaProThrLeuProProAlaTTPGlnProPheLeuLysAspHisArgIleSer 20
 Db 40 ATGGGTGCCCCGAGCTTCCCTGCTGCGACGCCCTTTCTCAAGACACCGCATCTCT 99
 QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
 Db 100 ACATTCAAGAACTGGCCCTTCTTGAGAGGCTGCGCTGCACCCCGAGCGGATGCGCAG 159
 QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
 Db 160 GCTGCTTCATTCATCCATGCCCCACGTAGAACAGACGCTTGCCCGCTGTTCTTCTGCG 219
 QY 61 PheLysGluLeuGluGlyTTPGluProAspAspProIleGluGluHisLysLysHis 80
 Db 220 TTCAAGAGAGCTGAGAGCTGGAGCCAGATGACGCCCATAGAGAACTAAAGACAT 279
 QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
 Db 280 TCGTCGGGTGGCGCTTCTCTTCTGTCAGAAAGCAGTTTGAAGATTAACTTGCTGCGAA 339
 QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
 Db 340 TTTTGAACCTGACAGAGAAAGACCAAGAACAAATTTGCAAGAGAAACCAACATTAAG 399
 QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAlaAla 140
 Db 400 AAGAAAGAAATTGAGAAACTGCGAAGAAAGTGGCGCTGCATCGAAGCACTGCGTGGCC 459
 QY 141 MetAsp 142
 Db 460 ATGGAT 465

RESULT 35
 BU171608 826 bp mRNA linear EST 04-SEP-2002
 LOCUS BU171608
 DEFINITION AGENCOURT_7945706 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6149893
 5', mRNA sequence.
 ACCESSION BU171608.1 GI:22685592
 VERSION BU171608
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 826)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: ATCC/DCTD/DTF
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLNL13483 row: k column: 14
 High quality sequence stop: 733.
 Location/Qualifiers
 1. 826
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6149893"
 /tissue_type="melanotic melanoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_1ib="NIH MGC 72"
 /note="Organ: skin; Vector: pCMV-Sport6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 2 kb. Library constructed by Life
 Technologies."

FEATURES

source

ORIGIN

Alignment Scores:

Pred. No.:	1.19e-148	Length:	826
Score:	142.00	Matches:	142
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	13	Gaps:	0

US-09-690-825-34 (1-142) x BU171608 (1-826)

QY 1 MetGlyAlaProThrLeuProProAlaTTPGlnProPheLeuLysAspHisArgIleSer 20
 Db 25 ATGGGTGCCCCGAGCTTCCCTGCTGCGACGCCCTTTCTCAAGACACCGCATCTCT 84
 QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
 Db 85 ACATTCAAGAACTGGCCCTTCTTGAGAGGCTGCGCTGCACCCCGAGCGGATGCGCAG 144
 QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
 Db 145 GCTGCTTCATTCATCCATGCCCCACGTAGAACAGACGCTTGCCCGCTGTTCTTCTGCG 204
 QY 61 PheLysGluLeuGluGlyTTPGluProAspAspProIleGluGluHisLysLysHis 80
 Db 205 TTCAAGAGAGCTGAGAGCTGGAGCCAGATGACGCCCATAGAGAACTAAAGACAT 264
 QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
 Db 265 TCGTCGGGTGGCGCTTCTCTTCTGTCAGAAAGCAGTTTGAAGATTAACTTGCTGCGAA 324
 QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
 Db 325 TTTTGAACCTGACAGAGAAAGACCAAGAACAAATTTGCAAGAGAAACCAACATTAAG 384
 QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAlaAla 140
 Db 385 AAGAAAGAAATTGAGAAACTGCGAAGAAAGTGGCGCTGCATCGAAGCACTGCGTGGCC 444
 QY 141 MetAsp 142
 Db 445 ATGGAT 450

RESULT 36
 BU600854 828 bp mRNA linear EST 20-SEP-2002
 LOCUS BU600854
 DEFINITION AGENCOURT_10058678 NIH_MGC_142 Homo sapiens cDNA clone
 IMAGE:6454689 5', mRNA sequence.
 ACCESSION BU600854
 VERSION BU600854.1 GI:23252613
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 828)
AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs@mail.nih.gov
Tissue Procurement: NCI

cDNA Library Preparation: Michael Brownstein Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: ULCM2671 row: f column: 02
High quality sequence stop: 574.
Location/Qualifiers

FEATURES

source

```
1..828
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="TAGS:649469"
/tissue_type="mixed (pool of 40 RNAs)"
/lab_host="DH10B (T1-phage-resistant)"
/clone_lib="NIH MGC 142"
/notes="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc);
Site 2: SfiI (ggccgcctggcc); Double-stranded cDNA was
prepared from a pool of 40 cell line polyA+ RNAs (ladder
- 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon -
4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%,
kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%,
ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary
gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were
used in cloning as follows:
5'-AACGATCGATTCACGCGAGTGGCCATTACGCCGG-3' and
5'-ATTCTAGAGCCGAGCGCGCCGACATG-AT(30)NN-3'. Full-length
enriched library was constructed using the Clontech
Creator SMART kit and size-selected to contain the >0.5 kb
size fraction (other fractions present in NIH MGC 141).
Library created in the laboratory of M. Brownstein (NIH,
NIH). Note: this is a NIH_MGC library."
```

ORIGIN

Alignment Scores:

Pred. No.:	1.19e-148	Length:	828
Score:	142.00	Matches:	142
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	13	Gaps:	0

US-09-690-825-34 (1-142) x BU60854 (1-828)

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QY 1 MetGlyAlaProThrLeuProProAlaTTPGInProPheLeuLeuAspHisArgIleSer 20
DB 68 ATGGGTCGCCCCGACGTTGGCCCTGGCTGGCAGCCCTTTCTCAAGAGCACCGCATCTCT 127
QY 21 ThrPheLeuAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 128 ACATTCAAGAACTGGGCCCTTCTTGGAGGGCTCGCGCTGACCCCGAGACGGATGGCCGAG 187
QY 41 AlaGlyPheIleHisCysProThrGluLeuGluProAspLeuAlaGlnCysPhePheCys 60
DB 188 GCTGGGTTATCATCAGTCCCGCCACTAGAAAGGAGCAAGCTTGGCCCAAGTTCTCTTCGC 247
QY 61 PheLeuGluLeuGluGlyTTPGInProAspAspAspPhePheIleGluGluHisIleLeuHis 80
DB 248 TTCAAGAGACTGGAAGGCTGGAGGACCAATGACGCCCATAGAGAACATTAAGAAT 307
QY 81 SerSerGlyCysAlaPheLeuSerValIleLeuGluGluLeuGluLeuThrLeuGlyGlu 100
DB 308 TCGTCGGTTGGGCTTCTCTTCTGCAAGAGAGTTTGAAGATTAACTCTTGCTGA 367
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QY 101 PheLeuLeuLeuAspArgGluArgAlaIleAsnIleAlaIleGluGluThrAsnAsnIys 120
DB 368 TTTTTCAACTCGACACAGAGAAAGAGCCAAACAAATTCAGAAAGAAACCAATTAAG 427
QY 121 LysLeuGluPheGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 140
DB 428 AAGAAAGAAATTGAGGAATCTGGAGAAAGAGAAAGTGGCGGTCCATCGACGAGCTGGCTGC 487
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QY 141 MetAsp 142
DB 488 ATGAT 493

RESULT 37

LOCUS

AUI26048 836 bp mRNA linear EST 01-AUG-2002

DEFINITION

AUI26048 NT2RM4 Homo sapiens cDNA clone NT2RM4002626 5', mRNA

ACCESSION

AUI26048

VERSION

AUI26048

KEYWORDS

EST

SOURCE

AUI26048.1 GI:10950764

ORGANISM

Homo sapiens (human)

REFERENCE

Ota, T., Wakamatsu, A., Ozawa, M., Ishii, S., Saito, K., Yamamoto, J.,

AUTHORS

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

TITLE

1 (bases 1 to 836)

JOURNAL

Unpublished (2000)

COMMENT

Contact: Takao Isegai

Genomics Laboratory

Helix Research Institute

1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

Tel: 81-438-52-3975

Fax: 81-438-52-3986

Email: genomics@hri.co.jp

HRI human cDNA project: 5'- & 3'-end one pass sequencing: Helix

Research Institute; cDNA library construction: Department of

Virology, Institute of Medical Science, University of Tokyo, and

Helix Research Institute.

Location/Qualifiers

precursor cells"

FEATURES

source

Pred. No.:	1.2e-148	Length:	836
Score:	142.00 <td>Matches:</td> <td>142</td>	Matches:	142
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-690-825-34 (1-142) x AUI26048 (1-836)

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QY 1 MetGlyAlaProThrLeuProProAlaTTPGInProPheLeuLeuAspHisArgIleSer 20
DB 55 ATGGGTCGCCCCGACGTTGGCCCTGGCTGGCAGCCCTTTCTCAAGAGCACCGCATCTCT 114
QY 21 ThrPheLeuAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 115 ACATTCAAGAACTGGGCCCTTCTTGGAGGGCTCGCGCTGACCCCGAGACGGATGGCCGAG 174
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OY		41	AlaAlyPheIleHIScysProThGluAsnGluProkaspLeuAlaGlnCysPhePheCys	60
Db		175	GCTGGCTTCATCCACTGCCCACTGAGACGACCACATTGGCCCGATGTTCCTTCTGC	234
OY		61	PheUysGluLeuGluGluYTTPGluProkaspPaspProIlegluGluHISLysLysHis	80
Db		235	TTCAGAGAGCTGGAAAGCGCTGGAGGACGATGATCACACCCCATAAGAGGAACAATAAAAAAGCAT	294
OY		81	SerSerArgLYCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu	100
Db		295	TGTCGCGGTGGCGCTTCCTTCCTTCGTCAAGAAGCAGTTTGAAAGATTACCTTGGTGAA	354
OY		101	PheLeuLysLeuAspArgLysGluArGAlaLysAsnLysIleAlaLysGluThrAsnAsnLys	120
Db		355	TTTTTGAAACCTGGACAGAGAAAGAACGCCAAGAACAAAATTGCAGAGAAACCAACAAATTAAG	414
OY		121	LysLysGluGluPheGluGluGluThrAlaLysLysValArgArgAlaIleGluGluLeuAlaAla	140
Db		415	AAGAAAGAAATTTGAGAAACTGCGAAGAAAGTGCGCCTGTGCATGAGCAAGCTGGCTGCC	474
OY		141	MetAsp	142
Db		475	ATGGAT	480
RESULT 38				
BQ438198			861 bp	mRNA linear EST 24-MAY-2002
LOCUS				
DEFINITION			AGENCOURT 7889851 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:6175596	
ACCESSION			BQ438198	
VERSIONS			BQ438198.1 GI:21177274	
KEYWORDS			EST.	
SOURCE			Homo sapiens (human)	
ORGANISM			Homo sapiens	
REFERENCE			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS			Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
JOURNAL			1 (bases 1 to 861)	
COMMENT			NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Life Technologies, Inc. DNA Sequencing Arrayed by: The I.M.A.G.E. Consortium (LLNL) Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM13550 row: j column: 13 High quality sequence stop: 573. Location/Qualifiers 1. 861 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:6175596" /tissue_type="leiomyosarcoma" /lab_host="DH10B (phage-resistant)" /clone_lib="NIH MGC 71" /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: Not.; Site 2: Salt; cloned unidirectionally. Primer: Oligo dt. Average insert size 2.1 kb."	
ORIGIN				
Alignment Scores:				
Pred. No.:			1,23e-148	Length: 861
Score:			142.00%	Matches: 142
Percent Similarity:			100.00%	Conservative: 0
Best Local Similarity:			100.00%	Mismatches: 0
Query Match:			100.00%	Indels: 0
DB:			13	Gaps: 0

US-09-690-825-34 (1-142) x BQ438198 (1-861)

Qy	1	MetGlyAlaIaProIhrleuPProPolaIrrGlnProPheLeuIysAspHisArgIleSer	20
Db	5	ATGGGATCCCCCGAAGCTTGGCCCCCTGCTGCTGGACAGCCCTTTCTCAAGACACACCGCATCTCT	64
Qy	21	ThrPheIysAntTppProPheLeuGlyGlyCysAlaCysThrProGluIaArgMetAlaGlu	40
Db	65	ACATTCAAGAACTGGAGCCCTCTTGGAGGGCTGGCCCTGCACCCCGGAGCGGATGGCCGAG	124
Qy	41	AlaGlyPheIleHisCysProIrrhGluAsnGluProAspLeuIaGlnCysPhePheCys	60
Db	125	GCTGGCTTCATCCACTGCCCCCACTGAAGAGAGCCAGCACTTGGCCCACTGTTCTTCTGCG	184
Qy	61	PheIysGluLeuGluGlyIrrPgiuProAspAspAspProIlegIuHisIlysIysHis	80
Db	185	TTCAAGAGAGCTGGAAAGCTGGAGCCAGATGACACACCCCTAGAGGAACATATAAAAACAT	244
Qy	81	SerSerGlyCysAlaPheLeuSerValIysIysGlnPheGluGluLeuTrrLeuGlyGlu	100
Db	245	TCGTCGGATTCGGCTTTCCTTCTTCGTCAAGAGCAGTTTGAAGATTAACTTCTTGCTGAA	304
Qy	101	PheLeuIysIleuAspArgIuArgAlaIysAsnIysIleAlaIysGluTrrAsnAsnIys	120
Db	305	TTTTTGAACCTGGACAGAGAAAGAGCCAGAAACAAATTCGAAAGAAACCAACAAATAG	364
Qy	121	LysIysGluPheGluGluTrrhAlaIysIysValaArgArgAlaIleGluGluLeuAlaAla	140
Db	365	AAGAAAGAAATTTGAGAAACTGCAGAAAGAAATGTCGCGCTGCATGAGCACTGGCTGCC	424
Qy	141	MetAsp	142
Db	425	ATGGAT	430

RESULT 39

LOCUS	BQ882604	868 bp	mRNA	linear	EST 16-AUG-2002
DEFINITION	AGNCOCURT 8726226 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:6341045				
ACCESSION	BQ882604				
VERSION	BQ882604.1	GI:22274612			
KEYWORDS	EST.				
SOURCE	Homo sapiens				
ORGANISM	Homo sapiens (human)				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
TITLE	1 (bases 1 to 868)				
JOURNAL	NIH-MGC http://mhc.nci.nih.gov/ .				
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)				
	Unpublished (1999)				
	Contact: Robert Strausberg, Ph.D.				
	Email: cgabbs-remail.nih.gov				
	Tissue Procurement: ATCC				
	cDNA Library Preparation: Rubin Laboratory				
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)				
	DNA Sequencing by: Agencourt Bioscience Corporation				
	Clone distribution: MGC clone distribution information can be				
	found through the I.M.A.G.E. Consortium/LIML at:				
	http://limc.nlm.gov				
	Plate: LMC2538 row: h column: 06				
	High quality sequence stop: 649.				

FEATURES

source

1..868

location/Qualifiers

organism="Homo sapiens"

molecule_type="mRNA"

db_xref="taxon:9606"

clone="IMAGE:6341045"

tissue_type="neuroblastoma, cell line"

lab_host="DH10B (phage-resistant)"

clone_id="NIH_MGC_47"

note="organ: brain; Vector: pOT37; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally

ORIGIN

cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the Laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC library."

Alignment Scores:

Pred. No.:	Length:	Score:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
1.24e-148	668	142.00	142	0	0	0	0
Percent Similarity:		100.00%					
Best Local Similarity:		100.00%					
Query Match:		100.00%					

US-09-690-825-34 (1-142) x B0882604 (1-868)

```

QY 1 MetGlyAlaProThrLeuProAlaTPGInProPheLeuLysAspHisArgIleSer 20
DB 44 ATGGGGGCCCGACGCTGGCCCTGCTGCGAGCCCTTTCTAAGACACCGCATCTCT 103
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetLaglu 40
DB 104 ACAATTCAGAACTGGCCCTTCTTGAGGGCTGCGCTGCAACCCGAGCGGATGGCCGAG 163
QY 41 AlaGlyPheIleHisCysProThrGluLeuGluProAspLeuAlaGlnCysPhePheCys 60
DB 164 GCTGGCTTATCATCAGCTGCCCCACGTGAAAGAGCCAGCTTGCCCAATGTTCTTCTG 223
QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHisLysLysHis 80
DB 224 TTCAGAGAGCTGGAAGGCTGGAGCCAGATGACGACCCCATAGAGAACATTAAGCAT 283
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGluGlu 100
DB 284 TCGTCCGCTTGCCTTCTTCTTCTGCAAGAGCATTTGAAGATTAACTTGGTGA 343
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120
DB 344 TTTTGAACCTGACAGAGAAAGACCAAAATTCAGAGAACCAACCAATTAAG 403
QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGluLeuAla 140
DB 404 AAGAAAGATTGAGAGAAATCGGAAAGAGCGCCGTCGATGAGACAGCTGGCTGCC 463
QY 141 MetAsp 142
DB 464 ATGGAT 469

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RESULT 40 BE883968 874 bp mRNA linear EST 20-OCT-2000
 LOCUS 601505487F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3907388 5',
 DEFINITION mRNA sequence.
 ACCESSION BE883968
 VERSION BE883968.1 GI:10332744
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 874)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-riemail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
 DNA Sequencing by: Incyte Genomics, Inc.

FEATURES

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at: <http://image.llnl.gov>
 Plate: L14K9717 row: n column: 21
 High quality sequence stop: 648.
 Location/Qualifiers
 1..874
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3907388"
 /tissue_type="leptomysarcoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_71"
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 2.1 kb."

ORIGIN

Alignment Scores:

Pred. No.:	Length:	Score:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
1.25e-148	874	142.00	142	0	0	0	0
Percent Similarity:		100.00%					
Best Local Similarity:		100.00%					
Query Match:		100.00%					

US-09-690-825-34 (1-142) x BE883968 (1-874)

```

QY 1 MetGlyAlaProThrLeuProAlaTPGInProPheLeuLysAspHisArgIleSer 20
DB 40 ATGGGGGCCCGACGCTGGCCCTGCTGCGAGCCCTTTCTAAGACACCGCATCTCT 99
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetLaglu 40
DB 100 ACAATTCAGAACTGGCCCTTCTTGAGGGCTGCGCTGCAACCCGAGCGGATGGCCGAG 159
QY 41 AlaGlyPheIleHisCysProThrGluLeuGluProAspLeuAlaGlnCysPhePheCys 60
DB 160 GCTGGCTTATCATCAGCTGCCCCACGTGAAAGAGCCAGATTTGGCCAGATTTCTTCTG 219
QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHisLysLysHis 80
DB 220 TTCAGAGAGCTGGAAGGCTGGAGCCAGATGACGACCCCATAGAGAACATTAAGCAT 279
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGluGlu 100
DB 280 TCGTCCGCTTGCCTTCTTCTTCTGCAAGAGCATTTGAAGATTAACTTGGTGA 339
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120
DB 340 TTTTGAACCTGACAGAGAAAGACCAAAATTCAGAGAACCAACCAATTAAG 399
QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGluLeuAla 140
DB 400 AAGAAAGATTGAGAGAAATCGGAAAGAGCGCCGTCGATGAGACAGCTGGCTGCC 459
QY 141 MetAsp 142
DB 460 ATGGAT 465

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RESULT 41 BE898710 875 bp mRNA linear EST 29-SEP-2000
 LOCUS 60161673F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951667 5',
 DEFINITION mRNA sequence.
 ACCESSION BE898710
 VERSION BE898710.1 GI:10365480
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 875)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-riemail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
 DNA Sequencing by: Incyte Genomics, Inc.

REFERENCE 1 (bases 1 to 875)
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@b-remail.nih.gov
Tissue Procurement: DCTD/BTP

CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: image.llnl.gov
Plate: LCM830 row: b column: 20
High quality sequence stop: 709.
Location/Qualifiers

FEATURES
source

1..875
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3951667"
/issue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_9"
/note="Organ: ovary; Vector: pOT7; Site 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Alignment Scores:

Pred. No.:	1,25e-148	Length:	875
Score:	142.00	Matches:	142
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-09-690-825-34 (1-142) x BE896710 (1-875)

QY 1 MetGtAlaProThrLeuProAlaTrpGlnProPheLeuYsAspHisArgIleSer 20
DB 6 ATGGGTGCGCCGAGCTTCCCTCCCTGCGAGCCCTTCTCAAGACACCGCATCTCT 65
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 66 ACATTCAGAACTGGCCCTTCTTGAGGGCTGGCCCTCCACCCGAGCGAGTATGCGGAG 125
QY 41 AlaglyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
DB 126 GCTGCTTCATCCATGCTCCCTCCCTGAGACGAGCCAGCTTGCCCATGTTCTTCGCG 185
QY 61 PheLysGluLeuGluGlyTTPGluProAspAspProIleGluGluHisLysLysHis 80
DB 186 TTCAGAGGAGCTGGAAGGCTGGAGGCGAGTACGACCCCAAGAGAAACATMAAAGAT 245
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
DB 246 TGTGCGGATGGCTTCTTCTCTGTCAGAGAGCGAGTTGAAGATTAACTTCGCTGAA 305
QY 101 PheLeuYsLeuAspArgGluArgAlaYsAsnYsIleAlaLysGluThrAsnAsnLys 120
DB 306 TTTTCAAACTGAGACGAGAAAGAGCAAAATTTGCAAAAGAAACCAACATATAG 365
QY 121 LysLysGluPheGluGluThrAlaLysLysValaArgAlaIleGluGluLeuAlaIa 140
DB 366 AAGAAAGAAATTTGAGAAACTGGAAGAAAGTGGCGGCGGATGAGAGAGCTGCTGCC 425
QY 141 MetAsp 142
|||||

DB 426 ATGCAT 431

RESULT 42
LOCUS BG528273 875 bp mRNA linear EST 03-APR-2001
DEFINITION 602557679P1 NIH_MGC_59 Homo sapiens CDNA clone IMAGE:4686547 5',
RNA sequence.
ACCESSION BG528273
VERSION BG528273.1 GI:13519810
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 875)
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@b-remail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
Plate: LCM1497 row: n column: 20
High quality sequence stop: 692.
Location/Qualifiers

FEATURES
source

1..875
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4686547"
/issue_type="mucoepidermoid carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/clone_id="NIH_MGC_59"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggccgctcgagc); Site 2: SfiI (ggccatcgagc); Double-stranded CDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-ATTCTAGAGGCGGAGCGCGGAGCATG-dT(30)BN-3' (where B = A, C, G, or T). Average insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	1,25e-148	Length:	875
Score:	142.00	Matches:	142
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	12	Gaps:	0

US-09-690-825-34 (1-142) x BG528273 (1-875)

QY 1 MetGtAlaProThrLeuProAlaTrpGlnProPheLeuYsAspHisArgIleSer 20
DB 46 ATGGGTGCGCCGAGCTTCCCTCCCTGCGAGCCCTTCTCAAGACACCGCATCTCT 105
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 106 ACATTCAGAACTGGCCCTTCTTGAGGGCTGGAGGCGGAGCGAGCGAGTATGCGGAG 165
QY 41 AlaglyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
DB 166 GCTGCTTCATCCATGCTCCCTCCCTGAGACGAGCCAGCTTGCCCATGTTCTTCGCG 225

ORIGIN

of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

Alignment Scores:

Pred. No.:	1,266-148	Length:	883
Score:	142.00	Matches:	142
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	13	Gaps:	0

US-09-690-825-34 (1-142) x BQ650551 (1-883)

QY 1 MetGlyAlaProThrLeuProProAlaTTPGlnProPheLeuYsAspHisArgIleSer 20
Db 29 ATGGGTGCCCCGAGCTTGCCCTGCTGGAGCGCTTTCTCAAGAGCACACCGCATCTCT 88
QY 21 ThrPheLeuAsnTrpProPheLeuGluGlyCysValAcysThrProGluArgMetAlaGlu 40
Db 89 ACATTCAAGAACTGCGCCCTTCTTGAGGGCTGCGCTGCACCCCGAGCGGATGGCCGAG 148
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
Db 149 GCTGGCTTCATCCACTGCCCCACTGAGACAGCACACTTGCGCCCATGTTCTTCTGTC 208
QY 61 PheLeuGluLeuGluGlyTTPGlnProAspAspProIleGluGluHis 80
Db 209 TTCAAGAGAGCTGGAAGCTGGAGGACGATGACGACCCCATAGAGAACTAAAGACAT 268
QY 81 SerSerGlyCysAlaPheLeuSerValIlyslsGlnPheGluGluLeuThrLeuGlyGlu 100
Db 269 TCGTCCGGTTCGCTTCTTCTTCTGTCAGAGAGCGCTTTGAAGAAATTACCCCTTGAGAA 328
QY 101 PheLeuYsLeuAspArgGluArgAlaIlyslsAsnIlyleAlaIlyslsGluThrAsnAsnIly 120
Db 329 TTTTGAAGAACTGACAGAGAAAGAGCCAAAGAAATTTGCAAGAGAAACCAACATTAAG 388
QY 121 LysIlyslsGluPheGluGluThrAlaIlyslsValArgArgAlaIleGluGlnLeuAlaIle 140
Db 389 AAGAAAGAAATTTGAGAGAACTGCGAAGAGTGGCGCTGCATGAGCAGCTGGCTGCC 448
QY 141 MetAsp 142
Db 449 ATGGAT 454

RESULT 45

BQ227378

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

ORGANISM

SOURCE

COMMENT

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

REFERENCE

AUTHORS

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JOURNAL

COMMENT

REFERENCE

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLML0289 row: k column: 24
High quality sequence stop: 682.

FEATURES

source

Location/Qualifiers
1..889
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4471055"
/issue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_90"
/note="Organ: liver; Vector: pCMV-SPORT6; Site: 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 1.27e-148 Length: 889
Score: 142.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-690-825-34 (1-142) x BG250436 (1-889)

QY 1 MetGlyAlaProThrLeuProProAlaTTPGInProPheLeuYAspHisArgIleSer 20
DB 15 ATGGGTGCCCCGACGCTTGCCCTGCTGGCAGCCCTTCTCAAGGACCAACCGCATCTCT 74
QY 21 ThrPheYAsnTTPProPheLeuGluGlyCysAlaCyStrProGluArgMetAlaGlu 40
DB 75 ACATTCAAGAACTGGGCGCTTCTTGAGGGCTCGGCTGCACCCCGGAGCGATGGCCGAG 134
QY 41 AlaGlyPheIleHisCysProThrGluLeuGluProAspLeuAlaGlnCysPhePheCys 60
DB 135 GCTGGCTTCATCCACTGCCCCCACTAGAACGAGCGACGCTTGCCGAGTGTCTTCTGC 194
QY 61 PheYsGluLeuGluGlyTTPGluProAspAspProIleGluGluHisIleYsYsHis 80
DB 195 TTCAGAGAGCTGGAAGGCTGGGAGCGACATGACGCCCATAGAGAACTAAAGAT 254
QY 81 SerSerGlyCysAlaPheLeuSerValYsYsGlnPheGluGluLeuThrLeuGlyGlu 100
DB 255 TGGTCCGGTTGGCTTCTTCTTCTGCAAGAGCGTTTGAAGATTAACTTGGTGA 314
QY 101 PheLeuYsLeuAspArgGluArgAlaYsAsnYsIleAlaYsGluThrAsnAsnYs 120
DB 315 TTTTGAAGCTGACAGAGAAAGACCAAGAAATTGCAAGAGAAACCAACATAG 374
QY 121 YsYsGluPheGluGluThrAlaYsYsValaArgArgAlaIleGluGluLeuAla 140
DB 375 AAGAAAGAAATTGAGAAACCTGCAAGAAAGTGCCTGCATGACACACTGCTGCC 434
QY 141 MetAsp 142
DB 435 ATGGAT 440

RESULT 47
BX425472

LOCUS BX425472 896 bp mRNA linear EST 15-MAY-2003
DEFINITION BX425472 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
ACCESSION CL08B015ZEB06 5-PRIME, mRNA sequence.
VERSION BX425472
KEYWORDS BX425472.1 GI:30778469
SOURCE EST.
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 896)
AUTHORS Li W.B., Gruber, C., Jesse, J. and Polyes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segre@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 8555.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CL08B015ZEB06R1aCluster=8555.r. Contact :
Feng Liang Email: fliang@life.techn.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CL08B015ZEB06R1.

FEATURES

source

Location/Qualifiers
1..896
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CL08B015ZEB06"
/issue_type="NEUROBLASTOMA"
/clone_lib="Homo sapiens NEUROBLASTOMA"
/note="Vector: pCMVSPORT_6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

ORIGIN

Alignment Scores:

Pred. No.: 1.27e-148 Length: 896
Score: 142.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-09-690-825-34 (1-142) x BX425472 (1-896)

QY 1 MetGlyAlaProThrLeuProProAlaTTPGInProPheLeuYAspHisArgIleSer 20
DB 75 ATGGGTGCCCCGACGCTTGCCCTGCTGGCAGCCCTTCTCAAGGACCAACCGCATCTCT 134
QY 21 ThrPheYAsnTTPProPheLeuGluGlyCysAlaCyStrProGluArgMetAlaGlu 40
DB 135 ACATTCAAGAACTGGGCGCTTCTTGAGGGCTCGGCTGCACCCCGGAGCGATGGCCGAG 194
QY 41 AlaGlyPheIleHisCysProThrGluLeuGluProAspLeuAlaGlnCysPhePheCys 60
DB 195 GCTGGCTTCATCCACTGCCCCCACTAGAACGAGCGACCTTGCCGAGTGTCTTCTGC 254
QY 61 PheYsGluLeuGluGlyTTPGluProAspAspProIleGluGluHisIleYsYsHis 80
DB 255 TTCAGAGAGCTGGAAGGCTGGGAGCGACATGACGCCCATAGAGAACTAAAGAT 314
QY 81 SerSerGlyCysAlaPheLeuSerValYsYsGlnPheGluGluLeuThrLeuGlyGlu 100
DB 315 TGGTCCGGTTGGCTTCTTCTTCTGCAAGAGCGTTTGAAGATTAACTTGGTGA 374
QY 101 PheLeuYsLeuAspArgGluArgAlaYsAsnYsIleAlaYsGluThrAsnAsnYs 120

Db 375 TTTTGAACCTGCAGAGAAAGCCAGAACCAATTTGCAAGAAACCAATTAAG 434

Qy 121 LysylsGluPheGluGluThrAlaLysValArgAlaIleGluGluLeuAla 140

Db 435 AAGAAAGAAATTTGAGAACTGCAGAAAGAAAGTGCCTGCATCGAGCAGTGGCTGCC 494

Qy 141 MetAsp 142

Db 495 ATGGAT 500

RESULT 48
BF972840 908 bp mRNA linear EST 22-JAN-2001
LOCUS 602241117F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4329509 5',
DEFINITION mRNA sequence.
ACCESSION BF972840
VERSION BF972840.1 GI:12340055
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 908)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L10M191 row: b column: 06
High quality sequence stop: 687.
Location/Qualifiers
1. 908
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4329509"
/tissue_type="leiomyosarcoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 46"
/note="Organ: uterus; Vector: POTB7; Site 1: XhoI; Site 2:
EcoRI; CDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-CDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

ORIGIN

Alignment Scores:

Pred. No.:	1.29e-148	Length:	908
Score:	142.00	Matches:	142
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-09-690-825-34 (1-142) x BF972840 (1-908)

Qy 1 MetGlyAlaProThrLeuProProAlaITpGlnProPheLeuLysAspHisArgIleSer 20

Db 13 ATGGGAGCCCGCGAGTGGCCCTGCGAGCCCTTTCTCAAGAGCAACCGCATCTCT 72

Qy 21 ThrPheLysAsnTrpProPheLeuGluGlyValAlaCysThrProGluArgValaGlu 40

Db 73 ACATTCAAGAACTGCGCTCTTCTTGAGGAGCTGCGCTGCACCCCGAGCGGAGCGCCGAG 132

Qy 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGluCysPhePheCys 60

Db 133 GCTGCTTCATCTACCTGCCCCCTAGAAACGAGCCACTTGCCCATGTTCTTCTTCC 192

Qy 61 PheLysGluLeuGluGlyTyrGluProAspAspProIleGluHisLysLysHis 80

Db 193 TTCAGAGAGCTGGAAGGCTGGAGCCAGATGCACCCCATAGAGAACTMAAAGCAT 252

Qy 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluLeuThrLeuGlyGlu 100

Db 253 TCGTCCGTTGGCTTCTTCTTCTGTCAGAGAGGTTGAAGAACTAACCTTGATGA 312

Qy 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120

Db 313 TTTTGAACCTGCAGACAGAAAGAGCCAGAAATTTGCAGAGAAACCAATTAAG 372

Qy 121 LysylsGluPheGluGluThrAlaLysLysValArgAlaIleGluGluLeuAla 140

Db 373 AAGAAAGAAATTTGAGAAACTGCAGAAAGAAAGTGCCTGCATGAGCAGCTGGCTGCC 432

Qy 141 MetAsp 142

Db 433 ATGGAT 438

RESULT 49
BG110508 915 bp mRNA linear EST 30-JAN-2001
LOCUS 602278934F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:4366425 5',
DEFINITION mRNA sequence.
ACCESSION BG110508
VERSION BG110508.1 GI:12604014
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 915)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L10M1017 row: d column: 10
High quality sequence stop: 606.
Location/Qualifiers
1. 915
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4366425"
/tissue_type="osteosarcoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 86"
/note="Organ: bone; Vector: PCMV-Spore6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.53 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	1.3e-148	Length:	915
Score:	142.00	Matches:	142
Percent Similarity:	100.00%	Conservative:	0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-690-825-34 (1-142) x BG110508 (1-915)

QY 1 MetG1YAlaProThreupProAlaATPGLnProPhelenuSAsphIsarG1leser 20
DB 31 ATGGGTCCTCATTGAGTGGCCCTGCTGAGCCCTTCTCAAGAACACCGCATCTCT 90
QY 21 ThrPhelYsAsnTrpProPhelenuG1YCySa1aCySthrProGluArgMetA1aGlu 40
DB 91 ACATTGAGAACTGGCCCTTCTTGAGGGCTGCGCTGACCCCGAGCGGATGGCCGAG 150
QY 41 A1aG1YPhel1ehIsCySproThrg1uaenGluProAsp1eua1aG1nCySphheCyS 60
DB 151 GCTGGCTTCATCAGTCCGACCCCACTGAGAACGAGCCGAGCTTGCCCAAGTTCCTTCC 210
QY 61 PhelYsG1uLeuG1YTrpG1uProAspAspPro1eG1uG1uH1s1Ys1YsH1s 80
DB 211 TTCAGAGAGCTGAGAGCTGGAGCCAGTGAAGCCCATAGAGAAATMAAAGCAT 270
QY 81 SerSerG1YCySa1aPhelenuSerVal1Ys1YsG1nPhelG1uLeuThre1uG1Y 100
DB 271 TCGTCGGTGGCTTCTTCTTCTGTCAGAAAGCATTTGAAGATTAACCTTGCTGA 330
QY 101 PhelenuYsLeuSAspArgG1uArgAla1YsAsn1Ys1leAla1YsG1uThrasn1Ys 120
DB 331 TTTTAAACTGACAGAGAAAGCCAGAACTTGAAGAAAGAAACCAACATAG 390
QY 121 Lys1YsG1uPhelG1uThra1a1Ys1YsVal1ArgAG1a1leG1uG1uLeu1a1a 140
DB 391 AAGAAAGAAATTTGAGAAACTGCGAAGAAAGTCCCGCTGCATGAGAGCTGCTGCC 450
QY 141 MetAsp 142
DB 451 ATGGAT 456

RESULT 50
B1760504 924 bp mRNA linear EST 25-SEP-2001
LOCUS B1760504
DEFINITION 603045042F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5185114 5',
mRNA sequence.
ACCESSION B1760504
VERSION B1760504.1 GI:15752082
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE NIH-MGC http://mgs.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMW at:
http://image.llnl.gov
Plate: LMW11462 row: d column: 11
High quality sequence stop: 862.
Location/Qualifiers
1..924
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5185114"
/lab_host="DH10B"
/clone_11b="NIH_MGC_116"

FEATURES
source

/note="Organ: pooled colon, kidney, stomach; Vector:
pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 3 clones, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
Pred. No.: 1,31e-148 Length: 924
Score: 142.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-690-825-34 (1-142) x B1760504 (1-924)

QY 1 MetG1YAlaProThreupProAlaATPGLnProPhelenuSAsphIsarG1leser 20
DB 10 ATGGGTCCTCATTGAGTGGCCCTGCTGAGCCCTTCTCAAGAACACCGCATCTCT 69
QY 21 ThrPhelYsAsnTrpProPhelenuG1YCySa1aCySthrProGluArgMetA1aGlu 40
DB 70 ACATTGAGAACTGGCCCTTCTTGAGGGCTGCGCTGACCCCGAGCGGATGGCCGAG 129
QY 41 A1aG1YPhel1ehIsCySproThrg1uaenGluProAsp1eua1aG1nCySphheCyS 60
DB 130 GCTGGCTTCATCAGTCCGACCCCACTGAGAACGAGCCGAGCTTGCCCAAGTTCCTTCTCC 189
QY 61 PhelYsG1uLeuG1YTrpG1uProAspAspPro1eG1uG1uH1s1Ys1YsH1s 80
DB 190 TTCAGAGAGCTGAGAGCTGGAGCCAGATGAGACCCCATAGAGAAATMAAAGCAT 249
QY 81 SerSerG1YCySa1aPhelenuSerVal1Ys1YsG1nPhelG1uLeuThre1uG1Y 100
DB 250 TCGTCGGTGGCTTCTTCTTCTGTCAGAAAGCATTTGAAGATTAACCTTGCTGA 309
QY 101 PhelenuYsLeuSAspArgG1uArgAla1YsAsn1Ys1leAla1YsG1uThrasn1Ys 120
DB 310 TTTTAAACTGACAGAGAAAGCCAGAACTTGAAGAAAGAAACCAACATAG 369
QY 121 Lys1YsG1uPhelG1uThra1a1Ys1YsVal1ArgAG1a1leG1uG1uLeu1a1a 140
DB 370 AAGAAAGAAATTTGAGAAACTGCGAAGAAAGTCCCGCTGCATGAGAGCTGCTGCC 429
QY 141 MetAsp 142
DB 430 ATGGAT 435

RESULT 51
BQ959492 933 bp mRNA linear EST 21-AUG-2002
LOCUS BQ959492
DEFINITION AGENCOURT 8922878 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:4473127
5' mRNA sequence.
ACCESSION BQ959492
VERSION BQ959492.1 GI:22374970
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE NIH-MGC http://mgs.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov

Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLM4008 row: c column: 16
High quality sequence stop: 630.
Location/Qualifiers

FEATURES

source

1. 933
/organism="Homo sapiens"
/mol_type="rRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6473127"
/tissue_type="leiomysarcoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 71"
/note="Organ: uterus; Vector: PCMV-SPORT6; Site 1: Notif;
Site 2: SalI; Cloned unidirectionally. Primer: oligo dt.
Average insert size 2.1 kb."

ORIGIN

Alignment Scores:

Pred. No.: 1.32e-148 Length: 933
Score: 142.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-690-825-34 (1-142) x BQ959492 (1-933)

QY 1 MetGlyAlaProThrLeuProProAlaTPGInPProPheLeuLysAspHisArgIleSer 20
DB 25 ATGGGTGCCCCGACGCTTCCCTCCCTGCGAGCCCTTCTCAAGAGCACCCGACTCT 84
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 85 ACATTCAAGAACTGGCCCTTCTTGAGGGCTGCGCTGCACCCCGAGCGGATGGCCGAG 144
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAlaPheLeuAlaGlnCysPhePheYs 60
DB 145 GCTGCTTCATCCATGCGCCCACTAGAACGACGACCTGGCCCACTGTTCTTCTGCG 204
QY 61 PheLysGluLeuGluGlyTTPGluProAspAspAspProIleGluGluHisLysLysHis 80
DB 205 TTCAAGAGCTGGAAGCGCTGGAGGACAGATGACGCCCATAGAGAACTAAAGAT 264
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
DB 265 TCGTCGGGTGGCTTCTTCTCTCAAGAGCGATTGAAAGATTAAACCTTGTGAA 324
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120
DB 325 TTTTGAACCTGACAGAGAAAGCCAGAACAAATTGCCAAGAAACCAACATAG 384
QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGluLeuAla 140
DB 385 AAGAAAGATTGAGAGAACTGCGAAGAAAGTGGCCCGTCATGACAGCTGCTGCC 444
QY 141 MetAsp 142
DB 445 ATGGAT 450

RESULT 52
BF982118 934 bp mRNA linear EST 23-JAN-2001
LOCUS BF982118
DEFINITION 602308926f1 NIH_MGC_88 Homo sapiens CDNA clone IMAGE:4400190 5',
mRNA sequence.
ACCESSION BF982118
VERSION BF982118.1 GI:12384930
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLM40105 row: c column: 07
High quality sequence stop: 639.
Location/Qualifiers

FEATURES

source

1. 934
/organism="Homo sapiens"
/mol_type="rRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4400190"
/tissue_type="duodenal adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 88"
/note="Organ: small_intestine; Vector: PCMV-SPORT6;
Site 1: Notif; Site 2: SalI; Cloned unidirectionally;
oligo-dt primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 1.32e-148 Length: 934
Score: 142.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-690-825-34 (1-142) x BF982118 (1-934)

QY 1 MetGlyAlaProThrLeuProProAlaTPGInPProPheLeuLysAspHisArgIleSer 20
DB 13 ATGGGTGCCCCGACGCTTCCCTCCCTGCGAGCCCTTCTCAAGAGCACCCGACTCT 72
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 73 ACATTCAAGAACTGGCCCTTCTTGAGGGCTGCGCTGCACCCCGAGCGGATGGCCGAG 132
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheYs 60
DB 133 GCTGCTTCATCCATGCGCCCACTAGAACGACGACCTGGCCCACTGTTCTTCTGCG 192
QY 61 PheLysGluLeuGluGlyTTPGluProAspAspAspProIleGluGluHisLysLysHis 80
DB 193 TTCAAGAGCTGGAAGCGCTGGAGGACAGATGAGACGCCCATAGAGAACTAAAGAT 252
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
DB 253 TCGTCGGGTGGCTTCTTCTCTCAAGAGCGATTGAAAGATTAAACCTTGTGAA 312
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120
DB 313 TTTTGAACCTGACAGAGAAAGCCAGAACAAATTGCCAAGAAACCAACATAG 372
QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGluLeuAla 140
DB 373 AAGAAAGATTGAGAGAACTGCGAAGAAAGTGGCCCGTCATGACAGCTGCTGCC 432

QY 141 Met-Asp 142
Db 433 ATGGAT 438
RESULT 53
BE883927
LOCUS BE883927 935 bp mRNA linear EST 20-OCT-2000
DEFINITION 601505442F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3907138 5',
mRNA sequence.
ACCESSION BE883927
VERSION BE883927
KEYWORDS EST.
SOURCE BE883927.1 GI:10332703
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE NIH-MGC <http://imgc.ncl.nih.gov/>.
1 (bases 1 to 935)
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM9717 row: c column: 11
High quality sequence stop: 694.
Location/Qualifiers
1..935
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3907138"
/tissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_71"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2.1 kb."
ORIGIN
Alignment Scores:
Pred. No.: 1,32e-148 Length: 935
Score: 142.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
US-09-690-825-34 (1-142) x BE883927 (1-935)
ORIGIN
QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
Db 5 ATGGGTGGCCCGACGCTGGCCCTGCTGGACGCTTTCACAGACACACGATCTCT 64
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
Db 65 AACTTCACAGACTGGCCCTCTCTTGGAGGGCTGCGCTCCACCCCGAGCGATGGCCAG 124
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
Db 125 GCTGGCTTCATCCTACCTGCGCCCACTGAGAACGACGACGACTGGCCCACTGTTCTTCGC 184
QY 61 PheLysGluLeuGluGlyThrGluProPheAspArgProIleGluGluHisLysLysHis 80
Db 185 TTCACAGACTGGAAGGCTGGAGCGACATGACGACCCCATPAGAGAAACATPAAAAAGCAT 244
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100

Db 245 TCGTCGGTTCGCGCTTTCCTTCTGTCACAGACGACTTGAAGATTACCTTGATGA 304
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120
Db 305 TTTTGAACCTGACAGAGAAAGCCACAGAACAAATTTCACAGAAACCAATTAAG 364
QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAla 140
Db 365 AAGAAAGAAATTGAGAACTGCGAAGAAAGTCCGCTGCATCGAGACGCTGCTGCC 424
QY 141 Met-Asp 142
Db 425 ATGGAT 430
RESULT 54
BF981768 943 bp mRNA linear EST 23-JAN-2001
LOCUS BF981768
DEFINITION 602305433F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:4396689 5',
mRNA sequence.
ACCESSION BF981768
VERSION BF981768
KEYWORDS EST.
SOURCE BF981768.1 GI:12384580
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE NIH-MGC <http://imgc.ncl.nih.gov/>.
1 (bases 1 to 943)
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM10096 row: a column: 10
High quality sequence stop: 672.
Location/Qualifiers
1..943
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4396689"
/tissue_type="duodenal adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_88"
/note="Organ: small intestine; Vector: pCMV-SPORT6;
Site 1: NotI; Site 2: SalI; Cloned unidirectionally;
Oligo-dt primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH_MGC Library."
ORIGIN
Alignment Scores:
Pred. No.: 1,33e-148 Length: 943
Score: 142.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
US-09-690-825-34 (1-142) x BF981768 (1-943)
ORIGIN
QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
Db 9 ATGGGTGGCCCGACGCTGGCCCTGCTGGACGCTTTCACAGACACGATCTCT 68
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40

Db ACATTCAAGAACTGCGCCCTTCTTGAGGGCTGCGCTTGACCCCGAGCGGATGCGCGAG 128

Qy 41 AAGAGYPhelIeHISySProThrGluAbnGluProAspLeuAlaGInCySPhPheCys 60

Db 129 GCTGGCTTCATCCTGACCTGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAG 188

Qy 61 PheLysGluLeuGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 80

Db 189 TTCAAGAGAGCTGGAAGCTGGGAGGACATGACGACCCCATAGAGAAACATTAATAAAGCAT 248

Qy 81 SerSerGlyCySAIaphLeuSerValIySylSylGlnPheGluGluLeuThreGluGlu 100

Db 249 TCGTCGGCTTACCTCTTCTTCTGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 308

Qy 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrasnAsnLys 120

Db 309 TTTTGAACCTGACAG 368

Qy 121 LysLysGluPheGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 140

Db 369 AAGAAAGAAATTGAGAGAACTGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 428

Qy 141 MetAsp 142

Db 429 ATGGAT 434

RESULT 55

BQ929774 943 bp mRNA linear EST 20-AUG-2002

LOCUS BQ929774

DEFINITION AGENCOURT_8950028 NIH_MGC_71 Homo sapiens CDNA clone IMAGE:6471370

ACCESSION BQ929774.1 GI:22344805

VERSION BQ929774.1

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 943)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabs-remail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>

Plate: LLM14003 row: 5 column: 11

High quality sequence stop: 636.

Location/Qualifiers

1..943

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6471370"

/tissue_type="leiomyosarcoma"

/lab_host="DH10B (phage-resistant)"

/note="Organ: uterus; Vector: pCMV-SPORT6; Site: 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 2.1 kb.

DB: US-09-690-825-34 (1-142) x BQ929774 (1-943) 13 Gaps: 0

Qy 1 MetGlyAlaProThreProProAlaATPginProPheLeuLysAspHisArgIleSer 20

Db 32 ATGGATGCCCCGACGCTTGGCCCCCTGCTGCGAGCCCTTCTCTAGAGACACCGCATCTCT 91

Qy 21 ThrPheLysAsnTrpProPheLeuGluGluGlyCySAIaCysThrProGluArgLysGlu 40

Db 92 ACATTCAAGAACTGCGCCCTTCTTGAGAGGAGCTGCGCTGACCCCGAGAGCGGATGCGGAG 151

Qy 41 AAGAGYPhelIeHISySProThrGluAbnGluProAspLeuAlaGInCySPhPheCys 60

Db 152 GCTGGCTTCATCCTGACCTGCGCCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 211

Qy 61 PheLysGluLeuGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 80

Db 212 TTCAAGAGAGCTGGAAGCTGGGAGGACATGACGACCCCATAGAGAGACATTAATAAAGCAT 271

Qy 81 SerSerGlyCySAIaphLeuSerValIySylSylGlnPheGluGluLeuThreGluGlu 100

Db 272 TCGTCGGCTTACCTCTTCTTCTGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 331

Qy 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrasnAsnLys 120

Db 332 TTTTGAACCTGACAG 391

Qy 121 LysLysGluPheGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 140

Db 392 AAGAAAGAAATTGAGAGAACTGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 451

Qy 141 MetAsp 142

Db 452 ATGGAT 457

RESULT 56

BQ649501 962 bp mRNA linear EST 15-JUN-2002

LOCUS BQ649501

DEFINITION AGENCOURT_8492482 NIH_MGC_100 Homo sapiens CDNA clone IMAGE:6296575

ACCESSION BQ649501

VERSION BQ649501.1

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 962)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabs-remail.nih.gov

Tissue Procurement: CGAP (Stanford)

CDNA Library Preparation: Rubin Laboratory

DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>

Plate: LLM2504 row: 8 column: 08

High quality sequence stop: 618.

Location/Qualifiers

1..962

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6296575"

/tissue_type="hepatocellular carcinoma, cell line"

/lab_host="DH10B (phage-resistant)"

/clone_id="NIH_MGC_100"

/note="Organ: liver; Vector: pOT87; Site: 1: XhoI; Site 2:

FEATURES

source

ECOR1: cDNA made by oligo-RT printing. Directionally cloned into ECOR1/XhoI sites using the following 5' adaptor: GCGCAGGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-DNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH-MGC library."

ORIGIN

Alignment Scores:	
Pred. No.:	1,35e-148
Score:	142.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	13
	Gaps:
	0
US-09-690-825-34 (1-142) x BQ649501 (1-962)	

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VERSION      BUS01647.1  GI:22804718
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE    NIH-MGC http://mgi.nci.nih.gov/.
              1 (bases 1 to 965)
AUTHORS      National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE        Unpublished (1999)
JOURNAL      Contact: Robert Strausberg, Ph.D.
              Email: cgaabs-remail.nih.gov
COMMENT      Tissue Procurement: ATCC
              cDNA Library Preparation: Rubin Laboratory
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
              DNA Sequencing by: Agencourt Bioscience Corporation
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LNL at:
              http://image.lnl.gov
              Plate: L1CM2539 row: K column: 03
              High quality sequence stop: 517.
              Location/Qualifiers
                1..965
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:6341498"
                /tissue_type="neuroblastoma, cell line"
                /lab_host="DH10B (phage-resistant)"
                /clone_1lb="NIH_MGC_47"
                /note="Organ: brain; Vector: pOT7; Site: 1: XhoI; Site 2:
                EcoRI; cDNA made by oligo-dt priming. Directionally
                cloned into EcoRI/XhoI sites using the following 5'
                adaptor: GGCAAGGAG(G). Size-selected >500bp for average
                insert size 1.8kb. Library constructed by Ling Hong in
                the laboratory of Gerald M. Rubin (University of
                California, Berkeley) using Zap-cDNA synthesis kit
                (Stratagene) and Superscript II RT (Life Technologies).
                Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.:      1,36e-148      Length:      965
Score:          142.00        Matches:      142
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:             Gaps:        0

US-09-690-825-34 (1-142) x BUS01647 (1-965)

QY      1 MetGlyAlaProThrLeuProProAlaATPGLNPropheLeuYsAspHisArgIleSer 20
        |||
DB      54 ATGGGTGCCCCGACGTTGCCCCCTGCTGGAGCCCTTTCTCAAGACACACGATCTCT 113
        |||
QY      21 ThrPheLYsAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
        |||
DB      114 ACATTCAAGAACTGGCCCTTCTTGAGGGCTCGGCTGACCCCGAGGGATGGCCAG 173
        |||
QY      41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
        |||
DB      174 GCTGGCTTATCATCGTCCCTCACTGAACAGACCACTTGGCCAGAGTTCCTTCG 233
        |||
QY      61 PheLYsGluLeuGluGlyTrpGluProAspAspAspProIleGluGlnHisLYsLYsHis 80
        |||
DB      234 TTCAGAGACTGGAGGCTGGAGGCGACATGACACCCCATAGAGAGAACATMAAAGCAT 293
        |||
QY      81 SerSerGlyCysAlaPheLeuSerValLYsLYsGlnPheGluGluLeuThrLeuGluGlu 100
        |||
DB      294 TCTCCGGGTGGCCCTTCTTCTTGCAAGAACCACTTGAAGAAATTAACCTTGGTGA 353
        |||
QY      101 PheLeuLYsLeuAspArgGluArgAlaLYsAsnLYsIleAlaLYsGluThrAsnLYs 120
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DB      354 TTTTGAAACTGTGACAGAAAGCCAGAACAAATTCAGAAAGAAACCAACATTAAG 413
        |||
QY      121 LYsLYsGluPheGluGluThrAlaLYsLYsValArgArgAlaIleGluGluLeuAla 140
        |||
DB      414 AAGAAAGAAATTTGAGAAACTGGAAGAAAGGTCGCGCTCATGACGAGCTGGCTGC 473
        |||
QY      141 MetAsp 142
        |||
DB      474 ATCGAT 479

RESULT 59
BM463502
LOCUS    AGENCOURT 6433458 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:5585909
DEFINITION
5', mRNA sequence.
ACCESSION
BM463502
VERSION  BM463502.1  GI:18512544
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE NIH-MGC http://mgi.nci.nih.gov/.
          1 (bases 1 to 974)
AUTHORS   National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE     Unpublished (1999)
JOURNAL   Contact: Robert Strausberg, Ph.D.
          Email: cgaabs-remail.nih.gov
COMMENT   Tissue Procurement: ATCC
          cDNA Library Preparation: Life Technologies, Inc.
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
          DNA Sequencing by: Agencourt Bioscience Corporation
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LNL at:
          http://image.lnl.gov
          Plate: L1AM2352 row: P column: 06
          High quality sequence stop: 742.
          Location/Qualifiers
            1..974
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            /db_xref="taxon:9606"
            /clone="IMAGE:5585909"
            /tissue_type="embryonal carcinoma, cell line"
            /lab_host="DH10B (phage-resistant)"
            /clone_1lb="NIH_MGC_92"
            /note="Organ: testis; Vector: pCMV-SPORT6; Site: 1: NotI;
            Site 2: SalI; Cloned unidirectionally; oligo-dt primed.
            Average insert size 2.5 kb. Library enriched for
            full-length clones and constructed by Life Technologies.
            Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.:      1,37e-148      Length:      974
Score:          142.00        Matches:      142
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:             Gaps:        0

US-09-690-825-34 (1-142) x BM463502 (1-974)

QY      1 MetGlyAlaProThrLeuProProAlaATPGLNPropheLeuYsAspHisArgIleSer 20
        |||
DB      31 ATGGGTGCCCCGACGTTGCCCCCTGCTGGAGCCCTTTCTCAAGACACACGATCTCT 90
        |||
QY      21 ThrPheLYsAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
        |||
DB      91 ACATTCAAGAACTGGCCCTTCTTGAGGGCTGGCCCTGACCCCGAGGCGATGGCCAG 150
        |||
QY      41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
        |||

```

Db 151 GCTGGCTTCACTCAGTCCCGCCACTGAGAACGAGCCAGACTTGGCCCGCAGTCTTTCTTCG 210
Qy 61 PhelysGluLeuGluGlyTTPGluProAspAspProIleGluGluHisLysLysHis 80
Db 211 TTCAGAGAGCTGAGAGCTGGAGGAGCAGATGACGACCCCATGAGAGACATAAAAGCAT 270
Qy 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
Db 271 TCGTCCGCTTCCCTTCTTCTGTCAGAGACGATTTGAAGAAATTAACTTGGTGA 330
Qy 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
Db 331 TTTTGAAGACTGACAGAGAAAGCCAGAACCAAAATTGCAAGAGAAACCAACATAG 390
Qy 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGluLeuAla 140
Db 391 AAGAAAGAAATTGAGAGAACTGAGAGAAAGTGCCGCGCATGAGAGAGCTGCTGCC 450
Qy 141 MetAsp 142
Db 451 ATGGAT 456

RESULT 60
BQ064557 976 bp mRNA linear EST 02-APR-2002
LOCUS AGENCOURT 6853415 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5926298
DEFINITION 5', mRNA sequence.
ACCESSION BQ064557
VERSION BQ064557.1 GI:19893301
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 976)
AUTHORS NIH-MGC http://mgi.mci.nih.gov/
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: Lou Staudt
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLMC2099 row: 9 column: 03
High quality sequence stop: 660.
Location/Qualifiers
1. 976
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5926298"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_11b="NIH_MGC_99"
/note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

ORIGIN
Alignment Scores:
Pctd. No.: 1.37e-148 Length: 976
Score: 142.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0
US-09-690-825-34 (1-142) x BQ064557 (1-976)

Qy 1 MetGlyAlaProThrLeuProPheAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
Db 57 ATGGGTCCTCCGAGCGTTGCCCTTGGAGGGGTGGCTGACCCCGAGCGGATGGCGGAG 116
Qy 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
Db 117 ACATTCAAGAACTGGCCCTTCTTGAGAGGGGTGGCTGACCCCGAGCGGATGGCGGAG 176
Qy 41 AlaGlyPheLeuHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
Db 177 GCTGGCTTCACTCAGTCCCGCCACTGAGAACGAGCCAGACTTGGCCCGAGTCTTCTTCG 236
Qy 61 PheLeuGluLeuGluGlyTTPGluProAspAspProIleGluGluHisLysLysHis 80
Db 237 TTCAGAGAGCTGAGAGCTGGAGGAGCAGATGACGACCCCATGAGAGACATAAAAGCAT 296
Qy 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
Db 297 TCGTCCGCTTCCCTTCTTCTGTCAGAGACGATTTGAAGAAATTAACTTGGTGA 356
Qy 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
Db 357 TTTTGAAGACTGACAGAGAAAGCCAGAACCAAAATTGCAAGAGAAACCAACATAG 416
Qy 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGluLeuAla 140
Db 417 AAGAAAGAAATTGAGAGAACTGAGAGAAAGTGCCGCGCATGAGAGAGCTGCTGCC 476
Qy 141 MetAsp 142
Db 477 ATGGAT 482

RESULT 61
BMS02009 985 bp mRNA linear EST 05-MAR-2002
LOCUS AGENCOURT_6459567 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:5582026
DEFINITION 5', mRNA sequence.
ACCESSION BMS02009
VERSION BMS02009.1 GI:19118832
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 985)
AUTHORS NIH-MGC http://mgi.mci.nih.gov/
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLMC2342 row: n column: 11
High quality sequence stop: 747.
Location/Qualifiers
1. 985
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5582026"
/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"

/clone.lib="NIH_MGC_67"
 /note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NcoI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.75 Kb. Library constructed by Life
 Technologies."

ORIGIN

Alignment Scores:

Pred. No.:	1,39e-148	Length:	985
Score:	142.00	Matches:	142
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	12	Gaps:	0

US-09-690-825-34 (1-142) x BM80209 (1-985)

QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
 DB 63 ATGGGTGCCCGACGCTGCCCCCTGCTGCAGCCCTTTCTCAAGACACCGCATCTCT 122

QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
 DB 123 ACATTCAGAACTGGCCCTTCTTGAGGGCTGCGCTTGCACCCCGAGCGATGGCCGAG 182

QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
 DB 183 GCTGCTTCATCACTGCCGCCCATGAGAACGACGACACTGGCCCACTGTTCTTCTGCG 242

QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHisLysLysHis 80
 DB 243 TTCAAGAGCTGGAGGCTGGAGCCAGATGACGCCCATAGAGAACTAAAGATCAT 302

QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
 DB 303 TCGTCGGTGGCGCTTCTTCTTCTGTCAGAAAGCATTTGAAGATTAACTTGGTGA 362

QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
 DB 363 TTTTGAACCTGACAGAGAAAGACCCAAAGAAATTGCAAGAAACCAACATATAG 422

QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAlaAla 140
 DB 423 AAGAAAGATTGAGAAACTGCAAGAAAGTGGCGCTGCATGAGCAGCTGCTGCC 482

QY 141 MetAsp 142
 DB 483 ATGGAT 488

QY 141 MetAsp 142
 DB 483 ATGGAT 488

QY 141 MetAsp 142
 DB 483 ATGGAT 488

QY 141 MetAsp 142
 DB 483 ATGGAT 488

QY 141 MetAsp 142
 DB 483 ATGGAT 488

QY 141 MetAsp 142
 DB 483 ATGGAT 488

QY 141 MetAsp 142
 DB 483 ATGGAT 488

QY 141 MetAsp 142
 DB 483 ATGGAT 488

QY 141 MetAsp 142
 DB 483 ATGGAT 488

QY 141 MetAsp 142
 DB 483 ATGGAT 488

QY 141 MetAsp 142
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QY 141 MetAsp 142
 DB 483 ATGGAT 488

QY 141 MetAsp 142
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QY 141 MetAsp 142
 DB 483 ATGGAT 488

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 DB 483 ATGGAT 488

QY 141 MetAsp 142
 DB 483 ATGGAT 488

http://image.llnl.gov
 Plate: L10M2678 row: d column: 18
 High quality sequence stop: 777.
 Location/Qualifiers
 1.990

FEATURES

Source

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6497345"
 /tissue_type="epidermoid carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone.lib="NIH_MGC_101"
 /note="Organ: lung; Vector: pMT7; Site 1: EcoRI; Site 2:
 XhoI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCAAGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC library."

ORIGIN

Alignment Scores:

Pred. No.:	1,39e-148	Length:	990
Score:	142.00	Matches:	142
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	13	Gaps:	0

US-09-690-825-34 (1-142) x BQ958253 (1-990)

QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
 DB 65 ATGGGTGCCCGACGCTGCCCCCTGCTGCAGCCCTTTCTCAAGACACCGCATCTCT 124

QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
 DB 125 ACATTCAGAACTGGCCCTTCTTGAGGGCTGCGCTTGCACCCCGAGCGATGGCCGAG 184

QY 125 ACATTCAGAACTGGCCCTTCTTGAGGGCTGCGCTTGCACCCCGAGCGATGGCCGAG 184
 DB 185 GCTGCTTCATCACTGCCGCCCATGAGAACGACGACACTGGCCCACTGTTCTTCTGCG 244

QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
 DB 185 GCTGCTTCATCACTGCCGCCCATGAGAACGACGACACTGGCCCACTGTTCTTCTGCG 244

QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHisLysLysHis 80
 DB 245 TTCAAGAGCTGGAGGCTGGAGCCAGATGACGCCCATAGAGAACTAAAGATCAT 304

QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
 DB 305 TCGTCGGTGGCGCTTCTTCTTCTGTCAGAAAGCATTTGAAGATTAACTTGGTGA 364

QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
 DB 365 TTTTGAACCTGACAGAGAAAGACCCAAAGAAATTGCAAGAAACCAACATATAG 424

QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAlaAla 140
 DB 425 AAGAAAGATTGAGAAACTGCAAGAAAGTGGCGCTGCATGAGCAGCTGCTGCC 484

QY 141 MetAsp 142
 DB 485 ATGGAT 490

QY 141 MetAsp 142
 DB 485 ATGGAT 490

QY 141 MetAsp 142
 DB 485 ATGGAT 490

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 DB 485 ATGGAT 490

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 DB 485 ATGGAT 490

QY 141 MetAsp 142
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QY 141 MetAsp 142
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QY 141 MetAsp 142
 DB 485 ATGGAT 490

QY 141 MetAsp 142
 DB 485 ATGGAT 490

QY 141 MetAsp 142
 DB 485 ATGGAT 490

QY 141 MetAsp 142
 DB 485 ATGGAT 490

QY 141 MetAsp 142
 DB 485 ATGGAT 490

QY 141 MetAsp 142
 DB 485 ATGGAT 490

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

RESULT 62
 BQ958253 990 bp mRNA linear EST 21-AUG-2002
 LOCUS
 DEFINITION
 AGENCOURT 10016123 NIH_MGC_101 Homo sapiens cDNA clone
 IMAGE:6497345 5', mRNA sequence.
 BQ958253
 ACCESSION
 BQ958253.1 GI:22373731
 VERSION
 EST.
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NIH-MGC http://mgi.nci.nih.gov/
 1 (bases 1 to 990)
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 993)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINT)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINT at:
http://image.llnl.gov
Plate: LHAM2254 row: d column: 14
High quality sequence stop: 643.
Location/Qualifiers
1. 993
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5547229"
/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site: 1: NotI;
Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Library constructed by Life
Technologies."

ORIGIN
Alignment Scores:
Pred. No.: 1,39e-148 Length: 993
Score: 142.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-690-825-34 (1-142) x BMS64739 (1-993)

QY 1 MetG1yAlaProthreupropProAlaTpgInpPhelLeuLysAspHisArgIleSer 20
Db 40 ATGGGTGCCCCGACGTTGGCCCTGCTGCGACGCCCTTCTCAAGACACCGCATCTCT 99
QY 21 ThPhelYsAsnTrpProPhelLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
Db 100 ACATTCAAGACCTGGCCCTTCTTGAGGGCTGCGGCTGCACCCCGAGGAGATGGCGAG 159
QY 41 AlaGlyPheIleHisCysProThrGluWangluProAspLeuAlaGlnCysPhePheCys 60
Db 160 GCTGGCTTATCCACTGCCCCCACTGAGACGAGCAGACTTGGCCAGTGTCTTCTTGC 219
QY 61 PheLysGluLeuGluGlyTyrGluProAspAspProIleGluGluHisLysLysHis 80
Db 220 TTCAAGACCTGAGAGGCTGGAGCGAGTACGACCCCATAGAGAACATTAAGAT 279
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
Db 280 TCGTCCGATTGCGCTTCTTCTGTCAAGACGATTGAAGATTAACTTGTGTAA 339
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
Db 340 TTTTGAACCTGACAGAGAAAGACCAAGAAATTGCAAGAGAAACCAACATAG 399
QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGluLeuAlaAla 140
Db 400 AAGAAAGATTGAGAGAACTGCAAGAAAGTGGCCGTGCATGACACACTGCTGCC 459
QY 141 MetAsp 142
|||||

Db 460 ATGGAT 465
RESULT 64
EM471181
LOCUS BM471181 995 bp mRNA linear EST 05-FEB-2002
DEFINITION AGENCOURT 6478298 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5563046
5', mRNA sequence.
ACCESSION BM471181.1 GI:18520223
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 995)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DMF
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINT)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINT at:
http://image.llnl.gov
Plate: LHAM2293 row: g column: 15
High quality sequence stop: 751.
Location/Qualifiers
1. 995
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5563046"
/tissue_type="melanotic melanoma"
/lab_host="DH103 (phage-resistant)"
/clone_lib="NIH_MGC_72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site: 1: NotI;
Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."

ORIGIN
Alignment Scores:
Pred. No.: 1,39e-148 Length: 995
Score: 142.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-690-825-34 (1-142) x BM471181 (1-995)

QY 1 MetG1yAlaProthreupropProAlaTpgInpPhelLeuLysAspHisArgIleSer 20
Db 39 ATGGGTGCCCCGACGTTGGCCCTGCTGCGACGCCCTTCTCAAGACACCGCATCTCT 98
QY 21 ThPhelYsAsnTrpProPhelLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
Db 99 ACATTCAAGACCTGGCCCTTCTTGAGGGCTGCGGCTGCACCCCGAGGAGATGGCGAG 158
QY 41 AlaGlyPheIleHisCysProThrGluWangluProAspLeuAlaGlnCysPhePheCys 60
Db 159 GCTGGCTTATCCACTGCCCCCACTGAGACGAGCAGACTTGGCCAGTGTCTTCTTGC 218
QY 61 PheLysGluLeuGluGlyTyrGluProAspAspProIleGluGluHisLysLysHis 80
Db 219 TTCAAGACCTGAGAGGCTGGAGCGAGTACGACCCCATAGAGAACATTAAGAT 278
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
Db 279 TCGTCCGATTGCGCTTCTTCTGTCAAGACGATTGAAGATTAACTTGTGTAA 338
|||||

QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
 Db 339 TTTTGAACCTGACAGAGAAAGAGCCAGCAAAATTCGCAAGAAACCAACCAATTAAG 398
 QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGluThrLeuAlaAla 140
 Db 399 AAGAAAGAAATTGGAGAAACTGCAAGAAAGTGGCCGCTGCATCGAGAGCTGCTGCC 458
 QY 141 MetAsp 142
 Db 459 ATGGAT 464
 RESULT 65
 AL545180 1009 bp mRNA linear EST 31-MAY-2003
 LOCUS
 DEFINITION AL545180 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
 clone CSOD1028YH13 5-PRIME, mRNA sequence.
 AL545180
 VERSION AL545180.2 GI:31267016
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1009)
 AUTHORS Li, N.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length CDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT On Feb 15, 2001 this sequence version replaced gi:12877661.
 CONTACT Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 8555.r for
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CSOD1028CD07QP1&cluster=8555.r. Contact :
 Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CSOD1028CD07QP1.
 FEATURES
 source
 1..1009
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CSOD1028YH13"
 /tissue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-cligo(dT)
 primer. Five primers end enriched, double-strand cDNA was
 digested with NotI and cloned into the NotI and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."
 ORIGIN
 Alignment Scores:
 Pred. No.: 1,41e-148 Length: 1009
 Score: 142.00 Matches: 142
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0
 US-09-690-825-34 (1-142) x AL545180 (1-1009)
 QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
 Db 91 ATGGGGGCCCGACGCTGGCCCTGCTGGACGCCCTTTCTCAAGACACCGCATCTCT 150
 QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
 Db 151 ACATTCAAGAACTGGCCCTTTCTTGGAGGGCTGCGCTGCACCCCGAGCGGATGCCGAG 210

QY 41 AlaGlyPheIleHisCysProThrGluLeuGluProAspLeuAlaGlnCysPheCys 60
 Db 211 GGTGGCTTCATCCTACCTGCCCCCTAGAAACGAGCGAGCTTGGCCAGTGTCTTCTGC 270
 QY 61 PheLysGluLeuGluGlyTrpGluProAspAspArgPheIleGluGluHisLysLysHis 80
 Db 271 TTCAGAGAGCTGGAAGCGCTGGAGCCAGATGACGCCCATGAGAGCAATTAAGCAT 330
 QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluThrLeuGluGlu 100
 Db 331 TCGTCGGGTGGCGCTTCTCTCTCTCAAGAAAGAGTGGAAATTAACCTTGCTGAA 390
 QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
 Db 391 TTTTGAACCTGACAGAGAAAGAGCCAGCAAAATTCGCAAGAAACCAACCAATTAAG 450
 QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGluThrLeuAlaAla 140
 Db 451 AAGAAAGAAATTGGAGAAACTGCAAGAAAGTGGCCCGCTGCATCGAGAGCTGCTGCC 510
 QY 141 MetAsp 142
 Db 511 ATGGAT 516
 RESULT 66
 BF033760 1031 bp mRNA linear EST 20-OCT-2000
 LOCUS BF033760
 DEFINITION 601454095F1 NIH_MGC_66 Homo sapiens CDNA clone IMAGE:3857879 5',
 mRNA sequence.
 BF033760
 VERSION BF033760.1 GI:10741472
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1031)
 AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps@remail.nih.gov
 Tissue Procurement: DCTD/DTF
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.jnl.gov
 Plate: LHAM9588 row: n column: 24
 High quality sequence stop: 691.
 FEATURES
 source
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3857879"
 /tissue_type="adenocarcinoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC 66"
 /note="Organ: ovary; Vector: pCMV-SPORE6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.8 kb. Library constructed by Life
 Technologies."
 ORIGIN
 Alignment Scores:
 Pred. No.: 1,44e-148 Length: 1031
 Score: 142.00 Matches: 142
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0

DB: 10 Gaps: 0

US-09-690-825-34 (1-142) x BF033760 (1-1031)

QY 1 MetGlyAlaProThrLeuProProAlaTPGInProPheLeuLysAspHisArgIleSer 20
DB 7 ATGGAGTCCCCGACGCTTCCCTGCTGACGCTTTCTCAAGACACCGCATCTCT 66
QY 21 ThPheLysAsnTPProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 67 ACATTCAGAGACTGGCCCTTCTTGAGAGGCTGGCTTCGACCCCGAGCGATGCGCGAG 126
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGluCysPhePheCys 60
DB 127 GCTGGCTTCATCCACTGCCCCACTGAGAGAGACCACTGACCAAGTTCCTCTGTC 186
QY 61 PheLeuGluLeuGluGlyTTPGluProAspAspAspProIleGluGluHisLysLysHis 80
DB 187 TTCAGAGAGCTGGAAGCTGGAGGACAGATGACGCCCATAGAGAAATATAAAGCAT 246
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGluPheGluGluLeuThrLeuGluGlu 100
DB 247 TCGTCCGGTGGCTTCTTCTGTCAGAGACGATTTGAAGAAATTAACCTTGTTGTA 306
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
DB 307 TTTTGAACCTGACAGAGAAAGAGCCAGAAACAAATTGCAAGGAAACCAACAATAG 366
QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGluLeuAla 140
DB 367 AAGAAAGAAATTGAGAAAGCTGCAAGAAAGTCCGCGCATGAGAGAGCTGGCTGCC 426
QY 141 MetAsp 142
DB 427 ATGGAT 432

RESULT 67
BM552163 1035 bp mRNA linear EST 20-FEB-2002
LOCUS AGENCOURT 6543744 NIH_MGC_71 Homo sapiens cDNA IMAGE:5549540
DEFINITION 5', mRNA sequence.
ACCESSION BM552163
VERSION BM552163.1 GI:18789795
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1035)
AUTHORS NIH-MGC <http://mhc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLM12260 row: d column: 21
High quality sequence stop: 552.
Location/Qualifiers
1..1035
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5549540"
/tissue_type="telomysarcoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_71"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;

ORIGIN

Alignment Scores:

Pred. No.: 1,44e-148 Length: 1035
Score: 142.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-690-825-34 (1-142) x BM552163 (1-1035)

QY 1 MetGlyAlaProThrLeuProProAlaTPGInProPheLeuLysAspHisArgIleSer 20
DB 8 ATGGAGTCCCCGACGCTTCCCTGCTGACGCTTTCTCAAGACACCGCATCTCT 67
QY 21 ThPheLysAsnTPProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 68 ACATTCAGAGACTGGCCCTTCTTGAGAGGCTGGCTTCGACCCCGAGCGATGCGCGAG 127
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGluCysPhePheCys 60
DB 128 GCTGGCTTCATCCACTGCCCCACTGAGAGAGACCACTGACCAAGTTCCTCTGTC 187
QY 61 PheLeuGluLeuGluGlyTTPGluProAspAspAspProIleGluGluHisLysLysHis 80
DB 188 TTCAGAGAGCTGGAAGCTGGAGGACAGATGACGCCCATAGAGAAATATAAAGCAT 247
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGluPheGluGluLeuThrLeuGluGlu 100
DB 248 TCGTCCGGTGGCTTCTTCTGTCAGAGACGATTTGAAGAAATTAACCTTGTTGTA 307
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
DB 308 TTTTGAACCTGACAGAGAAAGAGCCAGAAACAAATTGCAAGGAAACCAACAATAG 367
QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGluLeuAla 140
DB 368 AAGAAAGAAATTGAGAAAGCTGCAAGAAAGTCCGCGCATGAGAGAGCTGGCTGCC 427
QY 141 MetAsp 142
DB 428 ATGGAT 433

RESULT 68
B0048975 1047 bp mRNA linear EST 29-MAR-2002
LOCUS AGENCOURT 6832768 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:5789750
DEFINITION 5', mRNA sequence.
ACCESSION B0048975
VERSION B0048975.1 GI:19808315
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1047)
AUTHORS NIH-MGC <http://mhc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLM12883 row: m column: 15
High quality sequence stop: 612.

FEATURES
source

Location/Qualifiers
1..1047
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5789750"
/tissue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_92"
/note="Organ: testis; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 2.5 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC library."

ORIGIN

Alignment Scores:

Pred. No.:	1,45e-148	Length:	1047
Score:	142.00	Matches:	142
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	12	Gaps:	0

US-09-690-825-34 (1-142) x BG048975 (1-1047)

QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
Db 41 ATGGGTGCCCCGACGTTGGCCCCCTGGCGAGCCCTTTCTCAAGAGCACCCGATCTT 100
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGln 40
Db 101 ACATTCAAGAACTGGCCCTTCTTGGAGGGCTGGCCCTGCACCCCGAGCGGATGGCCGAG 160
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
Db 161 GCTGGCTTCATCCACTGCCCTGACGAGACGAGCCAGCTTGGCCCAAGTGTTCCTTCGC 220
QY 61 PheLysGluLeuGluGlyTrpGluProAspAspAspProIleGluGluHisIleLysLysHis 80
Db 221 TTCAAGAGCGTGAAGAGCTGGAGACGATGACGACCCCATAGAGAACTAAATAACAT 280
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGluGlu 100
Db 281 TCGTCCGGTTCGCTTCCTTCCTGTCAGAAAGAGATTGAAGATTAAACCTTGGTGA 340
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
Db 341 TTTTGAACACTGACAGAGAAAGACCAAGAACTTGAAGAGAAACCAACATTAAG 400
QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAlaAla 140
Db 401 AAGAAAGAAATTGAGGAAGAACTGCGAAGAAAGTGGCGCTGCATCGAGCACTGGCTGCC 460
QY 141 MetAsp 142
Db 461 ATGGAT 466

RESULT 69
BG035337

LOCUS 603224964f1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:4413183 5',
DEFINITION mRNA sequence.

ACCESSION BG035337
VERSION BG035337.1 GI:12429369

KEYWORDS
SOURCE

ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1051)
AUTHORS NIH-MGC <http://mgi.mci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL
COMMENT

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/BLNI at:
<http://image.llnl.gov>
Plate: LMAN1038 row: p column: 16
High quality sequence stop: 714.

FEATURES
source

Location/Qualifiers
1..1051
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4413183"
/tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_90"
/note="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC library."

ORIGIN

Alignment Scores:

Pred. No.:	1,46e-148	Length:	1051
Score:	142.00	Matches:	142
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-09-690-825-34 (1-142) x BG035337 (1-1051)

QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
Db 50 ATGGGTGCCCCGACGTTGGCCCCCTGGCGAGCCCTTTCTCAAGAGCACCCGATCTT 109
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGln 40
Db 110 ACATTCAAGAACTGGCCCTTCTTGGAGGGCTGGCCCTGCACCCCGAGCGGATGGCCGAG 169
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
Db 170 GCTGGCTTCATCCACTGCCCTGACGAGACGAGCCAGACTTGGCCCAAGTGTTCCTTC 229
QY 61 PheLysGluLeuGluGlyTrpGluProAspAspAspProIleGluGluHisIleLysLysHis 80
Db 230 TTCAAGAGCTGAAGAGCTGGAGACGATGACGACCCCATAGAGAACTAAATAACAT 289
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGluGlu 100
Db 290 TCGTCCGGTTCGCTTCCTTCCTGTCAGAAAGAGATTGAAGATTAAACCTTGGTGA 349
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
Db 350 TTTTGAACACTGACAGAGAAAGACCAAGAACTTGAAGAGAAACCAACATTAAG 409
QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAlaAla 140
Db 410 AAGAAAGAAATTGAGGAAGAACTGCGAAGAAAGTGGCGCTGCATCGAGCACTGGCTGCC 469
QY 141 MetAsp 142
Db 470 ATGGAT 475

RESULT 70
B1518504

LOCUS B1518504 1052 bp mRNA linear EST 29-AUG-2001

DEFINITION 603061622F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5211005 5', mRNA sequence.

ACCESSION B1518504

VERSION B1518504.1 GI:15343296

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1052)

AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc. (LNLN)
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: <http://image.llnl.gov>
plate: LLM11529 row: k column: 06
High quality sequence stop: 834.

FEATURES

source

1..1052

location/Qualifiers

1..1052

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5211005"

/tissue_type="leukocyte"

/lab_host="DH10B"

/clone_lib="NIH_MGC_118"

/note="Vector: PCMV-SPORT6, Site_1: NotI, Site_2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 1,466-148 Length: 1052

Score: 142.00 Matches: 142

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

Gaps: 0

DB: 12

US-09-690-825-34 (1-142) x B1518504 (1-1052)

QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20

DB 49 ATGGGTGCCCCCAGCCCTTCCCTGCGAGCCCTTTCACAGACACCGCATCTCT 108

QY 21 ThrPheLysAsnTrpProPheLeuGlnGlyCysAlaCysThrProGluArgMetAlaGlu 40

DB 109 ACATTCAAGAACTGCCCCCTTCTTGAGAGGCTGCGCTCACCAGCGAGATGCGAG 168

QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60

DB 169 GCTGCTCATCATCAGTCCCGCCAGACAGACAGACAGCTGGCCCAAGTCTTCTTCTGC 228

QY 61 PheLysGluLeuGlnGlyTrpGlnProAspAspProIleGluGlnHisIleLysHis 80

DB 229 TTCAAGAGAGCTGGAAGGCTGGAGCCAGATAGACACCCATAGAGAAACATAAAGCAT 288

QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100

DB 289 TCGTCCGATGGCTTCTTCTTCTGCAAGAGAGAGGTTTGAAGATTAACTTGTGTA 348

QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120

DB 349 TTTTGAACCTGCACAGAGAAAGCCAGCAAAATTGCCAAGAAACCAACATATAG 408

QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAla 140

DB 409 AAGAAAAGATTTCAGGAAACTGCGAAGAAAGCGCCGTCATCAGACGCTGCTGCC 468

QY 141 MetAsp 142

DB 469 ATGGAT 474

RESULT 71

BQ073169 1071 bp mRNA linear EST 02-APR-2002

LOCUS AGENCOURT 6817956 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5757525

DEFINITION 5', mRNA sequence.

ACCESSION BQ073169

VERSION BQ073169.1 GI:19902215

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1071)

AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: <http://image.llnl.gov>
plate: LLM12799 row: n column: 22
High quality sequence stop: 711.

FEATURES

source

1..1071

location/Qualifiers

1..1071

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5757525"

/tissue_type="leukocyte"

/lab_host="DH10B"

/clone_lib="NIH_MGC_118"

/note="Vector: PCMV-SPORT6, Site_1: NotI, Site_2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 1,486-148 Length: 1071

Score: 142.00 Matches: 142

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

Gaps: 0

DB: 13

US-09-690-825-34 (1-142) x BQ073169 (1-1071)

QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20

DB 19 ATGGGTGCCCCCAGCCCTTCCCTGCGAGCCCTTTCACAGACACCGCATCTCT 78

QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
 Db 79 ACATTCAAGAACTGGCCCTTCTTGGAGGGCTGGCCCTCCACCCCGAGCCGAGTGGCCGAG 138
 QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
 Db 139 GCTGGCTTCATCCACTGCCCCACCTGAGAACAGAGCCACACTGGCCCGCTTCTTCTGCG 198
 QY 61 PheLysGluLeuGluGlyTrpGluProAspAspAspProIleGluGluHis 80
 Db 199 TTCAGAGGCTGGAGAGGCTGGAGCCCGATGACACCCCATAGAGAACTTAAACCAT 258
 QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluLeuThrLeuGlyGlu 100
 Db 259 TCGTCCGGTTGGCTTCTTCTTCTGTCAGAGAACAGATTGAGAAATTAACCTTGGTGA 318
 QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
 Db 319 TTTTGGAACTGACAGAGAAAGCCAGAACAAATTTGCCAAGGAAACCAATTAAG 378
 QY 121 LysLysGluPheGluGluGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAlaAla 140
 Db 379 AAGAAAGAAATTTGAGAAACTGCCAAGAAAGTGGCCGCTGCATCGACAGCTGGCTGCC 438
 QY 141 MetAsp 142
 Db 439 ATGGAT 444
 RESULT 72
 EC394560 1073 bp mRNA linear EST 12-MAR-2001
 LOCUS 60245894F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:4579367 5'
 DEFINITION mRNA sequence.
 ACCESSION EC394560 GI:13288008
 VERSION EC394560.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1073)
 NIH-MGC http://mhc.nci.nih.gov/.
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
 Plate: LLM1296 row: 1 column: 24
 High quality sequence stop: 635.
 Location/Qualifiers
 1..1073
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4579367"
 /tissue_type="retinoblastoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_id="NIH_MGC_16"
 /note="Organ: eye; Vector: pCR37; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dt priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCACGAG(G). Library constructed by Ling Hong
 in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
 Pred. No.: 1,496-148 Length: 1073
 Score: 142.00 Matches: 142
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 12 Gaps: 0
 US-09-690-825-34 (1-142) x EC394560 (1-1073)
 QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
 Db 77 ATGGGTCGCCCGACAGCTGGCCCTTCTGTCAGAGAACAGATTGAGAAATTAACCTTGGTGA 136
 QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
 Db 137 ACATTCAAGAACTGGCCCTTCTTGGAGGGCTGGCCCTCCACCCCGAGCCGAGTGGCCGAG 196
 QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
 Db 197 GCTGGCTTCATCCACTGCCCCACCTGAGAACAGAGCCACACTGGCCCGCTTCTTCTGCG 256
 QY 61 PheLysGluLeuGluGlyTrpGluProAspAspAspProIleGluGluHis 80
 Db 257 TTCAGAGGCTGGAGAGGCTGGAGCCCGATGACACCCCATAGAGAACTTAAACCAT 316
 QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluLeuThrLeuGlyGlu 100
 Db 317 TCGTCCGGTTGGCTTCTTCTTCTGTCAGAGAACAGATTGAGAAATTAACCTTGGTGA 376
 QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
 Db 377 TTTTGGAACTGACAGAGAAAGCCAGAACAAATTTGCCAAGGAAACCAATTAAG 436
 QY 121 LysLysGluPheGluGluGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAlaAla 140
 Db 437 AAGAAAGAAATTTGAGAAACTGCCAAGAAAGTGGCCGCTGCATCGACAGCTGGCTGCC 496
 QY 141 MetAsp 142
 Db 497 ATGGAT 502
 RESULT 73
 BM551159 1114 bp mRNA linear EST 20-FEB-2002
 LOCUS BM551159
 DEFINITION AGENCOURT_6545015 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5738595
 5', mRNA sequence.
 ACCESSION BM551159
 VERSION BM551159.1 GI:18787966
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1114)
 NIH-MGC http://mhc.nci.nih.gov/.
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov
 Plate: LLM12750 row: 3 column: 04
 High quality sequence stop: 542.
 Location/Qualifiers
 1..1114
 /organism="Homo sapiens"

FEATURES

source

```

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5738595"
/tissue_type="duodenal adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_1ib="NIH_MGC_88"
/notes="Organ: small intestine; Vector: pCMV-SPORT6;
Site 1: NotI; Site 2: SalI; Cloned unidirectionally;
oligo-dt primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by life
technologies. Note: this is a NIH_MGC Library."

```

ORIGIN

Alignment Scores:

Pred. No.:	1,53e-148	Length:	1114
Score:	142.00	Matches:	142
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	12	Gaps:	0

US-09-690-825-34 (1-142) x BMS51159 (1-1114)

ORIGIN

Alignment Scores:

Pred. No.:	1,53e-148	Length:	1114
Score:	142.00	Matches:	142
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	12	Gaps:	0

US-09-690-825-34 (1-142) x BQ053391 (1-1115)

ORIGIN

Alignment Scores:

Pred. No.:	1,54e-148	Length:	1115
Score:	142.00	Matches:	142
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	12	Gaps:	0

Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LICM2122 row: e column: 17
 High quality sequence step: 613.
 Location/Qualifiers
 1. 1115
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5935096"
 /tissue_type="natural killer cells, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_1ib="NIH_MGC_106"
 /notes="Organ: blood; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; CDNA made by oligo-dt priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCACGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using zap-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."

FEATURES

source

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5738595"
/tissue_type="duodenal adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_1ib="NIH_MGC_88"
/notes="Organ: small intestine; Vector: pCMV-SPORT6;
Site 1: NotI; Site 2: SalI; Cloned unidirectionally;
oligo-dt primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by life
technologies. Note: this is a NIH_MGC Library."

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5935096"
/tissue_type="natural killer cells, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_1ib="NIH_MGC_106"
/notes="Organ: blood; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; CDNA made by oligo-dt priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using zap-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

```

DEFINITION AL549362 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 clone CSODI052Y011 5-PRIME, mRNA sequence.
 ACCESSION AL549362
 VERSION AL549362.2 GI:31271180
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1138)
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Playes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT On Feb 15, 2001 this sequence version replaced gi:12885275.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 8555.r For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CSODI052CE06Q1&cluster=8555.r. Contact :
 Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CSODI052CE06Q1.

FEATURES

Location/Qualifiers
 1..1138
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CSODI052Y011"
 /issue_type="PLACENTA COT 25-NORMALIZED"
 /clone_id="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="First strand cDNA was primed with a NotI-oligo (dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:

Pred. No.: 1,566-148 Length: 1138
 Score: 142.00 Matches: 142
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-690-825-34 (1-142) x AL549362 (1-1138)

QY 1 MetGtYAlaProThLeuProProAlaTtPgLnProPhelLeuLysAspHisArgTleser 20
 DB 76 ATGGGTGCCCGACGCTTCCCCCTGCGCAGCCCTTCTCAAGAACACCGCATCTCT 135
 QY 21 ThrPhelLysAntTtProPhelLeuGlnGlyCysAlaCysThrProGluArgMetAlaGln 40
 DB 136 ACATTCAAGAACTGGCCCTTCTTGAGGGGCTGGCCCTGACCCCGAGCGGATGGCCGAG 195
 QY 41 AlaGlyPheIleHisCysProThGlnGlnGlnProAspLeuAlaGlnCysPhePheCys 60
 DB 196 GGTGGCTTCATCATCTGCCCCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 255
 QY 61 PheLysGlnLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
 DB 256 TTCAAGGAGCTGAGAGCTGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 315
 QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGlnGlnGlnGlnGlnGlnGlnGln 100
 DB 316 TCGTCGGGTGGCTTCTTCTTCTGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 375
 QY 101 PheLeuLysLeuLysAspArgGlnArgAlaLysAsnLysIleAlaLysGlnThrAsnAsnLys 120
 DB 376 TTTTGAAGACTGGACAG 435

QY 121 LysLysGlnPheGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 140
 DB 436 AAGAAAGAAATTGGAGGAAACTCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 495
 QY 141 MetAsp 142
 DB 496 ATGGAT 501

Search completed: August 16, 2004, 03:23:12
 Job time : 2780 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 16, 2004, 00:13:04 / Search time 453 Seconds

(without alignments)
1331.665 Million cell updates/sec

Title: US-09-690-825-34

Perfect score: 142

Sequence: 1 MGATLPAPAMPFLKDHRI.....EFETAKKRAIEQLAAND 142

Scoring table:

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Ygapop 60.0	Ygapext 60.0	
Fgapop 6.0	Fgapext 7.0	
Delop 6.0	Delext 7.0	

Searched: 3373863 seqs, 212409041 residues

Word size: 1

Total number of hits satisfying chosen parameters: 6745138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Command line parameters:

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-O=/sgn_1/USPRO.spool/US09690825/runat_11082004_141014_13783/app_query.fasta_1.327
-DB=N Geneseq 29Jan04 -QMT=fastcap -SUFFIX=oligo.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=100 -DOCALLING=200 -THR SCORE=quality -THR MIN=1 -ALIGN=75 -MODE=LOCAL
-OUTMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09690825 @CGN_1_1_470 @runat_11082004_141014_13783 -NCPB=6 -ICPB=3
-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

N Geneseq 29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	142	100.0	426	2	AA231037 Open read
2	142	100.0	426	2	AA142859 Survivin
3	142	100.0	429	9	AA142859 Survivin
4	142	100.0	1024	7	AA283360 Tox1colog
5	142	100.0	1619	3	AA089303 Human sur
6	142	100.0	1619	5	AA21617 DNA encod
7	142	100.0	1619	7	ABX76199 Lung cand
8	142	100.0	1619	7	AA153734 Survivin

9	142	100.0	1619	7	AA249666 Human sur
10	142	100.0	1619	9	ABE85228 Farnesyl
11	142	100.0	1662	7	ABZ58106 Human Sur
12	142	100.0	2404	7	ACA03988 CDNA down
13	142	100.0	2404	7	AAQ93052 Human EPR
14	142	100.0	2404	7	ACA56320 Human sig
15	142	100.0	2404	7	AAQ93052 Human EPR
16	142	100.0	2404	7	AAQ93052 Human EPR
17	142	100.0	2404	7	AAQ93052 Human EPR
18	142	100.0	2404	7	AAQ93052 Human EPR
19	142	100.0	2404	7	AAQ93052 Human EPR
20	142	100.0	2404	7	AAQ93052 Human EPR
21	142	100.0	2404	7	AAQ93052 Human EPR
22	142	100.0	2404	7	AAQ93052 Human EPR
23	142	100.0	2404	7	AAQ93052 Human EPR
24	142	100.0	2404	7	AAQ93052 Human EPR
25	142	100.0	2404	7	AAQ93052 Human EPR
26	142	100.0	2404	7	AAQ93052 Human EPR
27	142	100.0	2404	7	AAQ93052 Human EPR
28	142	100.0	2404	7	AAQ93052 Human EPR
29	142	100.0	2404	7	AAQ93052 Human EPR
30	142	100.0	2404	7	AAQ93052 Human EPR
31	142	100.0	2404	7	AAQ93052 Human EPR
32	142	100.0	2404	7	AAQ93052 Human EPR
33	142	100.0	2404	7	AAQ93052 Human EPR
34	142	100.0	2404	7	AAQ93052 Human EPR
35	142	100.0	2404	7	AAQ93052 Human EPR
36	142	100.0	2404	7	AAQ93052 Human EPR
37	142	100.0	2404	7	AAQ93052 Human EPR
38	142	100.0	2404	7	AAQ93052 Human EPR
39	142	100.0	2404	7	AAQ93052 Human EPR
40	142	100.0	2404	7	AAQ93052 Human EPR
41	142	100.0	2404	7	AAQ93052 Human EPR
42	142	100.0	2404	7	AAQ93052 Human EPR
43	142	100.0	2404	7	AAQ93052 Human EPR
44	142	100.0	2404	7	AAQ93052 Human EPR
45	142	100.0	2404	7	AAQ93052 Human EPR
46	142	100.0	2404	7	AAQ93052 Human EPR
47	142	100.0	2404	7	AAQ93052 Human EPR
48	142	100.0	2404	7	AAQ93052 Human EPR
49	142	100.0	2404	7	AAQ93052 Human EPR
50	142	100.0	2404	7	AAQ93052 Human EPR
51	142	100.0	2404	7	AAQ93052 Human EPR
52	142	100.0	2404	7	AAQ93052 Human EPR
53	142	100.0	2404	7	AAQ93052 Human EPR
54	142	100.0	2404	7	AAQ93052 Human EPR
55	142	100.0	2404	7	AAQ93052 Human EPR
56	142	100.0	2404	7	AAQ93052 Human EPR
57	142	100.0	2404	7	AAQ93052 Human EPR
58	142	100.0	2404	7	AAQ93052 Human EPR
59	142	100.0	2404	7	AAQ93052 Human EPR
60	142	100.0	2404	7	AAQ93052 Human EPR
61	142	100.0	2404	7	AAQ93052 Human EPR
62	142	100.0	2404	7	AAQ93052 Human EPR
63	142	100.0	2404	7	AAQ93052 Human EPR
64	142	100.0	2404	7	AAQ93052 Human EPR
65	142	100.0	2404	7	AAQ93052 Human EPR
66	142	100.0	2404	7	AAQ93052 Human EPR
67	142	100.0	2404	7	AAQ93052 Human EPR
68	142	100.0	2404	7	AAQ93052 Human EPR
69	142	100.0	2404	7	AAQ93052 Human EPR
70	142	100.0	2404	7	AAQ93052 Human EPR
71	142	100.0	2404	7	AAQ93052 Human EPR
72	142	100.0	2404	7	AAQ93052 Human EPR
73	142	100.0	2404	7	AAQ93052 Human EPR
74	142	100.0	2404	7	AAQ93052 Human EPR
75	142	100.0	2404	7	AAQ93052 Human EPR
76	142	100.0	2404	7	AAQ93052 Human EPR
77	142	100.0	2404	7	AAQ93052 Human EPR
78	142	100.0	2404	7	AAQ93052 Human EPR
79	142	100.0	2404	7	AAQ93052 Human EPR
80	142	100.0	2404	7	AAQ93052 Human EPR
81	142	100.0	2404	7	AAQ93052 Human EPR

```

82 8 5.6 1734 7 ACA60388 ACA60388 Novel hum
83 8 5.6 1734 7 ACA72257 ACA72257 Novel hum
84 8 5.6 1734 7 ACD04781 ACD04781 Novel hum
85 8 5.6 1734 7 ACD18242 ACD18242 Human sec
86 8 5.6 1734 7 ACD08249 ACD08249 Human sec
87 8 5.6 1734 7 ACA88683 ACA88683 Novel hum
88 8 5.6 1734 7 ACA04997 ACA04997 Novel hum
89 8 5.6 1734 7 ACA70125 ACA70125 Novel hum
90 8 5.6 1734 7 ACD12347 ACD12347 Novel hum
91 8 5.6 1734 7 ACD74262 ACD74262 Human sec
92 8 5.6 1734 7 ACD15890 ACD15890 Human sec
93 8 5.6 1734 7 ACD25458 ACD25458 Novel hum
94 8 5.6 1734 7 ACD17935 ACD17935 Human sec
95 8 5.6 1734 7 ACC88222 ACC88222 Human sec
96 8 5.6 1734 7 ACD21576 ACD21576 Human sec
97 8 5.6 1734 7 ACD18643 ACD18643 Human sec
98 8 5.6 1734 7 ACA58835 ACA58835 CDNA enco
99 8 5.6 1734 7 ABX98253 ABX98253 Human CDN
100 8 5.6 1734 7 ACD14004 ACD14004 Human PRO

```

ALIGNMENTS

```

RESULT 1
AAZ31037
ID AAZ31037 standard; DNA; 426 BP.
XX
XX AAZ31037;

```

```

XX 17-JAN-2000 (first entry)
XX
XX Open reading frame of human Survivin gene.
XX
XX Survivin; open reading frame; IAP; apoptosis inhibitor; tumour cell;
XX effector cell protease receptor-1; Bpr-1; embryonic tissue; tubulin;
XX mitotic spindle; abnormal cell growth; tumorigenesis; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..426
XX FT /tag= a
XX FT /product= "Survivin"
XX
XX PN W09950440-A2.
XX
XX PD 07-OCT-1999.
XX
XX PF 01-APR-1999; 99M0-US007205.
XX
XX PR 01-APR-1998; 98US-0080288P.
XX
XX (UYVA ) UNIV YALE.
XX
XX Altieri DC;
XX
XX WPI; 1999-591329/50.
XX P-PSDB; AAY49080.
XX
XX Identifying agents that modulate Survivin interactions.
XX
XX Example; Fig 8B; 56pp; English.
XX
XX
XX This sequence is the open reading frame of the human survivin gene.
XX Survivin is a 142 amino acid protein of approximately 16.5kd. Survivin is
XX a member of the IAP family of apoptosis inhibitors, and the gene is
XX located on chromosome 17q25. The nucleic acid sequence of Survivin is
XX related to the Effector Cell Protease Receptor-1 (BPR-1). Survivin is
XX expressed in tumour cells and embryonic tissue. The sequence is used in
XX the invention which involves identifying an agent that modulates
XX interactions between Survivin and tubulin. Agents that modulate
XX interaction between Survivin and tubulin or mitotic spindles may be
XX administered to a mammal to modulate biological or pathological processes

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```

CC mediated by Survivin, for example Survivin-mediated inhibition of
CC cellular apoptosis. Thus an inhibiting agent may be used to block
CC abnormal cell growth, for example during tumorigenesis. An agent that
CC increases interaction may be used to extend cell growth in culture
XX
SQ Sequence 426 BP; 115 A; 112 C; 113 G; 86 T; 0 U; 0 Other;

```

```

Alignment Scores:
Pred. No.: 1,15e-141 Length: 426
Score: 142.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

```

```

US-09-690-825-34 (1-142) x AAZ31037 (1-426)

```

```

QY 1 MetGlyAlaProThrLeuProProAlaTTPGlnProPheLeuLysAspHisArgIleSer 20
Db 1 ATGGGTGCCCCGACGCTTGCCCCCTGCTGCGACGCCCTTCTCAAGACACCGCATCTCT 60
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
Db 61 ACATTCAAGACTGAGCCCTTTCTTGAGAGGCTGCGCTGCACCCGAGCGATGCGCGAG 120
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
Db 121 GTGGCTTCATCCACGCCCCCACTGAGACGACGACGACCTTGAGCCAGTGTCTTCTTCC 180
QY 61 PheLysGluLeuGluGluGluTrpGluProAspAspAspProIleGluGluHisLysHis 80
Db 181 TTCAAGAGCTGAGAGGCTGGGAGCGACGAGACGACCCCATGAGAGACATTAAGACAT 240
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
Db 241 TCGTCGGGTGGCCCTTCTTCTTCTGTCAGAGACGACTTGAAGATTACCTTGCTGTA 300
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrSerLys 120
Db 301 TTTTGAACATGACGACGAGAGAGCAAGCAAAATTTGCAAGAGAAACCAACATTAAG 360
QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGluLeuAla 140
Db 361 AAGAAAGATTGTAGAGAACTGCGAAGAAAGTGGCGCGTGCATGAGACGCTGGCTCC 420
QY 141 MetAsp 142
Db 421 ATGGAT 426

```

```

RESULT 2
AAL42859
ID AAL42859 standard; DNA; 426 BP.
XX
XX AAL42859;
XX
XX DT 05-AUG-2002 (first entry)
XX
XX Survivin-like protein coding sequence 6.
XX
XX Survivin-like protein; diagnosis; screening; cancer; gene; ds;
XX apoptosis abnormality; gene therapy.
XX
XX Unidentified.
XX
XX
XX Key Location/Qualifiers
XX FT 1..426
XX FT /tag= a
XX FT /partial=
XX FT /product= "Survivin-like protein 6"
XX FT /note= "No stop codon is given"
XX
XX PN W0200233071-A1.
XX

```


BD 25-APR-2002.
 XX 16-OCT-2001; 2001WO-JP009071.
 XX 17-OCT-2000; 2000JP-00316721.
 PR 20-DEC-2000; 2000JP-00386809.
 XX
 XX (TAKE) TAKEDA CHEM IND LTD.
 XX Tanaka H, Kaieda I;
 XX WPI; 2002-435536/46.
 DR P-PSDB; AAO14948.
 XX
 PT Baculovirus IAP repeat domain or RING-finger domain-containing survivin-
 PT like polypeptides and encoded DNAs, applicable in diagnosis and screening
 PT compounds for treating various cancers and apoptosis abnormality.
 XX
 PS Disclosure; Page 123-124; 136pp; Japanese.
 CC The invention comprises the amino acid and coding sequences of survivin-
 CC like proteins. The survivin-like DNA and protein sequences are useful in
 CC diagnostics and screening compounds for treating various cancers and
 CC apoptosis abnormality, including gene therapy. The present DNA sequence
 CC encodes a survivin-like protein of the invention
 XX
 SQ Sequence 426 BP; 115 A; 112 C; 113 G; 86 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1,15e-141 Length: 426
 Score: 142.00 Matches: 142
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: Gaps: 0
 US-09-690-825-34 (1-142) x AAL42859 (1-426)
 QY 1 MetGlyAlaProThrLeuProAlaTrpGlnProPheLeuYsAspHisArgIleSer 20
 DB 1 ATGGGTGCCCCGACGCTTCCCTCCGCGAGCCCTTCTCAAGAACACCGCATCTCT 60
 QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
 DB 61 ACATTCAGAACTGGCCCTCTCTTGGAGGGCTGCGCTGCACACCCGAGCGGATG3CCGAG 120
 QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
 DB 121 GCTGCTTCATCCACTGCCCCCACTAGAACAGCCAGCCTTGCCCGCATGTTCTTCTG 180
 QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGlnHisLysLysHis 80
 DB 181 TTCAAGAGAGCTGAGAGCTGGAGCCAGATGACGACCCCATAGAGAAACATAAAGCAT 240
 QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
 DB 241 TCGTCGGGTGGCTTCTCTTCTCTCAAGAAAGCAGTTTGAAGATTAAACCTTGATGA 300
 QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
 DB 301 TTTTGAAGACTGACAGAGAAAGAGCAAGAAACAAATTTGCAAGAGAAACCAACATVAG 360
 QY 121 LysLysGluPheGluGluThrAlaLysLysValAlaGaaGalaIleGluGlnLeuAlaAla 140
 DB 361 AAGAAAGAAATTTGAGAAACTGCGAAGAAAGTGCAGTGCATCGAGCACTGGCTGCC 420
 QY 141 MetAsp 142
 DB 421 ATGGAT 426
 RESULT 3
 ACF58071
 ID ACF58071 standard; DNA; 429 BP.

XX ACF58071;
 AC 15-JAN-2004 (first entry)
 DT Human survivin protein encoding DNA.
 XX
 DE Human survivin protein encoding DNA.
 XX
 KM RasGAP; Aurora kinase; cytostatic; anti-tumoural; human; survivin; gene;
 XX ds.
 XX Homo sapiens.
 XX OS
 FH Key Location/Qualifiers
 FT CDS 1..429
 FT /tag= a
 FT /product= "survivin"
 XX
 XX WO2003087395-A2.
 XX
 XX 23-OCT-2003.
 XX
 XX 15-APR-2003; 2003WO-IB002972.
 XX
 XX 15-APR-2002; 2002US-0372483P.
 XX
 XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 XX
 XX Garbay C, Gigoux V, Camonis J, L'hoste S, Samson J;
 XX WPI; 2003-845340/78.
 DR P-PSDB; ABR61582.
 XX
 PT Identifying anti-tumoral compounds, comprises determining the capacity of
 PT a compound to inhibit interaction between RasGAP and Drosophila
 PT melanogaster (Dm) aurora kinase, or between RasGAP, Dm aurora kinase and
 PT aurora binding protein.
 XX
 XX
 XX Disclosure; Page 67; 0pp; English.
 XX
 CC The invention relates to identifying a biologically active compound with
 CC anti-tumoural properties, where the compound is studied for its capacity
 CC to inhibit the interaction between: (a) RasGAP and the Drosophila
 CC melanogaster Aurora kinase or an orthologue of the kinase, or its
 CC fragment able to interact with RasGAP; or (b) RasGAP, an Aurora-binding
 CC protein and the D. melanogaster Aurora kinase or an orthologue of the
 CC kinase, or its fragment. The method is useful for identifying anti-
 CC tumoural agents. The present sequence represents a DNA encoding a human
 CC survivin protein, an aurora-binding protein
 XX
 SQ Sequence 429 BP; 116 A; 112 C; 114 G; 87 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1,15e-141 Length: 429
 Score: 142.00 Matches: 142
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: Gaps: 0
 US-09-690-825-34 (1-142) x ACF58071 (1-429)
 QY 1 MetGlyAlaProThrLeuProAlaTrpGlnProPheLeuYsAspHisArgIleSer 20
 DB 1 ATGGGTGCCCCGACGCTTCCCTCCGCGAGCCCTTCTCAAGAACACCGCATCTCT 60
 QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
 DB 61 ACATTCAGAACTGGCCCTCTCTTGGAGGGCTGCGCTGCACACCCGAGCGGATG3CCGAG 120
 QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
 DB 121 GCTGCTTCATCCACTGCCCCCACTAGAACAGCCAGCCTTGCCCGCATGTTCTTCTG 180

XX 23-SEP-1999; 99WO-US022076.
 PF 23-SEP-1999; 99WO-US022076.
 XX 23-SEP-1999; 99WO-US022076.
 PR 29-SEP-1998; 98US-00163162.
 PR 05-APR-1999; 99US-00286407.
 XX (ISIS-) ISIS PHARM INC.
 PA (ISIS-) ISIS PHARM INC.
 XX Bennett CF, Ackermann EJ, Swayze EE, Cowse LM;
 PI Bennett CF, Ackermann EJ, Swayze EE, Cowse LM;
 XX WPI, 2000-293103/25.
 DR WPI, 2000-293103/25.
 XX Antisense molecules targeted to Survivin, useful for inducing apoptosis
 PT in cancer cells.
 XX Example 13; Page 61-62; 73pp; English.
 XX This is the DNA sequence of human survivin (GenBank U75285), a member of
 CC the IAP (inhibitor of apoptosis) caspase inhibitor family. Survivin has
 CC been found to be involved in cell cycle regulation and is expressed in
 CC the G2/M phase of the cell cycle in a cell cycle regulated manner and
 CC associates with microtubules of the mitotic spindle. Disruption of this
 CC interaction results in loss of survivin's anti-apoptotic function and
 CC increased caspase-3 activity during mitosis. Caspase-3 is associated with
 CC apoptotic cell death. It is therefore believed that survivin may
 CC counteract a default induction of apoptosis in the G2/M phase. It is also
 CC believed that the over expression of survivin in cancer may overcome this
 CC apoptotic check point, allowing undesired survival and division of cancer
 CC cells. Antisense oligonucleotides (ASO's) may be used to down regulate
 CC endogenous survivin and to increase caspase-3-dependent apoptosis in
 CC cells in the G2/M phase. ASO's that were analyzed for
 CC effect on survivin mRNA levels by quantitative real-time PCR. The data
 CC obtained were averaged from three experiments. It was found that ISIS
 CC 23667 (A08925) provided 70% inhibition of Survivin and ISIS 23672
 CC (A08930) provided 64% inhibition. The ASO's may be used to inhibit the
 CC expression of human survivin genes for the treatment of diseases
 CC associated with overexpression of survivin. In particular, they may be
 CC used to induce apoptosis in tumor cells
 XX

SO Sequence 1619 BP; 349 A; 392 C; 449 G; 429 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	4,04e-141	Length:	1619
Score:	142.00	Matches:	142
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	3	Gaps:	0

US-09-690-825-34 (1-142) x AAA08903 (1-1619)

QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
 Db 50 ATGGATGACCCGACCTTGCCTCCCTGCGAGCCCTTTCTCAAGAGACACCGCATCTCT 109
 QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysTrpTrpProGluArgMetAlaGlu 40
 Db 110 ACATTCAGAGACTGCGCTTCTTGAGAGGCTGCGCTGCAACCCGAGCGGATGCGCGAG 169
 QY 41 AlaGlyPheIleHisCysProThrGlnAsnGluProAspLeuAlaGlnCysPhePheCys 60
 Db 170 GCTGCTTCATCCATCCACCTGACGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 229
 QY 61 PheLysGluLeuGluGlyTrpGluProAspAspAspProIleGluGluLysLysLysHis 80
 Db 220 TTCAAGAGAGCTGGAGAGCTGGAGAGCATATGACGACCCCATATAGAGAAATATAAGCAT 289
 QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
 Db 290 TCGTCGGGTGGCTTCTCTTCTGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 349
 QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120

Db 350 TTTTGAACTGACAG 409
 QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGluLeuAlaIa 140
 Db 410 AAGAAAGAAATTTGAGAAAGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 469
 QY 141 MetAsp 142
 Db 470 ATGAT 475

RESULT 6
 AAS21617
 ID AAS21617 standard; cDNA, 1619 BP.
 XX AAS21617;
 AC AAS21617;
 XX 21-NOV-2001 (first entry)
 DT 21-NOV-2001 (first entry)
 XX DNA encoding human survivin.
 DE Survivin; human; mouse; cytostatic; antisense oligonucleotide;
 XX hyperproliferative condition; cancer; apoptosis; cytokinesis; ss.
 XX Homo sapiens.
 XX W0200157059-A1.
 PN W0200157059-A1.
 XX 09-AUG-2001.
 PD 09-AUG-2001.
 XX 30-JAN-2001; 2001WO-US002939.
 PF 30-JAN-2001; 2001WO-US002939.
 PR 02-FEB-2000; 2000US-00496694.
 XX (ISIS-) ISIS PHARM INC.
 PA Bennett CF, Ackermann EJ, Swayze EE, Cowse LM;
 PI Bennett CF, Ackermann EJ, Swayze EE, Cowse LM;
 XX WPI, 2001-48863/53.
 DR WPI, 2001-48863/53.
 XX Novel antisense compounds for modulating the expression of Survivin and
 PT treatment of cancer.
 PT Example 17; Page 56; 120pp; English.

The invention relates to antisense oligonucleotides targeted to a nucleic
 CC acid molecule encoding human Survivin, where the antisense
 CC oligonucleotide inhibits the expression of human Survivin. These
 CC antisense oligonucleotides are used in the treatment of an animal
 CC suffering from a disease or condition associated with Survivin, e.g. a
 CC hyperproliferative condition such as cancer, and comprises administering
 CC a therapeutically or prophylactically effective amount of the antisense
 CC oligonucleotide so that expression of Survivin is inhibited. The
 CC oligonucleotide can also be used to treat a human suffering from a
 CC disease or condition characterized by a reduction in apoptosis comprising
 CC administering the antisense oligonucleotide to a human. In addition, the
 CC antisense oligonucleotide and a cytotoxic chemotherapeutic agent e.g.
 CC taxol or cisplatin, can be used to modulate apoptosis, cytokinesis or the
 CC cell cycle, or inhibit the proliferation in a cancer cell by contacting
 CC the cell with the antisense oligonucleotide. AAS21521-AAS21768 represent
 CC Survivin nucleic acids, and antisense oligonucleotides targeted to
 CC Survivin, used in the method of the invention
 CC

SO Sequence 1619 BP; 349 A; 392 C; 449 G; 429 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	4,04e-141	Length:	1619
Score:	142.00	Matches:	142
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	5	Gaps:	0

US-09-690-825-34 (1-142) x AAS21617 (1-1619)

QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
DB 50 ATGGGGCCCCCAGCCCTGGCCCTGGCAGCCCTTTCTCAAGACACCGCATCTCT 109
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 110 ACATTCAAGAACTGGCCCTCTTCTGAGGGCTCCGCTCCACCCCGAGACGCGATGGCCGAG 169
QY 41 AlaGlyPheIleHisCysProThrGluLeuGluProAspLeuAlaGlnCysPhePheCys 60
DB 170 GGTGGTTTATCACCCTGCCCCCAGCAAGACGAGCAGCTGGCCAGTGTCTTCTGCG 229
QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHisLysLysHis 80
DB 230 TTCAAGAGACTGGAAAGCTGGGAGCCAGATGCGACCCCATAGAGAACATTAAGCAT 289
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
DB 290 TCGTCGGGTTCGCTTCTTCTGTCGCAAGACGATTGGAAGATTAACTTGTGTA 349
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAspAsnLys 120
DB 350 TTTTGAACCTGGACAGAGAAAGAGCCAGAACAAATTGCAAGAGAACCAACATTAAG 409
QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGluLeuAlaAla 140
DB 410 AAGAAAGATTGAGAGAACTGCAAGAAAGTGCCTGCGCATGACACAGCTGCTGCC 469
QY 141 MetAsp 142
DB 470 ATGGAT 475
RESULT 7
ABX76199
ID ABX76199 standard; DNA; 1619 BP.
AC ABX76199;
XX
DT 02-APR-2003 (first entry)
XX
DE Lung cancer-associated polynucleotide #70.
XX
KW Lung cancer-associated polynucleotide; gene: ds; cytostatic; emphysema;
anti-inflammation; antiasthmatic; non-small cell lung cancer; atelectasis;
small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
XX
OS Unidentified.
XX
PN WO200286443-A2.
XX
PD 31-OCT-2002.
XX
PF 18-APR-2002; 2002WO-US012476.
XX
PR 18-APR-2001; 2001US-0284770P.
PR 10-MAY-2001; 2001US-0290492P.
PR 09-NOV-2001; 2001US-0339245P.
PR 13-NOV-2001; 2001US-0350666P.
PR 29-NOV-2001; 2001US-0334370P.
PR 12-APR-2002; 2002US-0372246P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Aziz N, Murray R;
XX
XX
DR WPI; 2003-093161/08.
DR P-PDB; ABUS6477.
XX
PT Detecting a lung cancer-associated transcript in a cell from a patient
for treating lung cancer, by contacting a biological sample from the

PT patient with a polynucleotide that exhibits increased or decreased
XX expression in lung cancer.
XX
PS Claim 22, Page 242; 453bp; English.
XX
CC The invention relates to a method for detecting a lung cancer-associated
transcript in a cell from a patient, comprising contacting a biological
sample from the patient with a polynucleotide that selectively hybridizes
to a sequence that is at least 80 % identical to a gene that exhibits
increased or decreased expression in lung cancer samples. Lung cancer-
associated polynucleotides and polypeptides are used for identifying a
compound that modulates a lung cancer-associated polypeptide, for
inhibiting proliferation of a lung cancer-associated cell to treat lung
cancer in a patient and for treating a mammal having lung cancer by
administering a modulatory compound identified. The methods are useful
for treating lung cancer, such as small cell lung cancer, non-small cell
lung cancer or other benign or precancerous lesions, e.g. atelectasis,
emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
bronchiectasis. The genes, polynucleotides and polypeptides are useful
for diagnostic purposes and as targets for screening for therapeutic
compounds that modulate lung cancer, such as antibodies. Sequences
CC ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the
invention
XX
SQ Sequence 1619 BP; 349 A; 392 C; 449 G; 429 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 4,04e-141 Length: 1619
Score: 142.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
US-09-690-825-34 (1-142) x ABX76199 (1-1619)
QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
DB 50 ATGGGGCCCCCAGCCCTGGCCCTGGCAGCCCTTTCTCAAGACACCGCATCTCT 109
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 110 ACATTCAAGAACTGGCCCTCTTCTGAGGGCTCCGCTCCACCCCGAGACGCGATGGCCGAG 169
QY 41 AlaGlyPheIleHisCysProThrGluLeuGluProAspLeuAlaGlnCysPhePheCys 60
DB 170 GGTGGTTTATCACCCTGCCCCCAGCAAGACGAGCAGCTGGCCAGTGTCTTCTGCG 229
QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHisLysLysHis 80
DB 230 TTCAAGAGACTGGAAAGCTGGGAGCCAGATGCGACCCCATAGAGAACATTAAGCAT 289
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
DB 290 TCGTCGGGTTCGCTTCTTCTGTCGCAAGACGATTGGAAGATTAACTTGTGTA 349
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAspAsnLys 120
DB 350 TTTTGAACCTGGACAGAGAAAGAGCCAGAACAAATTGCAAGAGAACCAACATTAAG 409
QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGluLeuAlaAla 140
DB 410 AAGAAAGATTGAGAGAACTGCAAGAAAGTGCCTGCGCATGACACAGCTGCTGCC 469
QY 141 MetAsp 142
DB 470 ATGGAT 475
RESULT 8
AAL53734
ID AAL53734 standard; RNA; 1619 BP.
XX

AC AAL53734;
 XX 07-FEB-2003 (first entry)
 XX Survivin DNA sequence SEQ ID NO 28.
 DE
 XX Target RNA: target RNA:support-attached test compound; flow cytometry;
 KW mass spectrometry; high-throughput screening; ds.
 XX
 OS Homo sapiens.
 PN MO20283837-A1.
 PD 24-OCT-2002.
 XX 11-APR-2002; 2002WO-US011758.
 PF 11-APR-2001; 2001US-0282966P.
 PR (PTCT-) PTC THERAPEUTICS INC.
 PA
 PI Alimstead NG;
 PI WPI; 2003-075534/07.
 DR
 XX Identifying a test compound that binds to a target RNA molecule by
 PT separating the detectably labeled target RNA:support-attached test
 PT compound complex from uncomplexed target RNA molecules and test compounds
 PT by flow cytometry.
 PS Example; Page 81; 131pp; English.
 XX
 XX The invention relates to a novel method for identifying a test compound
 CC that binds to a target RNA molecule comprising separating the detectably
 CC labeled target RNA:support-attached test compound complex from
 CC uncomplexed target RNA molecules and test compounds. The separating
 CC process is carried out by flow cytometry and determining a structure of
 CC the type of test compound of the RNA:support-attached test compound
 CC complex by mass spectrometry. The method is useful for high-throughput
 CC screening of libraries of compounds to identify pharmaceutical leads.
 CC This polynucleotide sequence represents a DNA sequence related to the
 CC detecting method of the invention
 XX
 SQ Sequence 1619 BP; 349 A; 392 C; 449 G; 429 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 4,04e-141 Length: 1619
 Score: 142.00 Matches: 142
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 7 Gaps: 0
 US-09-690-825-34 (1-142) x AAL53734 (1-1619)

DB 290 TCGTCGGGTGGCTTTCCTTCTGTCAAGAACAGTGTGAAGATTAACCTTGATGA 349
 XX
 QY 101 PheLeuLyLeuAspArgGluArgAlaIysAsnLysIleAlaIysGluThrAspAsnLys 120
 DB 350 TTTTGAACCTGGACAGAGAAAGCCCAAGAACAAATTGCAGAGAAACCAACATAG 409
 QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluIleuAlaIa 140
 DB 410 AAGAAAGATTTTGAGGAAACTCCGAAGAAAGTCCCGCTGCATGAGAGAGCTGCTGCC 469
 QY 141 MetAsp 142
 DB 470 ATGAT 475
 RESULT 9
 AAD49666
 ID AAD49666 standard; DNA; 1619 BP.
 XX
 AC AAD49666;
 XX
 DT 24-MAR-2003 (first entry)
 XX
 DE Human survivin DNA.
 XX
 XX Amyloidosis; haemophilia; Alzheimer's disease; atherosclerosis; cancer;
 KW gigantism; dwarfism; hypothyroidism; hyperthyroidism; cystic fibrosis;
 KW autoimmune disorder; aging; inflammation; diabetes; obesity; anorectic;
 KW neurodegenerative disorder; Parkinson's disease; gene therapy; virucide;
 KW haemostatic; antibacterial; nootropic; neuroprotective; cytostatic; XIAP;
 KW fungicide; human; survivin; gene; ds.
 XX
 OS Homo sapiens.
 XX
 PN MO200283953-A1.
 PD 24-OCT-2002.
 XX
 XX 11-APR-2002; 2002WO-US011757.
 PF 11-APR-2001; 2001US-0282965P.
 PR (PTCT-) PTC THERAPEUTICS INC.
 PA
 PI Rando R, Welch E;
 PI WPI; 2003-075561/07.
 DR
 XX Identifying a test compound that binds to a target RNA molecule for
 PT treating or preventing amyloidosis, hemophilia, cancer, gigantism,
 PT diabetes, by contacting a detectably labeled target RNA molecule with a
 PT library of test compounds.
 XX
 XX Example; Page 89-90; 152pp; English.
 PS
 XX The invention relates to a method for identifying a test compound that
 CC binds to a target RNA molecule, which comprises contacting a detectably
 CC labelled target RNA molecule with a library of test compounds under
 CC conditions that permit direct binding of the labelled target RNA to a
 CC member of the library of test compounds so that a detectably labeled
 CC target RNA:test compound complex is formed. The method is useful for
 CC screening libraries of compounds for those that are selectively bind to a
 CC pre-selected target RNA. The compounds are useful for inhibiting the
 CC formation of a specific bound RNA: host cell factor complexes in vivo.
 CC They are also useful for treating or preventing diseases associated with
 CC overproduction or decreased protein function, such as amyloidosis,
 CC hemophilia, Alzheimer's disease, atherosclerosis, cancer, gigantism,
 CC dwarfism, hypothyroidism, hyperthyroidism, autoimmune disorders, aging,
 CC inflammation, cystic fibrosis, diabetes, obesity, neurodegenerative
 CC disorders, Parkinson's disease or infections (bacterial, viral, fungal).
 CC The invention is also used in gene therapy. The present sequence is human
 CC survivin DNA. This sequence is used to illustrate the method of the
 CC invention
 XX

XX Human; Survivin; inhibitor of apoptosis; cell death; apoptosis; cancer;
 KM cytostatic; cardiast; neuroprotective; gene therapy; gene; ss.
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT CDS 43..471
 FT /tag= a
 FT /product= "Survivin"
 XX WO2003004606-A2.
 PN 16-JAN-2003.
 XX
 XX 03-JUL-2002; 2002NC-US021002.
 XX
 XX 03-JUL-2001; 2001US-00898158.
 XX
 XX (UYCO) UNIV COLUMBIA NEW YORK.
 XX
 XX Troy CM, Shelanski ML;
 PI WPI; 2003-210351/20.
 XX P-PSDB; ABP72162.
 DR
 XX
 XX New nucleic acid encoding an inhibitor-of-apoptosis protein, useful for
 PT treating cancer, neurodegenerative disorder or cardiomyopathy.
 PT
 XX
 XX Disclosure; Fig 20B; 124bp; English.
 PS
 XX
 XX The present sequence is that of cDNA encoding human Survivin protein. The
 CC invention provides a nucleic acid, such as an antisense oligonucleotide,
 CC which specifically hybridizes to a nucleic acid encoding an inhibitor of
 CC apoptosis protein. Survivin is an example of an inhibitor of apoptosis or
 CC inducer of cell death protein of the invention. A claimed method for
 CC inducing a cell's death comprises contacting the cell with the nucleic
 CC acid under conditions permitting the nucleic acid to enter the cell;
 CC especially the use of a vector, liposome, or a mechanical or electrical
 CC means. The method is used to treat acute lymphocytic leukaemia, acute
 CC myelogenous leukaemia, lung cancer, breast cancer, ovarian cancer,
 CC prostate cancer, lymphoma, Hodgkin's disease, malignant melanoma,
 CC neuroblastoma, renal cell carcinoma and squamous cell carcinoma (all
 CC claimed). The invention also provides a second nucleic acid, which
 CC specifically hybridizes to a nucleic acid encoding a protein, other than
 CC caspase-2, that induces cell death. A claimed method for inhibiting a
 CC cell's death comprises contacting the cell with the nucleic acid under
 CC conditions permitting the nucleic acid to enter the cell. The method is
 CC used to treat a neurodegenerative disorder (especially a brain disorder
 CC or central nervous system disorder), or a heart disorder (especially
 CC cardiomyopathy) in a human (all claimed)
 CC
 XX
 XX Sequence 1662 BP; 396 A; 369 C; 451 G; 426 T; 0 U; 0 Other;
 SO
 Alignment Scores:
 Pred. No.: 4,14e-141 Length: 1662
 Score: 142.00 Matches: 142
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 7 Gaps: 0
 US-09-690-825-34 (1-142) X ABZ58106 (1-1662)

DB 163 GCTGCTTCATCCACTGCCACCTGAGAACGAGCAGACTTGCCGACGTGTTCTTCTGC 222
 QY PheLysGluLeuGluGlyTTPGluProAspAspProIleGluGluHisLysHis 80
 DB 223 TTCAGAGAGCTGGAAGGCTGGAGCCAGATGACACCCCATAGAGGAACATTAAGAGAT 282
 QY SerSerGlyCysAlaPheLeuSerValIleLysGlnPheGluGluLeuThrLeuGlyGlu 100
 DB 283 TCGTCGGGTGGCTTCTTCCTTCCTGTCAGAGAGAGATTGAAGATTAAACCTTGGA 342
 QY PheLeuLysLeuAspArgGluAlaAlaLysAsnLysIleAlaLysGluThrAsnLys 120
 DB 343 TTTTGAAGACTGAGACAGAGAAAGCCAGAACCAATTGCAAGAAAGCAACATTAAG 402
 QY 121 LysLysGluPheGluGluGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAla 140
 DB 403 AAGAAAGAAATTTGAGGAAGAACTGCCAGAAAGTGGCGGTCATCGACACTGGCTGCC 462
 QY 141 MetAsp 142
 DB 463 ATGGAT 468
 RESULT 12
 ID ACA03988 standard; cDNA; 2404 BP.
 AC ACA03988;
 XX
 XX 27-MAY-2003 (first entry)
 DT
 XX
 XX CDNA downregulated in senescent cells Inocyte ID NO: 251651.4.
 DE
 XX Human; senescence; ss; gene; cancer; proliferative disorder; leukaemia;
 XX adenocarcinoma; lymphoma; melanoma; myeloma; sarcoma; teratocarcinoma;
 XX adrenal gland cancer; bladder cancer; bone cancer; bone marrow cancer;
 XX brain cancer; breast cancer; cervical cancer; colon cancer; heart cancer;
 XX oesophageal cancer; gall bladder cancer; ganglial cancer; kidney cancer;
 XX liver cancer; lung cancer; muscle cancer; ovarian cancer; penile cancer;
 XX pancreatic cancer; parathyroid gland cancer; prostate cancer;
 XX salivary gland cancer; skin cancer; small intestine cancer;
 XX spleen cancer; stomach cancer; testicular cancer; thymic cancer;
 XX thyroid cancer; uterine cancer.
 KM
 XX
 XX Homo sapiens.
 OS
 XX US2002192678-A1.
 EN
 XX 19-DEC-2002.
 PD
 XX 07-FEB-2002; 2002US-00071766.
 PF
 XX
 XX 09-FEB-2001; 2001US-0268380P.
 PR
 XX
 XX (CHEN/) CHEN H.
 PA
 XX
 XX Chen H;
 PI
 XX WPI; 2003-328858/21.
 XX
 XX New combination comprising cDNAs or their complements, useful for
 PT detecting changes in expression of genes encoding proteins associated
 PT with senescence, and in diagnosing, staging or treating proliferative
 PT diseases, e.g. cancer.
 PT
 XX
 XX Example 13; Page 135-136; 155bp; English.
 PS
 XX The invention relates to a combination comprising a plurality of cDNAs,
 CC or their complements that are differentially expressed in cancer and
 CC other proliferative disorders. The combination is useful in detecting
 CC changes in expression of genes encoding proteins that are associated with
 CC senescence and in diagnosing, staging, treating, or monitoring the
 CC progression or treatment of subjects with proliferative diseases such as

CC cancer e.g. adenocarcinoma, leukaemia, lymphoma, melanoma, myeloma,
 CC sarcoma, teratocarcinoma, cancer of the adrenal gland, bladder, bone,
 CC bone marrow, brain, breast, cervix, colon, oesophagus, gall bladder,
 CC ganglia, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid
 CC glands, penis, prostate, salivary glands, skin, small intestine, spleen,
 CC stomach, testis, thymus, thyroid and uterus. The present sequence
 CC represents cDNA of genes that are downregulated in senescent cells
 XX

SQ Sequence 2404 BP; 525 A; 588 C; 634 G; 628 T; 0 U; 29 Other;

Alignment Scores:

Pred. No.:	5,86e-141	Length:	2404
Score:	142.00	Matches:	142
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	7	Gaps:	0

US-09-690-825-34 (1-142) x ACA03988 (1-2404)

QY 1 MetGlyAlaProThrLeuProBProAlaTrpGlnProPheLeuYsAspHisArgIleSer 20
 DB 56 ATGGGGTCCCGACGTCGTCCTGCGCAGCCCTTTCAGAGACCGCATCTCT 115
 QY 21 ThrPheYsAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
 DB 116 ACATTCAAGAACTGGCCCTCTTGGAGGGCTGGCTCCACCCCGAGCGATGGCCGAG 175
 QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
 DB 176 GCTGGCTTATCCACATGCGCCCACTGAGAAGCAGACGATGGCCCAATGTTCTTCTGC 235
 QY 61 PheLeuYsLeuAspArgGluArgAlaYsAsnYsIleAlaYsGluThrAsnAsnYs 80
 DB 236 TTCAAGAGAGCTGGAAGCTGGAGCGCAGATGACGACCCCAAGAGAAACATMAAAGCAT 295
 QY 81 SerSerGlyCysAlaPheLeuSerValYsYsGlnPheGluGluLeuThrLeuGlyGlu 100
 DB 296 TCGTCGGTGGCTGCTTCTTCTCTCAAGAAAGCATTTGAAGATTAACTTGTGTA 355
 QY 101 PheLeuYsLeuAspArgGluArgAlaYsAsnYsIleAlaYsGluThrAsnAsnYs 120
 DB 356 TTTTGGAAACTGGACAGAAAGACCAAGCAAAATTGCAAGGAAACCAACAAATTAAG 415
 QY 121 LysLysGluPheGluGluThrAlaYsYsValArgArgAlaIleGluGlnLeuAla 140
 DB 416 AAGAAAGAAATTGAGGAAATCTCGAAGAAAGTGGCCCTGCAATCGAGCACTGGCTGCC 475
 QY 141 MetAsp 142
 DB 476 ATGGAT 481

RESULT 13

AAQ93052/C
 ID AAQ93052 standard; cDNA, 1165 BP.

XX AAQ93052;
 AC 25-MAR-2003 (revised)
 DT 07-DEC-1995 (first entry)
 XX
 DE Human EPR-1 cDNA.
 XX
 KW Effector cell protease receptor-1; EPR-1; lymphocyte;
 KW lymphoproliferative disorder; ss.
 XX
 OS Homo sapiens.

XX Key Location/Qualifiers
 FT 37..1050
 FT CDS /*tag=a
 XX
 PN W09520655-A1.

XX
 PD 03-AUG-1995.
 XX
 PF 18-JAN-1995; 95WC-US000666.
 XX
 PR 28-JAN-1994; 94US-00189309.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Altieri DC;
 XX
 DR WPI, 1995-275440/36.
 DR P-PSDB; AAR6744.
 XX
 PT New effector cell protease receptor-1 protein - used to develop prods.
 PT for inducing lymphocyte proliferation or diagnosis and treatment of
 PT lymphoproliferative disorders.
 XX
 PS Claim 10; Page 154-155; 181pp; English.
 XX

CC Immunoscreening of a human lymphocyte expression library in lambda. Still
 CC using a Mab raised against human EPR-1 yielded clone lambda-104. This was
 CC used as a probe in further screening of human cDNA libraries, and a
 CC consensus EPR-1 cDNA sequence was deduced from 28 isolated clones. The
 CC cDNA can be used for prodn. of recombinant EPR-1. (Updated on 25-MAR-2003
 CC to correct PN field.)
 XX

SQ Sequence 1165 BP; 293 A; 331 C; 300 G; 241 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	5.01e-104	Length:	1165
Score:	107.00	Matches:	138
Percent Similarity:	99.28%	Conservative:	0
Best Local Similarity:	99.28%	Mismatches:	1
Query Match:	75.35%	Indels:	1
DB:	2	Gaps:	0

US-09-690-825-34 (1-142) x AAQ93052 (1-1165)

QY 1 MetGlyAlaProThrLeuProBProAlaTrpGlnProPheLeuYsAspHisArgIleSer 20
 DB 1114 ATGGGGTCCCGACGTCGTCCTGCGCAGCCCTTTCAGAGACCGCATCTCT 1055
 QY 21 ThrPheYsAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
 DB 1054 ACATTCAAGAACTGGCCCTCTTGGAGGGCTGGCTCCACCCCGAGCGATGGCCGAG 996
 QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
 DB 995 GCTGGCTTATCCACATGCGCCCACTGAGAAGCAGACGATGGCCCAATGTTCTTCTGC 936
 QY 61 PheLeuYsLeuAspArgGluArgAlaYsAsnYsIleAlaYsGluThrAsnAsnYs 80
 DB 935 TTCAAGAGAGCTGGAAGCTGGAGCGCAGATGACGACCCCAAGAGAAACATMAAAGCAT 876
 QY 81 SerSerGlyCysAlaPheLeuSerValYsYsGlnPheGluGluLeuThrLeuGlyGlu 100
 DB 875 TCGTCGGTGGCTGCTTCTTCTCTCAAGAAAGCATTTGAAGATTAACTTGTGTA 816
 QY 101 PheLeuYsLeuAspArgGluArgAlaYsAsnYsIleAlaYsGluThrAsnAsnYs 120
 DB 815 TTTTGGAAACTGGACAGAAAGACCAAGCAAAATTGCAAGGAAACCAACAAATTAAG 756
 QY 121 LysLysGluPheGluGluThrAlaYsYsValArgArgAlaIleGluGlnLeuAla 139
 DB 755 AAGAAAGAAATTGAGGAAATCTCGAAGAAAGTGGCCCTGCAATCGAGCACTGGCTGCC 699

RESULT 14

ACA56320
 ID ACA56320 standard; cDNA, 740 BP.

XX ACA56320;
 AC

Alignment Scores:

Pred. No.: 1,72e-71 Length: 399
 Score: 76.00 Matches: 115
 Percent Similarity: 98.29% Conservative: 0
 Best Local Similarity: 98.29% Mismatches: 1
 Query Match: 53.52% Indels: 2
 DB: 3 Gaps: 0

US-09-690-825-34 (1-142) x AAC02317 (1-399)

QY 1 MetGlyAlaProThreLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
 DB 52 ATGGGGCCCCCGACGCTGGCCCCCTGGCGAGCCCTTCTCAAGACACCGCTCTCT 111
 QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysTrpProGluArgMetAlaGlu 40
 DB 112 AATTTCAGACACTGGCCCTTCTTGAAGGCTCCGCTGACCCCGGACCGGATGGCCGAG 171
 QY 41 AlaGlyPheIleHisCysProThrGluLysGlnProAspLeuAlaGlnCysPhePheCys 60
 DB 172 GCTGGCTTCATCCACTGCGCCCACTGAGAACGACGAGACTTGGCCGAGTCTTCTGCG 231
 QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHis-LysLysHis 80
 DB 232 TTCAGAGAGCTGAGAGGCTGGAGCCAGATGACGACCCCATGAGAGASA-TAAAGAGCA 290
 QY 80 sSerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGly 100
 DB 291 TTCGTCGGCTGCGCTTCTCTCTGTSAGAGAGAGTTTGAAGAAATTAAAGCTTGGCGA 350
 QY 100 uPheLeuLysLeuAspArgGluLysArgAlaLysAsnLysIleAlaLysGlu 116
 DB 351 ATTTTGAACCTGACAGAGAAAGCCAGAAACAAATTCGACAAAGAA 399

RESULT 16
 ADD33414
 ID ADD33414 standard; DNA; 300 BP.
 XX
 AC ADD33414;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Mouse mitochondrial DNA sequence SEQ ID NO:1186.
 XX
 KW ds; mouse; array; mitochondrial; hybridisation; energy-metabolism;
 KW mitochondrial disease; oxidative phosphorylation dysfunction;
 KW oxidative stress; apoptosis; aging.
 XX
 OS Mus musculus.
 XX
 PN MO2003020220-A2.
 XX
 PD 13-MAR-2003.
 XX
 PF 30-AUG-2002; 2002WO-US027886.
 XX
 PR 30-AUG-2001; 2001US-0316323P.
 PR 31-AUG-2001; 2001CA-02356540.
 XX
 PA (UYEM-) UNITV EMORY.
 XX
 PI Wallace DC, Levy S, Kerstann K, Procaccio V;
 DR WPI; 2003-300821/29.
 XX
 PT Array containing probes for genes involved in mitochondrial biology,
 PT useful for determining mitochondrial biology gene expression profiles for
 PT use in diagnosing pathologies and identifying biochemical pathways.
 XX
 PS Claim 2; SEQ ID NO 1186; 201pp; English.
 XX
 CC The invention relates to a novel array comprising at least two isolated
 CC nucleotide molecules, each molecule having a sequence capable of uniquely

CC hybridising to a nucleic acid molecule which is an expression product of
 CC a gene involved in mitochondrial biology. The array comprises two or more
 CC isolated nucleic acid molecules or spots, each molecule having a sequence
 CC chosen from sequence of 994 human probes and 2046 mouse probes. An array
 CC of the invention is useful for determining an expression profile of a
 CC mouse or human sample containing nucleic acid, by contacting the array
 CC with the sample under conditions allowing selective hybridisation, and
 CC measuring hybridisation of nucleic acid in the sample to the array to
 CC produce an expression profile. The array is also useful for determining
 CC an expression profile of a first labelled sample containing nucleic acid
 CC relative to a second, differently labelled sample containing nucleic
 CC acid. The second sample is a reference or a standard. An array is useful
 CC for determining an expression profile diagnostic of an energy-metabolism-
 CC related physiological condition. An array of the invention is useful for
 CC determining mitochondrial biology gene expression profiles of organisms,
 CC such as human, mice and closely related species, tissue and organs of
 CC such organisms, which are useful for determining expression profiles
 CC diagnostic of energy metabolism-related physiological conditions,
 CC diagnosing such physiological conditions, identifying biochemical
 CC pathways, genes, and mutations involved in such physiological conditions,
 CC identifying therapeutic agents useful for preventing and/or treating such
 CC physiological conditions, evaluating and/or monitoring the efficacy of
 CC such therapies, and creating and identifying animal models of human
 CC energy metabolism-related physiological conditions. An array is also
 CC useful for defining expression signatures or profiles for mitochondrial
 CC diseases, as well as distinguishing clinical disorders that result from
 CC oxidative phosphorylation (OXPHOS) dysfunction, oxidative stress,
 CC apoptosis and aging. An array of the invention contains probes of genes
 CC not previously recognised to participate in mitochondrial biology. The
 CC sequences shown in ADD33324-ADD33260 represent murine mitochondrial DNA
 CC clones used to make the probes of the invention. Some sequences are not
 CC present, these are SEQ ID NO's 295, 1174, 1213, 1700, 1728, 1730, 1905,
 CC 1906, 2408 and 2643.
 XX

SQ Sequence 300 BP; 66 A; 91 C; 84 G; 59 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2.22e-34 Length: 300
 Score: 41.00 Matches: 41
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 28.87% Indels: 0
 DB: 9 Gaps: 0

US-09-690-825-34 (1-142) x ADD33414 (1-300)

QY 31 CysAlaCysThrProGluArgMetAlaGluAlaGlyPheIleHisCysProThrGluLys 50
 DB 114 TGGGCTTGACCCCAAGCGGAATGGGGAGGCTGCTTCATGACCTGCCCTCCAGAAC 173
 QY 51 GluProAspLeuAlaGlnCysPhePheCysPheLysGluLeuGluGlyTrpGluProAsp 70
 DB 174 GAGCCTGATTGGCCCGAGTGTCTTCTTAAAGAAATGGAGGCTGGGAACCCGAT 233
 QY 71 Asp 71
 DB 234 GAC 236

RESULT 17
 AAT72714
 ID AAT72714 standard; DNA; 500 BP.
 XX
 AC AAT72714;
 XX
 DT 16-SEP-1997 (first entry)
 XX
 DE Mouse inhibitor of apoptosis protein homologue M1HD DNA.
 DE Inhibitor of apoptosis protein; IAP; mammalian IAP homologue; M1HD;
 KW degenerative disease; infectious disease; autoimmune disease; cancer;
 KW gene therapy; diagnosis; ss.
 XX
 OS Mus musculus.

XX Key Location/Qualifiers
FH CDS 48..470
FT /**tag= a
XX
XX MO9723501-A1.
XX
XX 03-JUL-1997.
XX
XX 20-DEC-1996; 96MO-AU000827.
XX
XX 22-DEC-1995; 95AU-00007275.
XX
XX (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
XX Vaux DL;
XX
XX WPI: 1997-350966/32.
XX P-PSDB; AAM19749.
XX
XX Isolated protein homologues of viral inhibitors of apoptosis - used to
XX PT modulate apoptosis for treatment of degenerative, infectious or
XX PT auto-immune diseases and cancer.
XX
XX Claim 28; Page 71-72; 136pp; English.
XX
XX An isolated nucleic acid molecule (AAT72714) codes for mammalian IAP
XX CC homologue D (MIHD) (AAM19749), a murine homologue of baculovirus
XX CC inhibitor of apoptosis protein (IAP). It was isolated following a
XX CC database search for sequences showing homology to a consensus sequence
XX CC (see also AAM19744) for IAP homologues. Animal IAP homologue nucleic
XX CC acids (see also AAT72710-13 and AAT72715-17) can be used to produce
XX CC polypeptides useful in methods for modulating apoptosis in animal cells,
XX CC specifically for treatment, by inhibition, of degenerative and infectious
XX CC disease or, by promotion, of cancer and autoimmune disease, and can be
XX CC used for gene therapy of these diseases
SQ Sequence 500 BP; 134 A; 131 C; 135 G; 100 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 3.6e-34 Length: 500
Score: 41.00 Matches: 41
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 28.87% Indels: 0
DB: 2 Gaps: 0
US-09-690-825-34 (1-142) x AAT72714 (1-500)
QY 31 CysAlaCysThrProGluArgMetAlaGluAlaGlyPheIleHisCysProThrGluAsn 50
Db 138 TGGCGCTGCACCCCGAGGAAATGGCGAGCTGCTTCATCCACTGCCCTACCGAGAAC 197
QY 51 GluProAspLeuAlaGlnCysPhePheCysPheIysGluLeuGluGlyTyrGluProAsp 70
Db 138 GAGCCTGATTGGCCAGAGTGTTCCTTGAAGAAATGGAGAGCTGGGAACCCGAT 257
QY 71 Asp 71
Db 258 GAC 260
RESULT 18
AAS21530
ID AAS21530 standard; cDNA; 955 BP.
XX
XX AAS21530;
XX
XX 21-NOV-2001 (first entry)
XX
XX DNA encoding mouse survivin.
XX
XX Survivin; human; mouse; cytosolic; antisense oligonucleotide;
XX hyperproliferative condition; cancer; apoptosis; cytokinesis; ss.
XX

XX Mus musculus.
OS
XX
XX WO200157059-A1.
XX
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US002939.
XX
XX 02-FEB-2000; 2000US-00436694.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Bennett CF, Ackermann EJ, Swayze EE, Cowseert LM;
XX WPI: 2001-48863/53.
XX
XX Novel antisense compounds for modulating the expression of Survivin and
XX PT treatment of cancer.
XX
XX Example 13; Page 80-81; 120pp; English.
XX
XX The invention relates to antisense oligonucleotides targeted to a nucleic
XX CC acid molecule encoding human Survivin, where the antisense
XX CC oligonucleotide inhibits the expression of human Survivin. These
XX CC antisense oligonucleotides are used in the treatment of an animal
XX CC suffering from a disease or condition associated with Survivin, e.g. a
XX CC hyperproliferative condition such as cancer, and comprises administering
XX CC a therapeutically or prophylactically effective amount of the antisense
XX CC oligonucleotide so that expression of Survivin is inhibited. The
XX CC oligonucleotides can also be used to treat a human suffering from a
XX CC disease or condition characterised by a reduction in apoptosis comprising
XX CC administering the antisense oligonucleotide to a human. In addition, the
XX CC antisense oligonucleotide and a cytotoxic chemotherapeutic agent e.g.
XX CC taxol or cisplatin, can be used to modulate apoptosis, cytokinesis or the
XX CC cell cycle, or inhibit the proliferation in a cancer cell by contacting
XX CC the cell with the antisense oligonucleotide. AAS21521-AAS21768 represent
XX CC Survivin nucleic acids, and antisense oligonucleotides targeted to
XX CC Survivin, used in the method of the invention
SQ Sequence 955 BP; 230 A; 227 C; 265 G; 233 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 6.63e-34 Length: 955
Score: 41.00 Matches: 41
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 28.87% Indels: 0
DB: 5 Gaps: 0
US-09-690-825-34 (1-142) x AAS21530 (1-955)
QY 31 CysAlaCysThrProGluArgMetAlaGluAlaGlyPheIleHisCysProThrGluAsn 50
Db 199 TGGCGCTGCACCCCGAGGAAATGGCGAGCTGCTTCATCCACTGCCCTACCGAGAAC 258
QY 51 GluProAspLeuAlaGlnCysPhePheCysPheIysGluLeuGluGlyTyrGluProAsp 70
Db 259 GAGCCTGATTGGCCAGAGTGTTCCTTGAAGAAATGGAGAGCTGGGAACCCGAT 318
QY 71 Asp 71
Db 319 GAC 321
RESULT 19
ABZ68313
ID ABZ68313 standard; DNA; 121 BP.
XX
XX ABZ68313;
XX
XX 22-APR-2003 (first entry)
XX
XX Nucleotide sequence of a target sequence from human survivin cDNA.
XX
XX

XX Stem-loop; resonance energy transfer; cancer; probe;
 KM nucleic acid detection; survival; ss.
 XX Homo sapiens.
 XX MO2003000933-A1.
 XX PD 03-JAN-2003.
 XX PF 25-JUN-2002; 2002WO-US020094.
 XX PR 25-JUN-2001; 2001US-030672P.
 XX PR 03-JUN-2001; 2001US-0303258P.
 XX PA (GEOR-) GEORGIA TECH RES CORP.
 XX PI Bao G, Tsourkas A, Xu Y;
 XX WPI; 2003-210160/20.
 XX Composition for detecting target nucleic acid for diagnosing cancer,
 PT comprises dual nucleic acid probes with resonance energy transfer
 PT moieties.
 XX Example 3; Page 45; 78pp; English.
 XX The specification describes a composition for the detection of a target
 CC polynucleotide. The composition comprises two nucleic acid probes that
 CC hybridize to a first and second nucleic acid target sequence on the
 CC target polynucleotide. The probes form a stem-loop structure when not
 CC bound to the target sequence, and incorporate a resonance energy transfer
 CC donor or acceptor moiety. When both probes hybridize to the target, an
 CC observable and detectable interaction occurs. The method is useful for
 CC detecting a subject polynucleotide in vivo. The probes are useful for
 CC detecting nucleic acid target hybridization, for the identification and
 CC quantification of tissue and cell-specific gene expression levels,
 CC including response to external stimuli, such as drug candidates, and
 CC genetic variations associated with disease such as cancer. The present
 CC sequence represents a fragment of human survival CDNA. Probes AB268314-15
 CC hybridize to this sequence, and are used to demonstrate the method of the
 CC invention.
 XX SQ Sequence 121 BP; 19 A; 44 C; 35 G; 23 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1.09e-33 Length: 121
 Score: 40.00 Matches: 40
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 28.17% Indels: 0
 DB: 7 Gaps: 0
 US-09-690-825-34 (1-142) x AB268313 (1-121)
 QY 1 MetGlyAlaProThLeuProProAlaTrpGlnProPhenLeuLysASP;IArgIleSer 20
 DB 1 AAGGGAGGCCCGACCTTCGCGAGCCCTTTCACAGACACCGCATCTCT 60
 QY 21 ThrPheLysAsnTrpProPhenLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
 DB 61 ACATTCAAGAACTGCGCCCTTCTGGAGGGCTGCGCTGCACCCGAGCGGATGGCCGAG 120
 RESULT 20
 ADB67958/C
 ID ADB67958 standard; CDNA; 1050 BP.
 XX ADB67958;
 XX 04-DEC-2003 (first entry)
 XX Human lung specific nucleic acid sequence SEQ ID NO:57.

XX human; lung specific polypeptide; LSP; lung specific nucleic acid; LSNA;
 KM lung; cytosolic; vaccine; gene therapy; immune response; lung cancer;
 KM metastasis; gene; ss.
 XX Homo sapiens.
 XX MO2003020899-A2.
 XX PD 13-MAR-2003.
 XX PF 29-AUG-2002; 2002WO-US027771.
 XX PF 31-AUG-2001; 2001US-0316260P.
 XX PR (DIAD-) DIADEXUS INC.
 XX PA Sun Y, Liu C, Chen S;
 XX WPI; 2003-300880/29.
 XX P-PSDB; ADB67863.
 XX Novel lung specific polypeptides and nucleic acids; useful for
 PT identifying, diagnosing, monitoring, staging, imaging and treating lung
 PT cancer and non-cancerous disease states in lung.
 XX Example 1; Page 200-201; 263pp; English.
 XX The present invention describes human lung specific polypeptides (LSP,
 CC (I)) and lung specific nucleic acids (LSNA, (II)). Also described: (1)
 CC determining (M1) the presence of an LSNA in a sample; (2) a vector (II)
 CC comprising (II); (3) a host cell comprising (II); (4) a polypeptide (IV)
 CC encoded by (II); (5) production of (IV); (6) an antibody (V) or its
 CC fragment that specifically binds to an LSP; (7) determining (M2) the
 CC presence of an LSP in a sample; (8) a kit for detecting a risk of cancer
 CC or presence of cancer in a patient, comprising a unit for determining the
 CC presence of (I) or (II) in a sample of the patient; and (9) a vaccine
 CC comprising (I) or (II). LSP and LSNA sequences have cytosolic
 CC activities, and can be used in vaccines, gene therapy, and as inducers of
 CC an immune response. (I) and (II) can be used for diagnosing or monitoring
 CC the presence and metastases of lung cancer in a patient, by determining
 CC the amount of (I) or (II) in a sample of a patient, and comparing the
 CC amount of the determined nucleic acid molecule or the polypeptide in the
 CC sample of the patient to the amount of the lung specific marker in a
 CC normal control, where the difference in the amount of the nucleic acid
 CC molecule or the polypeptide in the sample compared to the amount of the
 CC nucleic acid molecule or the polypeptide in the normal control is
 CC associated with the presence of lung cancer. (I) and (V) are useful for
 CC treating a patient with lung cancer, by administering (I) or (V), where
 CC the administration of (I) or (V) induces an immune response against the
 CC lung cancer cell expressing the nucleic acid molecule or a polypeptide.
 CC (I), (II) and (V) are also useful for identifying, diagnosing,
 CC monitoring, staging, imaging and treating lung cancer and non-cancerous
 CC disease states in lung, for identifying lung tissue, and monitoring,
 CC identifying and/or designing agonists and antagonists of (I). (II) can be
 CC used in gene therapy, for producing transgenic animals and cells, and for
 CC producing engineered lung tissue for treatment and research. (II) is also
 CC useful for detecting or amplifying nucleic acid molecules that have
 CC similar or identical nucleic acid sequences compared to (II). (I) is
 CC useful for producing engineered lung tissue. (V) is useful for
 CC identifying (I). (II) is also useful for driving in vivo expression of
 CC (I). The present sequence represents a human LSNA from the present
 CC invention.
 XX SQ Sequence 1050 BP; 316 A; 231 C; 178 G; 325 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 9.72e-32 Length: 1050
 Score: 39.00 Matches: 39
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 27.46% Indels: 0
 DB: 9 Gaps: 0

CC The survivin gene can be u

XX

CC The invention provides antisense compounds capable of inhibiting the
CC expression of human Her-3, a member of epidermal growth factor (EGF)
CC family of receptor/tyrosine kinases. The antisense oligonucleotides are
CC useful for inhibiting the expression of Her-3 in cells or tissues. They
CC are commonly used as research reagents and in diagnostics for example, to
CC elucidate the function of particular genes. The antisense compounds are
CC also useful for distinguishing between functions of various members of a
CC biological pathway and for research use. They are also utilized for
CC diagnostics, therapeutics, prophylaxis and in kits. They are useful
CC for prophylactically, e.g. to prevent or delay infection, inflammation or
CC tumor formation. The present sequence represents the human Her-3 DNA
CC sequence (GenBank Accession No. U75285)
XX
SQ Sequence 14796 BP; 3482 A; 3488 C; 3888 G; 3938 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1,18e-30 Length: 14796
Score: 39.00 Matches: 39
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 27.46% Indels: 0
DB: Gaps: 0

US-09-690-825-34 (1-142) x AAB47531 (1-14796)

QY 75 GluGluHisIysLysHisSerSerGlyCysAlaPheLeuSerValIlysglnPheGlu 94
Db 5159 GAGCAACATATAAAGCATTCGTCGCGTTCCTTCTGTCTCAAGAGCAGTTTGA 5218
QY 95 GluLeuThrLeuGlyGluPheLeuLysLeuAspArgGluArgAlaLysAsnIle 113
Db 5219 GAATTAACTCTTGTAATTTTGAACCTGACAGAGAAAGCCAGAAACAAAT 5275

RESULT 23
AAS21523
ID AAS21523 standard; cDNA; 14796 BP.
XX
AC AAS21523;
XX
DT 21-NOV-2001 (first entry)
XX
DE DNA encoding human survivin.
XX
KW Survivin; human; mouse; cytostatic; antisense oligonucleotide;
KM hyperproliferative condition; cancer; apoptosis; cytokinesis; ss.
XX
OS Homo sapiens.
XX
PN WO200157059-A1.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US002939.
XX
PR 02-FEB-2000; 2000US-00496694.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Ackermann EJ, Swayze EE, Cowsett LM;
XX
DR WPI, 2001-488663/53.
XX
PT Novel antisense compounds for modulating the expression of Survivin and
PI treatment of cancer.
XX
PS Example 13; Page 74-79; 120pp; English.
XX
CC The invention relates to antisense oligonucleotides targeted to a nucleic
CC acid molecule encoding human Survivin, where the antisense
CC oligonucleotide inhibits the expression of human Survivin. These
CC antisense oligonucleotides are used in the treatment of an animal
CC suffering from a disease or condition associated with Survivin, e.g. a
CC hyperproliferative condition such as cancer, and comprises administering

CC a therapeutically or prophylactically effective amount of the antisense
CC oligonucleotide so that expression of Survivin is inhibited. The
CC oligonucleotides can also be used to treat a human suffering from a
CC disease or condition characterised by a reduction in apoptosis comprising
CC administering the antisense oligonucleotide to a human. In addition, the
CC antisense oligonucleotide and a cytotoxic chemotherapeutic agent e.g.
CC taxol or cisplatin, can be used to modulate apoptosis, cytokinesis or the
CC cell cycle, or inhibit the proliferation in a cancer cell by contacting
CC the cell with the antisense oligonucleotide. AAS21521-AAS21768 represent
CC Survivin nucleic acids, and antisense oligonucleotides targeted to
CC Survivin, used in the method of the invention
XX
SQ Sequence 14796 BP; 3482 A; 3488 C; 3888 G; 3938 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1,18e-30 Length: 14796
Score: 39.00 Matches: 39
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 27.46% Indels: 0
DB: Gaps: 0

US-09-690-825-34 (1-142) x AAS21523 (1-14796)

QY 75 GluGluHisIysLysHisSerSerGlyCysAlaPheLeuSerValIlysglnPheGlu 94
Db 5159 GAGCAACATATAAAGCATTCGTCGCGTTCCTTCTGTCTCAAGAGCAGTTTGA 5218
QY 95 GluLeuThrLeuGlyGluPheLeuLysLeuAspArgGluArgAlaLysAsnIle 113
Db 5219 GAATTAACTCTTGTAATTTTGAACCTGACAGAGAAAGCCAGAAACAAAT 5275

RESULT 24
ABL68655
ID ABL68655 standard; DNA; 14796 BP.
XX
AC ABL68655;
XX
DT 15-MAY-2002 (first entry)
XX
DE Kidney cancer related gene sequence SEQ ID NO:6992.
XX
KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KM stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytostatic; gene therapy; antineoplastic; Wilms tumour; adenocarcinoma;
XX
OS Homo sapiens.
XX
PN WO200194629-A2.
XX
PD 13-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-US010838.
XX
PR 05-JUN-2000; 2000US-0209473P.
PR 05-JUN-2000; 2000US-0209531P.
PR 18-SEP-2000; 2000US-0233133P.
PR 18-SEP-2000; 2000US-0233617P.
PR 20-SEP-2000; 2000US-0234009P.
PR 20-SEP-2000; 2000US-0234034P.
PR 22-SEP-2000; 2000US-0234509P.
PR 22-SEP-2000; 2000US-0234567P.
PR 25-SEP-2000; 2000US-0234923P.
PR 25-SEP-2000; 2000US-0234924P.
PR 25-SEP-2000; 2000US-0235077P.
PR 25-SEP-2000; 2000US-0235082P.
PR 25-SEP-2000; 2000US-0235134P.
PR 25-SEP-2000; 2000US-0235280P.
PR 26-SEP-2000; 2000US-0235637P.
PR 26-SEP-2000; 2000US-0235638P.
PR 27-SEP-2000; 2000US-0235711P.

27-SEP-2000; 2000US-0235720P.
PR 27-SEP-2000; 2000US-0235840P.
PR 27-SEP-2000; 2000US-0235863P.
PR 28-SEP-2000; 2000US-0236028P.
PR 28-SEP-2000; 2000US-0236032P.
PR 28-SEP-2000; 2000US-0236033P.
PR 28-SEP-2000; 2000US-0236034P.
PR 28-SEP-2000; 2000US-0236109P.
PR 28-SEP-2000; 2000US-0236111P.
PR 29-SEP-2000; 2000US-0236842P.
PR 29-SEP-2000; 2000US-0236891P.
PR 02-OCT-2000; 2000US-0237172P.
PR 02-OCT-2000; 2000US-0237173P.
PR 02-OCT-2000; 2000US-0237278P.
PR 02-OCT-2000; 2000US-0237294P.
PR 02-OCT-2000; 2000US-0237295P.
PR 02-OCT-2000; 2000US-0237316P.
PR 03-OCT-2000; 2000US-0237425P.
PR 03-OCT-2000; 2000US-0237598P.
PR 03-OCT-2000; 2000US-0237604P.
PR 03-OCT-2000; 2000US-0237606P.
PR 03-OCT-2000; 2000US-0237608P.
PR 01-NOV-2000; 2000US-0244867P.
PR 01-NOV-2000; 2000US-0245084P.
XX (AVAL-) AVALON PHARM.
XX
XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppe DR, Weaver Z;
XX WPI; 2002-188264/24.
XX
XX Screening for anti-neoplastic agent involves exposing cells to a chemical
PT agent to be tested for anti-neoplastic activity, and determining a change
PT in expression of a gene of a signature gene set.
XX
XX Claim 1; SEQ ID NO 6992; 44pp; English.
XX
XX The present invention describes a method (M1) for screening for an anti-
CC neoplastic agent. The method involves exposing cells to a chemical agent
CC to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 847 sequences (given in AB61664
CC to AB670110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening an
CC anti-neoplastic agent, and can be used for producing a product which is
CC the data collected with respect to the anti-neoplastic agent as a result
CC of M1, and the data is sufficient to convey the chemical structure and/or
CC properties of the agent. M1 can be used in the treatment of cancer such
CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms
CC tumour
XX
XX Sequence 14796 BP; 3482 A; 3488 C; 3888 G; 3938 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 1.18e-30 Length: 14796
Score: 39.00 Matches: 39
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 27.46% Indels: 0
DB: 6 Gaps: 0
US-09-690-825-34 (1-142) x AB616655 (1-14796)
QY 75 GIUGIUIHSLYSLYSHISSEISERGLYCYSALAPHEUSEVALYSLYGLIPHEGLU 94
DB 5159 GAGGAACATTAATAAACCATTCGCGGTTCCGTTTCCCTTTGTCAGAAACCATTTGAA 5218
QY 95 GIULeuTHrLeuGLYGLuPHeuLyuLSLeuSparGLuARGAlaLYASnLYSle 113

Db. 5219 GAATTACCCCTGGTGAATTTTGGAACTGGACAGAGAAAGCCCAAGCAAAATT 5275
RESULT 25
AB616526
ID AB616526 standard; DNA, 14796 BP.
XX
XX
XX AB616526;
AC
XX
XX 15-MAY-2002 (first entry)
DT
XX
XX Lung cancer related gene sequence SEQ ID NO:4663.
DE
XX
XX Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytostatic; gene therapy; antineoplastic; Wilms tumour; adenocarcinoma;
KW gene; ds.
XX
XX Homo sapiens.
OS
XX
XX WO200194629-A2.
PN
XX
XX 13-DEC-2001.
PD
XX
XX 30-MAY-2001; 2001WO-US010838.
PF
XX
XX 05-JUN-2000; 2000US-0209473P.
PR 05-JUN-2000; 2000US-0209531P.
PR 18-SEP-2000; 2000US-0231133P.
PR 18-SEP-2000; 2000US-0233617P.
PR 20-SEP-2000; 2000US-0234009P.
PR 20-SEP-2000; 2000US-0234034P.
PR 20-SEP-2000; 2000US-0234052P.
PR 22-SEP-2000; 2000US-0234509P.
PR 22-SEP-2000; 2000US-0234567P.
PR 25-SEP-2000; 2000US-0234923P.
PR 25-SEP-2000; 2000US-0234924P.
PR 25-SEP-2000; 2000US-0235077P.
PR 25-SEP-2000; 2000US-0235082P.
PR 25-SEP-2000; 2000US-0235134P.
PR 25-SEP-2000; 2000US-0235280P.
PR 26-SEP-2000; 2000US-0235637P.
PR 26-SEP-2000; 2000US-0235638P.
PR 27-SEP-2000; 2000US-0235711P.
PR 27-SEP-2000; 2000US-0235720P.
PR 27-SEP-2000; 2000US-0235840P.
PR 27-SEP-2000; 2000US-0235863P.
PR 28-SEP-2000; 2000US-0236028P.
PR 28-SEP-2000; 2000US-0236032P.
PR 28-SEP-2000; 2000US-0236033P.
PR 28-SEP-2000; 2000US-0236034P.
PR 28-SEP-2000; 2000US-0236109P.
PR 28-SEP-2000; 2000US-0236111P.
PR 28-SEP-2000; 2000US-0236842P.
PR 28-SEP-2000; 2000US-0236891P.
PR 29-SEP-2000; 2000US-0237172P.
PR 02-OCT-2000; 2000US-0237173P.
PR 02-OCT-2000; 2000US-0237173P.
PR 02-OCT-2000; 2000US-0237278P.
PR 02-OCT-2000; 2000US-0237294P.
PR 02-OCT-2000; 2000US-0237295P.
PR 03-OCT-2000; 2000US-0237425P.
PR 03-OCT-2000; 2000US-0237598P.
PR 03-OCT-2000; 2000US-0237604P.
PR 03-OCT-2000; 2000US-0237606P.
PR 03-OCT-2000; 2000US-0237608P.
PR 01-NOV-2000; 2000US-0244867P.
PR 01-NOV-2000; 2000US-0245084P.
XX (AVAL-) AVALON PHARM.
XX
XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppe DR, Weaver Z;

Alignment Scores:

Pred. No.: 1.18e-30 Length: 14796
 Score: 39.00 Matches: 39
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 27.46% Indels: 0
 DB: 6 Gaps: 0

US-09-690-825-34 (1-142) x ABL65663 (1-14796)

Qy 75 GIUGLHISLYSHISSESSERGLYCYSALAPHELEUSERVALLYSYGLINPHEGLU 94

Db 5159 GAGGAACATMAAAGCATTCGCGCTTCCTTCCTTCGCAAGAGCAGTTTGA 5218

Qy 95 GLEUTHTLEUGLYGLUPHELEULYSLEUSPARGLUARGALALYSANLYSILE 113

Db 5219 GAATTAACTTGATTTTGAACCTGACAGAGAAAGCCAAAGCAAAAT 5275

RESULT 27

ABN96924 ID ABN96924 standard; DNA; 14796 BP.

AC ABN96924;

DT 13-AUG-2002 (first entry)

DE Gene #3422 used to diagnose liver cancer.

XX Gene, liver cancer; ds; hepatocellular carcinoma, hepatotropic;

KM metastatic liver tumour; cytostatic; expression profile; disease state;

KM disease progression; drug toxicity; drug efficacy; drug metabolism.

XX Homo sapiens.

XX WO200229103-A2.

PN 11-APR-2002;

PF 02-OCT-2001; 2001WO-US030589.

XX 02-OCT-2000; 2000US-0237054P.

XX (GENE-) GENE LOGIC INC.

PI Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;

XX WPI; 2002-426119/45.

PT Diagnosing and detecting the progression of liver cancer, hepatocellular

PT carcinoma or metastatic liver tumor in a patient, involves detecting the

PT level of expression of two or more genes in a liver tissue sample.

PS Claim 1; SEQ ID NO 3422; 298bp; English.

XX The invention relates to a novel method for diagnosing and detecting the
 CC progression of liver cancer, hepatocellular carcinoma or metastatic liver
 CC tumor in a patient, and differentiating metastatic liver cancer from
 CC hepatocellular carcinoma in a patient, involving detecting the level of
 CC expression of two or more genes represented in ABN93503-ABN97455 in a
 CC tissue sample. The method of the invention has hepatotropic, and
 CC cytostatic activity. The method is useful for diagnosing and detecting
 CC the progression of liver cancer, hepatocellular carcinoma and metastatic
 CC liver carcinoma in a patient. The method is useful for identifying
 CC expression profiles which serve as useful diagnostic markers as well as
 CC markers that can be used to monitor disease states, disease progression,
 CC drug toxicity, drug efficacy and drug metabolism. Note: The sequence data
 CC for this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 14796 BP; 3482 A; 3488 C; 3888 G; 3938 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.18e-30 Length: 14796
 Score: 39.00 Matches: 39
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 27.46% Indels: 0
 DB: 6 Gaps: 0

US-09-690-825-34 (1-142) x ABN96924 (1-14796)

Qy 75 GIUGLHISLYSHISSESSERGLYCYSALAPHELEUSERVALLYSYGLINPHEGLU 94

Db 5159 GAGGAACATMAAAGCATTCGCGCTTCCTTCCTTCGCAAGAGCAGTTTGA 5218

Qy 95 GLEUTHTLEUGLYGLUPHELEULYSLEUSPARGLUARGALALYSANLYSILE 113

Db 5219 GAATTAACTTGATTTTGAACCTGACAGAGAAAGCCAAAGCAAAAT 5275

RESULT 28

AAZ31036 ID AAZ31036 standard; DNA; 403 BP.

XX AAZ31036;

DT 17-JAN-2000 (first entry)

DE 5' flanking region of the human Survivin gene.

XX Effector, 5' flanking region; IAP; apoptosis inhibitor; tumour cell;

KM effector cell protease receptor-1; EPR-1; embryonic tissue; tubulin;

KM mitotic spindle; abnormal cell growth; tumorigenesis; ss.

XX Homo sapiens.

XX WO950440-A2.

PN 07-OCT-1999.

PF 01-APR-1999; 99WO-US007205.

XX 01-APR-1998; 98US-0080288P.

XX (UYVA) UNIT VALL.

PA Altieri DC;

PI WPI; 1999-591329/50.

XX Identifying agents that modulate Survivin interactions.

XX Example; Fig 3A; 56pp; English.

XX This sequence is the 5' flanking region of the human Survivin gene,
 CC (Survivin open reading frame: AAZ31037). Survivin is a 142 amino acid
 CC protein of approximately 16.5kD. Survivin is a member of the IAP family
 CC of apoptosis inhibitors, and the gene is located on chromosome 17q25. The
 CC nucleic acid sequence of Survivin is related to the Effector Cell
 CC Protease Receptor-1 (EPR-1). Survivin is expressed in tumour cells and
 CC embryonic tissue. The sequence is used in the invention which involves
 CC identifying an agent that modulates interactions between Survivin and
 CC tubulin. Agents that modulate interaction between Survivin and tubulin or
 CC mitotic spindles may be administered to a mammal to modulate biological
 CC or pathological processes mediated by Survivin, for example Survivin-
 CC mediated inhibition of cellular apoptosis. Thus an inhibiting agent may
 CC be used to block abnormal cell growth, for example during tumorigenesis.
 CC An agent that increases interaction may be used to extend cell growth in
 CC culture

SQ Sequence 403 BP; 63 A; 143 C; 140 G; 57 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 5.28e-30 Length: 403
 Score: 37.00 Matches: 37
 Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 26.06% Indels: 0
 DB: 2 Gaps: 0

US-09-690-825-34 (1-142) x AA231036 (1-403)

QY 1 MetGlyAlaProThreLeuProProAlaTTPGlnProPheLeuLysAspHisArgTleser 20

DB 291 ATGGGTGCCCCGACGCTGGCCCTGCGACGCCCTTCTCAAGACCCGCACTCT 350

QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArg 37

DB 351 ACATTCAAGAACTGGCCCTTCTTGAGGGCTGCGCTGCACCCCGGAGCGG 401

RESULT 29

AA82458

ID AA82458 standard; DNA; 1100 BP.

AC AA82458;

XX 29-UTN-2001 (first entry)

DE Human survivin promoter.

XX Human; Map4 promoter; cytosratic; gene therapy; apoptosis modulator;

KM survivin promoter; p53-mediated repression; cancer;

XX proliferative disorder; ds.

XX Homo sapiens.

XX WO200123522-A2.

XX PD 05-APR-2001.

XX PF 02-OCT-2000; 2000WO-US027076.

XX PR 30-SEP-1999; 99US-0157171P.

XX PA (FOX-) FOX CHASE CANCER CENT.

XX PI Murphy M;

XX DR WPI; 2001-308140/32.

XX PT Novel nucleic acid sequence comprising a promoter region containing p53

PT negative response elements are useful for treating cancers and other

PT cellular proliferative diseases.

PS Claim 15; Page 68-69; 84pp; English.

XX The present sequence is the human survivin promoter. The invention

CC relates to isolated nucleic acid molecules containing the Map4 or

CC survivin promoter. The Map4 and survivin genes are involved in p53-

CC mediated repression of gene expression. The sequences are useful for

CC determining the presence of an alteration in the Map 4 or survivin

CC promoter sequence, where an alteration is associated with a pathological

CC condition. They are also useful for screening novel therapeutic agents

CC for treating and diagnosing cancer and other cellular proliferative

CC disorders. Furthermore, the sequences may be used in gene therapy

XX

SO Sequence 1100 BP; 199 A; 343 C; 312 G; 246 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.58e-28 Length: 1100

Score: 36.00 Matches: 36

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 25.35% Indels: 0

DB: 4 Gaps: 0

US-09-690-825-34 (1-142) x AA82458 (1-1100)

QY 1 MetGlyAlaProThreLeuProProAlaTTPGlnProPheLeuLysAspHisArgTleser 20

DB 991 ATGGGTGCCCCGACGCTGGCCCTGCGACGCCCTTCTCAAGACCCGCACTCT 1050

QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGlu 36

DB 1051 ACATTCAAGAACTGGCCCTTCTTGAGGGCTGCGCTGCACCCCGGAG 1098

RESULT 30

ADCC32487/c

ID ADCC32487 standard; cDNA; 1596 BP.

AC ADCC32487;

XX 18-DEC-2003 (first entry)

DE Human novel cDNA contig sequence, SEQ ID NO:2569.

XX Human; diagnostic; drug screening; forensics; gene mapping;

KM biodiversity assessment; Parkinson's disease; Alzheimer's disease;

KM neurodegenerative diseases; anaemia; platelet disorder; wound; burns;

KM ulcers; osteoporosis; autoimmune disease; cancer;

KM molecular weight marker; food supplement; antiparkinsonian; nootropic;

KM neuroprotective; antihaemic; anticoagulant; thrombolytic; vienerary;

KM anticancer; osteopathic; immunosuppressive; antiinflammatory; cycostatic;

XX gene therapy; chromosome 17; ss.

XX Homo sapiens.

XX WO2003029271-A2.

XX PD 10-APR-2003.

XX PF 24-SEP-2002; 2002WO-US030474.

XX PR 24-SEP-2001; 2001US-0324631P.

XX PA (HYSE-) HYSEQ INC.

XX Tang TY, Zhang J, Ren F, Xue AJ, Zhao QA, Wang J, Wehrman T;

XX Zhou P, Ghosh M, Wang D, Ma Y, Asundi V, Wang Z, Wang G;

XX PI Haley-Vicence D, Dymnae RT;

XX DR WPI; 2003-371981/35.

XX P-PSDB; ADCC3254.

XX New polynucleotide and polypeptide useful for diagnosing, preventing or

PT treating conditions such as neurodegenerative diseases, anaemias, platelet

PT disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or

PT cancer.

PS Example 2; SEQ ID NO 2569; 1185pp; English.

XX The invention relates to 971 novel human cDNA sequences (ADCC29919-

CC ADCC30889) and the polypeptides they encode (ADCC30890-ADCC31860). The

CC invention also relates to nucleic acid sequences over 99% identical with

CC the novel human cDNAs. The invention additionally encompasses expression

CC vectors and host cells comprising a nucleic acid of the invention; the

CC recombinant production of a polypeptide of the invention; an antibody

CC against a polypeptide of the invention; a method of detecting

CC polynucleotides or polypeptides of the invention; and methods of

CC identifying a compound which binds to a polypeptide of the invention. The

CC invention further discloses methods of preventing, treating or

CC ameliorating a medical condition; kits comprising polynucleotide probes

CC and/or monoclonal antibodies for carrying out the methods of the

CC invention; methods for the identification of compounds that modulate the

CC expression or activity of the polynucleotide and/or polypeptide; and 767

CC contig sequences corresponding to the cDNA sequences of the invention

CC (ADCC1861-ADCC32627) and the polypeptides encoded by the contigs (ADCC32628

CC -ADCC33394). The nucleic acids and polypeptides of the invention are

CC useful in diagnostics, drug screening, forensics, gene mapping, in the

CC identification of mutations responsible for genetic disorders or other

CC traits, for assessing biodiversity, and in producing many other types of

CC data and products dependent on DNA and amino acid sequences. They are

CC also used for treating diseases such as Parkinson's disease, Alzheimer's
 CC disease and other neurodegenerative diseases, anemia, platelet
 CC disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
 CC cancer. The nucleic acids may also be used as hybridisation probes or
 CC primers, and in the recombinant production of a protein. The polypeptides
 CC are also useful in generating antibodies, as molecular weight markers,
 CC and as food supplements. The present sequence represents a human contig
 CC sequence used in an example of the invention. Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from Wipo at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 1596 BP, 328 A, 509 C, 470 G, 289 T, 0 U, 0 Other;

Alignment Scores:

Pred. No.:	Length:	Matches:	1596
Score:	15.00	Conservative:	0
Percent Similarity:	100.00%	Mismatches:	0
Best Local Similarity:	100.00%	Indels:	0
Query Match:	10.56%	Gaps:	0

DB: 9

US-09-690-825-34 (1-142) x ADC32487 (1-1596)

Oy 114 AAlaySGlUTrrArArArArLyLyLyGluPhheGluGluThraLa 128

Db 90 GCAAGAGAACCAACAAATTAAGAGAAAGAAATTGAGAGAACTGCG 46

RESULT 31
 ABK93852 ID ABK93852 standard; DNA; 30 BP.

XX ABK93852;

XX 26-AUG-2002 (first entry)

XX Human survivin Real Time-PCR probe.

XX Human; sb; antisense; inhibitor of apoptosis; H1A1, H1A2, XIAP;
 KW cytoskeletal; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;
 KW pancreatic cancer; embryonic development; viral pathogenesis;
 KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;
 KW lupus erythematosus; herpes virus infection; pox virus infection;
 KW adenovirus infection; proliferative disease; probe; real time PCR.

XX Homo sapiens.

XX WO200226968-A2.

XX 04-APR-2002.

XX 27-SEP-2001; 2001WO-CA001379.

XX 28-SEP-2000; 2000US-00672717.

XX (UYOT-) UNIV OTTAWA.

XX (ABGE-) ABERG THERAPEUTICS INC.

XX Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;

XX WPI; 2002-479562/51.

XX Novel antisense inhibitor of apoptosis nucleic acid useful for enhancing
 PT apoptosis in a cell, for treating cancer and other proliferative
 PT diseases.

XX Example 4; Page 42; 135pp; English.

XX The invention relates to an inhibitor of apoptosis (IAP) antisense
 CC nucleic acid (I) that inhibits IAP biological activity, regardless of
 CC length of the antisense nucleic acid, the IAP proteins may be mouse or
 CC human XIAP, H1A1 or H1A2. Also included are a pharmaceutical
 CC composition comprising a mammalian IAP antisense molecule and a method of

CC enhancing apoptosis in a cell, comprising administering a negative
 CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP
 CC antisense inhibitor is useful for enhancing apoptosis in a cell in a
 CC mammal diagnosed with a proliferative disease. The method is useful for
 CC treating a patient diagnosed with a proliferative disease like cancer.

CC The IAP antisense molecule is useful to treat, ameliorate, improve,
 CC sustain or prevent proliferative diseases (e.g. ovarian cancer,
 CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or
 CC conditions where apoptosis is involved or implicated (e.g. embryonic
 CC development, viral pathogenesis, autoimmune disorders, neurodegenerative
 CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes
 CC virus, pox virus and adenovirus). The present sequence is a real time PCR
 CC probe used to measure mRNA levels in an experiment showing that the
 CC antisense molecules of the invention reduce the levels of IAP mRNA in a
 CC cell

XX SQ Sequence 30 BP, 12 A, 8 C, 7 G, 3 T, 0 U, 0 Other;

Alignment Scores:

Pred. No.:	Length:	Matches:	30
Score:	0.276	Conservative:	9
Percent Similarity:	9.00%	Mismatches:	0
Best Local Similarity:	100.00%	Indels:	0
Query Match:	6.34%	Gaps:	0

DB: 6

US-09-690-825-34 (1-142) x ABK93852 (1-30)

Oy 69 ProASpASPpProlegluGluHis 77

Db 3 CCAGATGACGACCCCATAGAGACAT 29

RESULT 32
 AAS21533 ID AAS21533 standard; DNA; 26 BP.

XX AAS21533;

XX 21-NOV-2001 (first entry)

XX Mouse survivin PCR probe.

XX Survivin; human; mouse; cytoskeletal; antisense oligonucleotide;
 KW hyperproliferative condition; cancer; apoptosis; cytotoxicity; ss.

XX Mus musculus.

XX WO200157059-A1.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US002939.

XX 02-FEB-2000; 2000US-00496694.

XX (ISIS-) ISIS PHARM INC.

XX Bennett CF, Ackermann EJ, Swayze EE, Cowse LM;

XX WPI; 2001-48863/53.

XX Novel antisense compounds for modulating the expression of Survivin and
 PT treatment of cancer.

XX Example 13; Page 50; 120pp; English.

XX The invention relates to antisense oligonucleotides targeted to a nucleic
 CC acid molecule encoding human Survivin, where the antisense
 CC oligonucleotide inhibits the expression of human Survivin. These
 CC antisense oligonucleotides are used in the treatment of an animal
 CC suffering from a disease or condition associated with Survivin, e.g. a
 CC hyperproliferative condition such as cancer, and comprises administering
 CC a therapeutically or prophylactically effective amount of the antisense

CC oligonucleotide so that expression of Survivin is inhibited. The
CC oligonucleotides can also be used to treat a human suffering from a
CC disease or condition characterised by a reduction in apoptosis comprising
CC administering the antisense oligonucleotide to a human. In addition, the
CC antisense oligonucleotide and a cytotoxic chemotherapeutic agent e.g.
CC taxol or cisplatin, can be used to modulate apoptosis, cytokinesis or the
CC cell cycle, or inhibit the proliferation in a cancer cell by contacting
CC the cell with the antisense oligonucleotide. AAS21521-AAS21768 represent
CC Survivin nucleic acids, and antisense oligonucleotides targeted to
CC Survivin, used in the method of the invention

XX
SQ Sequence 26 BP; 8 A; 4 C; 10 G; 4 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2.79 Length: 26
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.63% Indels: 0
DB: Gaps: 0

US-09-690-825-34 (1-142) x AAS21533 (1-26)

QY 62 LysGluLeuGluGlyTyrGluPro 69
ABV52787
ID ABV52787 standard; cDNA; 509 BP.
XX
AC ABV52787;
XX
DT 17-SEP-2002 (first entry)
XX
DE Human prostate expression marker CDNA 52778.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW Pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US005171.
XX
PR 17-FEB-2000; 2000US-0183319P.
PR 16-MAR-2000; 2000US-0189862P.
PR 25-MAY-2000; 2000US-0207454P.
PR 09-JUN-2000; 2000US-0211314P.
PR 18-JUL-2000; 2000US-0219007P.
PR 13-DEC-2000; 2000US-0255281P.
XX
PA (MIL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JB;
XX
DR WPI, 2001-662795/76.
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer. Useful
PT for detecting presence of prostate cancer, stage of prostate cancer.
XX
PS Claim 1; Page 10233; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (1) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (1) is useful for: (a) assessing whether
CC a patient is afflicted with prostate cancer; (b) monitoring the efficacy
CC progression of prostate cancer in a patient; (c) assessing the efficacy
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing

CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC determining whether prostate cancer has metastasized in a patient; (h)
CC assessing the aggressiveness or incidence of prostate cancer in a patient
CC; (i) is also useful as a pharmacodynamic or pharmacogenomic marker

XX
SQ Sequence 509 BP; 212 A; 110 C; 73 G; 114 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 46.3 Length: 509
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.63% Indels: 0
DB: Gaps: 0

US-09-690-825-34 (1-142) x ABV52787 (1-509)

QY 115 LysGluThrAsnAsnLysLysLys 122
ABV52787
ID AAS21751 standard; cDNA; 515 BP.
XX
AC AAS21751;
XX
DT 21-NOV-2001 (first entry)
XX
DE DNA encoding mouse survivin.
XX
KW Survivin; human; mouse; cytostatic; antisense oligonucleotide;
KW hyperproliferative condition; cancer; apoptosis; cytokinesis; ss.
XX
OS Mus musculus.
XX
PN WO200157059-A1.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US002939.
XX
PR 02-FEB-2000; 2000US-00496694.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Ackermann EJ, Swayze EE, Cowser LM;
XX
DR WPI, 2001-488653/53.
XX
PT Novel antisense compounds for modulating the expression of Survivin and
PT treatment of cancer.
XX
PS Example 18; Page 116-117; 120pp; English.
XX
CC The invention relates to antisense oligonucleotides targeted to a nucleic
CC acid molecule encoding human Survivin, where the antisense
CC oligonucleotide inhibits the expression of human Survivin. These
CC antisense oligonucleotides are used in the treatment of an animal
CC suffering from a disease or condition associated with Survivin, e.g. a
CC hyperproliferative condition such as cancer, and comprises administering
CC a therapeutically or prophylactically effective amount of the antisense
CC oligonucleotide so that expression of Survivin is inhibited. The
CC oligonucleotides can also be used to treat a human suffering from a
CC disease or condition characterised by a reduction in apoptosis comprising
CC administering the antisense oligonucleotide to a human. In addition, the
CC antisense oligonucleotide and a cytotoxic chemotherapeutic agent e.g.
CC taxol or cisplatin, can be used to modulate apoptosis, cytokinesis or the
CC cell cycle, or inhibit the proliferation in a cancer cell by contacting
CC the cell with the antisense oligonucleotide. AAS21521-AAS21768 represent
CC Survivin nucleic acids, and antisense oligonucleotides targeted to

CC Survivin, used in the method of the invention
 XX Sequence 515 BP, 152 A, 120 C, 109 G, 133 T, 0 U, 1 Other;
 SQ Sequence 515 BP, 152 A, 120 C, 109 G, 133 T, 0 U, 1 Other;

Alignment Scores:
 Pred. No.: 46.8 Length: 515
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 5.63% Indels: 0
 DB: Gaps: 0

US-09-690-825-34 (1-142) x AAS21751 (1-515)

OY 122 LysGluPheGluGluThrAlaLys 129
 DB 325 AAAGGTTTGAAGAGACTGCAAG 348

RESULT 35
 ACH27866
 ID ACH27866 standard; CDNA; 587 BP.
 XX ACH27866;
 AC ACH27866;
 XX 13-OCT-2003 (first entry)
 DT 13-OCT-2003 (first entry)
 XX Human adult ovary cDNA #6246.
 DE Human adult ovary cDNA #6246.
 XX Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
 KM genome mapping; biodiversity; genetic disorder.
 XX Homo sapiens.
 OS US2003073623-A1.
 PN 17-APR-2003.
 PD 17-APR-2003.
 XX 30-JUN-2001; 2001US-00918995.
 PF 30-JUN-2001; 2001US-00918995.
 XX 30-JUN-2001; 2001US-00918995.
 PR (DRMA/) DRMANAC R T.
 PA (LABA/) LABAT I.
 PA (STRC/) STACHE-CRAIN B.
 PA (DICK/) DICKSON M C.
 PA (JONE/) JONES L W.
 XX Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
 PI WPI; 2003-615964/58.
 DR WPI; 2003-615964/58.
 XX New polynucleotide sequences obtained from various cDNA libraries, useful
 PT as hybridization probes, as oligomers for PCR, for chromosome and gene
 PT mapping, in the recombinant production of protein, or in generating
 PT antisense DNA or RNA.
 PS Claim 1; SEQ ID NO 15078; 44bp; English.
 XX The invention relates to an isolated polynucleotide comprising any one of
 CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
 CC determined by the technique of SBH (sequencing by hybridisation). Also
 CC included is a purified polypeptide comprising a sequence corresponding to
 CC a reading frame of the novel polynucleotide. The nucleic acid sequences
 CC are useful in diagnostics as expressed sequence tags (EST) for
 CC identifying expressed genes or for physical mapping of the human genome,
 CC in forensics, in assessing biodiversity, or in identifying mutations
 CC responsible for genetic disorders and other traits. The nucleotide
 CC sequences are also useful as hybridisation probes, as oligomers for PCR,
 CC for chromosome and gene mapping, in the recombinant production of
 CC protein, or in generating antisense DNA or RNA. The purified polypeptide
 CC is useful for generating antibodies specific for it. The present sequence
 CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
 CC for this patent did not form part of the printed specification, but was

CC obtained in electronic format directly from USPRO at
 CC seqdata.uspro.gov/sequence.html?docid=20030073623
 XX Sequence 587 BP, 133 A, 150 C, 110 G, 91 T, 0 U, 103 Other;
 SQ Sequence 587 BP, 133 A, 150 C, 110 G, 91 T, 0 U, 103 Other;

Alignment Scores:
 Pred. No.: 52.9 Length: 587
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 5.63% Indels: 0
 DB: Gaps: 0

US-09-690-825-34 (1-142) x ACH27866 (1-587)

OY 1 MetGlyAlaProThrLeuProPro 8
 DB 367 ATGGAGCCCCCACACTCCTCCT 390

RESULT 36
 ACA01764
 ID ACA01764 standard; DNA; 660 BP.
 XX ACA01764;
 AC ACA01764;
 XX 03-JUN-2003 (first entry)
 DT 03-JUN-2003 (first entry)
 XX C. glutamicum derived ORF SEQ ID 1755.
 DE C. glutamicum derived ORF SEQ ID 1755.
 XX Coryneform; nucleic acid array; fermentation; culture; ds.
 KM Coryneform; nucleic acid array; fermentation; culture; ds.
 XX Corynebacterium glutamicum.
 OS Corynebacterium glutamicum.
 PN DE10128510-A1.
 PD 19-DEC-2002.
 XX 13-JUN-2001; 2001DE-01028510.
 PF 13-JUN-2001; 2001DE-01028510.
 XX 13-JUN-2001; 2001DE-01028510.
 PR (DEGS) DEGUSSA AG.
 PA Farwick M, Moeckel B, Pfeifferle W, Bathe B, Hutmacher K;
 PI WPI; 2003-279970/28.
 DR WPI; 2003-279970/28.
 XX New nucleic acid array useful for monitoring mRNA expression of
 PT Corynebacterium glutamicum during fermentation, comprising nucleic acid
 PT from Corynebacterium glutamicum.
 PS Claim 1; Page 590; 709pp; German.
 XX This invention describes a novel nucleic acid array involving
 CC Corynebacterium glutamicum polynucleotides. The arrays are used to
 CC analyse C. glutamicum, particularly for monitoring a fermentation process
 CC to determine expression levels of C. glutamicum cellular mRNA. Such
 CC monitoring particularly differentiates between expression levels of
 CC different strains of C. glutamicum and allows the adjustment of different
 CC culture and fermentation conditions. ACA00010-ACA02188 represent C.
 CC glutamicum derived polynucleotides described in the disclosure of the
 CC invention
 XX Sequence 660 BP, 183 A, 190 C, 141 G, 146 T, 0 U, 0 Other;
 SQ Sequence 660 BP, 183 A, 190 C, 141 G, 146 T, 0 U, 0 Other;

Alignment Scores:
 Pred. No.: 59.1 Length: 660
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 5.63% Indels: 0
 DB: Gaps: 0

US-09-690-825-34 (1-142) x ACA01764 (1-660)

QY 4 ProthLeuProProAlaTrpGln 11
 |||||
 DB 152 CCGACGCTTCCCCCTGCATGCGAG 175

RESULT 37
 AAC69515
 ID AAC69515 standard; DNA; 1441 BP.
 XX
 AC AAC69515;
 XX
 DT 31-JAN-2001 (first entry)
 XX
 DE Human secreted protein gene 4 clone HKAJK47.
 XX
 KW Immunosuppressive; antiarthritic; antirheumatic; antiproliferative;
 KW cytostatic; cardiatic; vasotropic; cerebroprotective; neuroprotective;
 KW neurotropic; antibacterial; virocidic; fungicide; ophtalmological;
 KW vulnerary; gene therapy; infection; human; secreted protein; ss.
 XX
 OS Homo sapiens.
 XX
 PN MO200061623-A1.
 XX
 PD 19-OCT-2000.
 XX
 PF 06-APR-2000; 2000MO-US008979.
 XX
 PR 09-APR-1999; 99US-0128693P.
 PR 26-APR-1999; 99US-0130991P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Ruben SM, Ni J, Komatsculis GA, Rosen CA, Sceppe DR, Shi Y,
 PI Lafleur DW, Olsen HS, Ebner R, Florence KA, Moore PA, Birse CB,
 PI Young PE;
 XX
 DR WPI; 2000-647418/62.
 XX
 PT New nucleic acid molecules encoding 62 human secreted proteins for
 PT diagnosing, preventing, treating or ameliorating medical conditions and
 PT used as food additives or preservatives.
 XX
 PS Claim 1; Page 531; 716pp; English.
 XX
 CC The invention relates to the isolation of genes (AAC69512-C69587)
 CC encoding 62 human secreted proteins (AAB38321-B38396). The genes can be
 CC used to generate fusion proteins by linking to the gene for the human
 CC immunoglobulin G Fc portion (AAC69503) for increasing the stability of
 CC the fusion protein as compared to the human protein only. The genes and
 CC proteins are useful for preventing, ameliorating or treating medical
 CC conditions, e.g. by protein or gene therapy. The genes are isolated from
 CC a range of human tissues disclosed in the specification. The nucleic
 CC acids, proteins, antibodies and (ant)agonists are useful in the
 CC diagnosis, treatment and prevention of: (a) autoimmune diseases e.g.
 CC rheumatoid arthritis; (b) hyperproliferative disorders e.g. neoplasms of
 CC the breast or liver; (c) cardiovascular disorders e.g. cardiac arrest;
 CC (d) cerebrovascular disorders e.g. cerebral ischemia; (e) angiodysplasia;
 CC (f) nervous system disorders e.g. Alzheimer's disease; (g) infections
 CC caused by bacteria, viruses and fungi; and (h) ocular disorders e.g.
 CC corneal infection. The polypeptides can also be used to aid wound healing
 CC and epithelial cell proliferation, to prevent skin aging due to sunburn,
 CC to maintain organs before transplantation, for supporting cell culture of
 CC primary tissues, to regenerate tissues and in chemotaxis
 XX
 SQ Sequence 1441 BP; 348 A; 367 C; 503 G; 221 T; 0 U; 2 Other;
 XX
 Alignment Scores:
 Pred. No.: 123 Length: 1441
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0

Query Match: 5.63% Indels: 0
 DB: 3 Gaps: 0

US-09-690-825-34 (1-142) x AAC69515 (1-1441)

QY 1 MetGlyAlaProthLeuProPro 8
 |||||
 DB 1343 ATGGAGAGCCCCCACTCTCTCT 1366

RESULT 38
 ABS97149/c
 ID ABS97149 standard; DNA; 1469 BP.
 XX
 AC ABS97149;
 XX
 DT 23-DEC-2002 (first entry)
 XX
 DE Wild type human CYP450A1 gene.
 XX
 KW Human; ds; cytochrome P450 A1; CYP450A1; UGT2B4; MDR1;
 KW cytochrome P450 A2; CYP450A2; cytochrome P450 02E; CYP45002E1; LTF;
 KW adrenergic receptor beta1; ADRB1; aryl hydrocarbon; AHR; MRP3; NR112;
 KW aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;
 KW cyclooxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
 KW epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
 KW glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;
 KW HMMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NMMT;
 KW NADPH quinone oxidoreductase 2; NQO2; sulfoxidoreductase; STM;
 KW UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
 KW UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA;
 KW multidrug resistance 1; lactotransferrin; orphan nuclear receptor;
 KW multidrug resistance associated protein 3; cancer; prostate;
 KW acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;
 KW altered drug metabolism; cardiovascular function; colorectal tumour;
 KW central nervous system; pulmonary; immunological; SNP;
 KW single nucleotide polymorphism.
 XX
 OS Homo sapiens.
 XX
 PN MO200257410-A2.
 XX
 PD 25-JUL-2002.
 XX
 PF 28-NOV-2001; 2001MO-US044838.
 XX
 PR 28-NOV-2000; 2000US-00724389.
 XX
 PA (DNAS-) DNA SCI LAB INC.
 XX
 PI Guida M, Hall J;
 XX
 DR WPI; 2002-698522/75.
 XX
 PT Isolated nucleic acid molecules having polymorphisms in known human genes
 PT e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers
 PT for locating, identifying and characterizing the genes responsible for
 PT disorder-related traits.
 XX
 PS Example 1; Page 209; 714pp; English.
 XX
 CC This invention relates to the sequence of an isolated nucleic acid
 CC molecule comprising at least one base variation from that of a known
 CC human cytochrome P450 A1 (CYP450A1), cytochrome P450 A2 (CYP450A2),
 CC cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADRB1),
 CC aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator
 CC (ARNT), cathepsin S (CTSS), cyclooxygenase 2 (COX2), diazepam binding
 CC inhibitor (DBI), epoxide hydroxylase 2 (EPHX2), 5-lipoxygenase activating
 CC protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl
 CC transferase (HMMT), kallikrein 2 (KLK2), nicotinamide-N-methyl
 CC transferase (NMMT), NADPH quinone oxidoreductase 2 (NQO2),
 CC sulfoxidoreductase thermolabile (STM), UDP-glucuronosyl transferase 2B4
 CC (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl
 CC transferase (UGT2B15), urokinase receptor (uPA), multidrug resistance 1

```
CC (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3
CC (MRP3), orphan nuclear receptor (NR112), or acetylcholine muscarinic
CC receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.
CC The polymorphisms in the human genes cited in the invention are useful as
CC genetic linkage markers for locating and characterizing the genes that
CC are responsible for specific traits within the genome and eventually
CC identifying the genes responsible for a variety of disorder-related
CC traits as a result of their e.g., overexpression, constitutive
CC expression, mutation or underexpression, which may be used in diagnosing
CC and/or treating the disorders. The nucleic acid molecules comprising the
CC polymorphic sequences contained in CYP4501A1, CYP4501A2, CYP4502B1, AHR,
CC ARNT, EPH2, GST12, NNMT, NQO2, NR12, STM, UGT2B4, UGT2B15, AHR,
CC MDR1 and/or MDR3 are useful for screening individuals for altered drug
CC metabolism. The polymorphic sequences contained in CYP4501A1, CYP4501A2,
CC AHR, MDR1 and/or MDR3 may also be used to screen individuals for
CC susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are
CC used to screen for altered cardiovascular function, in COX2 for altered
CC susceptibility to colorectal tumors, in DBI or CHMR1 for altered central
CC nervous system function, in FLAP and HMT for altered pulmonary,
CC immunological or haematological function, in KIK2 for altered serine
CC protease activity in the prostate, in LTF for altered immunological or
CC haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and
CC peripheral nervous system function. The present sequence represents a
CC polymorphic DNA sequence of the invention
XX
SQ Sequence 1469 BP; 245 A; 497 C; 457 G; 270 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 126 Length: 1469
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.63% Indels: 0
Gaps: 0
DB: 6
US-09-690-825-34 (1-142) x ABS97149 (1-1469)
Oy 2 G1yAlaProThreProPron1a 9
Db 820 GAGGCCCCACCCTACCCCGGCT 797
XX
RESULT 39
AAZ43802
ID AAZ43802 standard; cDNA; 1493 BP.
XX
AC AAZ43802;
XX
DT 10-MAR-2000 (first entry)
XX
DE Human adult skin cDNA clone vcl_1.
XX
KW Human; secreted protein; treatment; nutritional activity; cytokine;
KW cell proliferation; cell differentiation; hematopoiesis regulation;
KW tissue growth; activin; inhibitor; chemoketic; chemoketic; hemostatic;
KW thrombolytic; anti-inflammatory; invasion suppressor; tumor inhibition;
KW gene therapy; ds.
XX
OS Homo sapiens.
XX
PN WO955721-A1.
XX
PD 04-NOV-1999.
XX
PF 23-APR-1999; 99WO-US008504.
XX
PR 24-APR-1998; 98US-0082904P.
PR 11-JUN-1998; 98US-0088994P.
PR 12-JUN-1998; 98US-0089278P.
PR 02-JUL-1998; 98US-0091647P.
PR 24-AUG-1998; 98US-0097639P.
PR 22-APR-1999; 99US-00097639.
XX
PA (ALPH-) ALPHAGENE INC.
XX
XX
XX Valenzuela D, Yuan O, Hoffman H, Hall J, Rapleyko F;
XX WPI; 2000-052801/04.
XX P-PSDB; AAY50939, AAY50940.
XX
XX New polynucleotides encoding secreted human proteins, derived from human
XX fetal brain, adult skin, adult brain, adult heart, adult thymus and adult
XX aorta cDNA libraries.
XX
XX Claim 60a; Page 252-253; 282pp; English.
XX
XX This invention describes novel human secreted proteins which are encoded
XX by polynucleotides obtained from fetal brain, adult skin, adult brain,
XX adult heart, adult thymus and adult aorta cDNA libraries. The
XX polynucleotides and proteins are predicted to have biological activities
XX which would make them suitable for treating, preventing or ameliorating
XX medical conditions in humans and animals. Although no supporting data is
XX given, suggested activities include nutritional activity, cytokine and
XX cell proliferation/differentiation activity, immune stimulating (e.g. as
XX vaccines) or suppressing activity, hematopoiesis regulating activity,
XX tissue growth activity, activin/inhibin activity,
XX chemotactic/chemokinetic activity, hemostatic and thrombolytic activity,
XX receptor/ligand activity, anti-inflammatory activity, cadherin/tumor
XX invasion suppressor activity, and tumor inhibition activity. The
XX polynucleotides are also stated to be useful for gene therapy. AAZ43777-
XX Z43808 represent the polynucleotides described in the invention which
XX encode the proteins represented in AAY50935-Y50947
XX
SQ Sequence 1493 BP; 429 A; 356 C; 492 G; 216 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 128 Length: 1493
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.63% Indels: 0
Gaps: 0
DB: 3
US-09-690-825-34 (1-142) x AAZ43802 (1-1493)
Oy 1 MetG1yAlaProThreProPro 8
Db 1312 ATGGAGCCCCCACCCTCCTCT 1335
XX
RESULT 40
AAZ437036
ID AAZ437036 standard; cDNA; 1733 BP.
XX
AC AAZ437036;
XX
DT 08-AUG-2000 (first entry)
XX
DE Human PRO1411 (UNQ729) cDNA sequence SEQ ID NO:51.
XX
KW Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
KW transmembrane; secretion; immunoadhesion; pharmaceutical; screening; ss.
XX
OS Homo sapiens.
XX
PN WO200012708-A2.
XX
PD 09-MAR-2000.
XX
PF 01-SEP-1999; 99WO-US020111.
XX
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098749P.
PR 01-SEP-1998; 98US-0098750P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0099536P.
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PR 09-SEP-1998; 98US-0099596P.
PR 09-SEP-1998; 98US-0099598P.
PR 09-SEP-1998; 98US-0099602P.
PR 09-SEP-1998; 98US-0099642P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099792P.
PR 10-SEP-1998; 98US-0099808P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98US-0099815P.
PR 10-SEP-1998; 98US-0099816P.
PR 15-SEP-1998; 98US-0100385P.
PR 15-SEP-1998; 98US-0100388P.
PR 15-SEP-1998; 98US-0100390P.
PR 16-SEP-1998; 98US-0100584P.
PR 16-SEP-1998; 98US-0100627P.
PR 16-SEP-1998; 98US-0100651P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100664P.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100710P.
PR 17-SEP-1998; 98US-0100711P.
PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.
PR 18-SEP-1998; 98US-0100848P.
PR 18-SEP-1998; 98US-0100849P.
PR 18-SEP-1998; 98US-0101014P.
PR 18-SEP-1998; 98US-0101068P.
PR 18-SEP-1998; 98US-0101071P.
PR 22-SEP-1998; 98US-0101279P.
PR 22-SEP-1998; 98US-0101471P.
PR 23-SEP-1998; 98US-0101472P.
PR 23-SEP-1998; 98US-0101474P.
PR 23-SEP-1998; 98US-0101475P.
PR 23-SEP-1998; 98US-0101476P.
PR 23-SEP-1998; 98US-0101477P.
PR 23-SEP-1998; 98US-0101479P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101741P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101915P.
PR 24-SEP-1998; 98US-0101916P.
PR 29-SEP-1998; 98US-0102070P.
PR 29-SEP-1998; 98US-0102240P.
PR 29-SEP-1998; 98US-0102307P.
PR 29-SEP-1998; 98US-0102330P.
PR 30-SEP-1998; 98US-0102331P.
PR 30-SEP-1998; 98US-0102484P.
PR 30-SEP-1998; 98US-0102487P.
PR 30-SEP-1998; 98US-0102570P.
PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.
PR 06-OCT-1998; 98US-0102965P.
PR 06-OCT-1998; 98US-0103258P.
PR 06-OCT-1998; 98US-0103449P.
PR 07-OCT-1998; 98US-0103314P.
PR 07-OCT-1998; 98US-0103315P.
PR 07-OCT-1998; 98US-0103328P.
PR 07-OCT-1998; 98US-0103355P.
PR 07-OCT-1998; 98US-0103396P.
PR 07-OCT-1998; 98US-0103401P.
PR 08-OCT-1998; 98US-0103633P.
PR 08-OCT-1998; 98US-0103678P.
PR 08-OCT-1998; 98US-0103679P.
PR 08-OCT-1998; 98US-0103711P.
PR 14-OCT-1998; 98US-0104257P.
PR 20-OCT-1998; 98US-0104987P.
PR 20-OCT-1998; 98US-0105000P.
PR 20-OCT-1998; 98US-0105002P.
PR 21-OCT-1998; 98US-0105104P.

PR 22-OCT-1998; 98US-0105169P.
PR 22-OCT-1998; 98US-0105266P.
PR 26-OCT-1998; 98US-0105693P.
PR 26-OCT-1998; 98US-0105694P.
PR 27-OCT-1998; 98US-0105807P.
PR 27-OCT-1998; 98US-0105811P.
PR 27-OCT-1998; 98US-0105822P.
PR 27-OCT-1998; 98US-0105823P.
PR 28-OCT-1998; 98US-0106023P.
PR 28-OCT-1998; 98US-0106029P.
PR 28-OCT-1998; 98US-0106030P.
PR 28-OCT-1998; 98US-0106032P.
PR 28-OCT-1998; 98US-0106033P.
PR 28-OCT-1998; 98US-0106178P.
PR 29-OCT-1998; 98US-0106248P.
PR 29-OCT-1998; 98US-0106384P.
PR 29-OCT-1998; 98US-0106500P.
PR 30-OCT-1998; 98US-0106464P.
PR 03-NOV-1998; 98US-0106856P.
PR 03-NOV-1998; 98US-0106902P.
PR 03-NOV-1998; 98US-0106905P.
PR 03-NOV-1998; 98US-0106919P.
PR 03-NOV-1998; 98US-0106932P.
PR 03-NOV-1998; 98US-0106934P.
PR 10-NOV-1998; 98US-0107783P.
PR 17-NOV-1998; 98US-0108275P.
PR 17-NOV-1998; 98US-0108779P.
PR 17-NOV-1998; 98US-0108787P.
PR 17-NOV-1998; 98US-0108788P.
PR 17-NOV-1998; 98US-0108801P.
PR 17-NOV-1998; 98US-0108802P.
PR 17-NOV-1998; 98US-0108806P.
PR 17-NOV-1998; 98US-0108807P.
PR 17-NOV-1998; 98US-0108867P.
PR 18-NOV-1998; 98US-0108925P.
PR 18-NOV-1998; 98US-0108848P.
PR 18-NOV-1998; 98US-0108849P.
PR 18-NOV-1998; 98US-0108850P.
PR 18-NOV-1998; 98US-0108851P.
PR 18-NOV-1998; 98US-0108852P.
PR 18-NOV-1998; 98US-0108858P.
PR 18-NOV-1998; 98US-0108904P.

(GRTH ) GENENTECH INC.
XX Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;
XX WPI, 2000-237871/20.
XX P-PSDB; AA99354.
XX New mammalian DNA sequences encoding transmembrane, receptor or secreted
XX PRO polypeptides, useful for screening of potential peptide or small
XX molecule inhibitors of the relevant receptor/ligand interactions.
XX
XX Claim 2, Fig 29; 773pp; English.
XX
XX AAA37022 to AAA37144 encode the new isolated human transmembrane,
XX receptor or secreted PRO polypeptides given in AA99340 to AA99462. The
XX transmembrane and receptor PRO proteins can be used for screening of
XX potential peptide or small molecule inhibitors of the relevant
XX receptor/ligand interactions. The polypeptides and nucleotide sequences
XX encoding them have various industrial applications, including uses as PCR
XX pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR
XX primers and hybridisation probes used in the isolation of the PRO
XX polypeptides from the present invention
XX
XX Sequence 1733 BP; 502 A; 397 C; 580 G; 254 T; 0 U; 0 Other;
XX
XX Alignment Scores: 147
XX Pred. No.: 8.00
XX Score: 100.00%
XX Percent Similarity: 100.00%
XX Best Local Similarity: 100.00%
XX Length: 1733
XX Matches: 8
XX Conservative: 0
XX Mismatches: 0

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Query Match: 5.63% Indels: 0
DB: 3 Gaps: 0
US-09-690-825-34 (1-142) x AAF54238 (1-1733)
CY 1 MetGlyAlaProThreProPro 8
DB 1534 ATGGAGCCCCCAGCTCCTCCT 1557

RESULT 41
ID AAF54238 standard; DNA; 1733 BP.
AC AAF54238;
XX
XX 02-APR-2001 (first entry)
DT
XX DNA encoding protein of the invention #15.
DE
XX Secreted; transmembrane; gene therapy; ss.
XX
XX Unidentified.
OS
XX MO200078961-A1.
XX
XX 28-DEC-2000.
XX
XX 18-FEB-2000; 2000MO-US004342.
XX
XX 23-JUN-1999; 99US-0141037P.
XX 20-JUL-1999; 99US-0144758P.
XX 26-JUL-1999; 99US-0145698P.
XX 01-SEP-1999; 99MO-US020111.
XX 29-OCT-1999; 99US-0162506P.
XX 30-NOV-1999; 99MO-US028313.
XX 02-DEC-1999; 99MO-US028551.
XX 16-DEC-1999; 99MO-US030095.
XX 05-JAN-2000; 2000MO-US000219.
XX 06-JAN-2000; 2000MO-US000376.
XX
XX (GETH) GENENTECH INC.
XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
XX Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
XX Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
XX Williams EM, Wood WI;
XX WPI; 2001-071395/08.
XX
XX Secreted and transmembrane proteins and nucleic acids designated PRO,
XX useful as hybridization probes, in chromosome and gene mapping and gene
XX therapy.
XX
XX Claim 2; Fig 29; 787pp; English.
XX
XX The present invention relates to secreted and transmembrane proteins.
XX These proteins and the DNA encoding them may be used as hybridization
XX probes, in chromosome and gene mapping and in the generation of anti-
XX sense RNA and DNA. They may also be used to generate either
XX transgenic animals or knockout animals which are in turn useful for
XX development and screening of therapeutically useful reagents. The nucleic
XX acids may also be used in gene therapy
XX
XX Sequence 1733 BP; 502 A; 397 C; 580 G; 254 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 147 Length: 1733
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.63% Indels: 0
DB: 4 Gaps: 0

US-09-690-825-34 (1-142) x AAF54238 (1-1733)
CY 1 MetGlyAlaProThreProPro 8
DB 1534 ATGGAGCCCCCAGCTCCTCCT 1557

RESULT 42
ID AAC87038 standard; cDNA; 1734 BP.
AC AAC87038;
XX
XX 20-APR-2001 (first entry)
DT
XX Nucleotide sequence of human polypeptide PRO1411.
XX
XX Human; secreted protein; transmembrane protein; PRO196; PRO444; PRO183;
XX PRO185; PRO210; PRO215; PRO217; PRO242; PRO288; PRO365; PRO1361; PRO1308;
XX PRO1183; PRO1272; PRO1419; PRO4999; PRO7170; PRO248; PRO353; PRO1318;
XX PRO1600; PRO9940; PRO533; PRO301; PRO187; PRO337; PRO1411; PRO4356;
XX PRO246; PRO265; PRO941; PRO10096; PRO6003; PRO6004; PRO350; PRO2630;
XX PRO6309; cell death; genetic disorder; transgenic animal; gene therapy;
XX ss.
XX
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX CDS 184..1506
XX FT /*tag= a
XX sig_peptide 184..246
XX FT /*tag= b
XX
XX MO200077037-A2.
XX
XX 21-DEC-2000.
XX
XX 22-MAY-2000; 2000MO-US014042.
XX
XX 15-JUN-1999; 99US-0139695P.
XX 20-JUL-1999; 99US-0145070P.
XX 26-JUL-1999; 99US-0145698P.
XX 17-AUG-1999; 99US-0149396P.
XX 01-SEP-1999; 99MO-US020111.
XX 08-SEP-1999; 99MO-US020594.
XX 15-SEP-1999; 99MO-US021090.
XX 15-SEP-1999; 99MO-US021547.
XX 30-NOV-1999; 99MO-US028313.
XX 01-DEC-1999; 99MO-US028301.
XX 02-DEC-1999; 99MO-US028565.
XX 07-DEC-1999; 99US-0169495P.
XX 05-JAN-2000; 2000MO-US000219.
XX 18-FEB-2000; 2000MO-US004341.
XX 18-FEB-2000; 2000MO-US004342.
XX 22-FEB-2000; 2000MO-US004414.
XX 01-MAR-2000; 2000MO-US005601.
XX 02-MAR-2000; 2000MO-US005841.
XX 20-MAR-2000; 2000MO-US007377.
XX 30-MAR-2000; 2000MO-US008439.
XX 15-MAY-2000; 2000MO-US013358.
XX 17-MAY-2000; 2000MO-US013705.
XX
XX (GETH) GENENTECH INC.
XX Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
XX Ferrara N, Fong S, Gao W, Garber H, Gerritsen ME, Goddard A;
XX Godowski PJ, Gurney AL, Kijavini JV, Mather JP, Napier MA, Pan J;
XX Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PJ;
XX Wood WI, Zhang Z;
XX WPI; 2001-050091/06.
XX P-FSDB; AAB31205.
XX
XX Isolated nucleic acid molecule encoding a PRO polypeptide which is a

transmembrane polypeptide is useful for gene therapy and identification of related polypeptides.

Claim 2; Fig 53; 24pp; English.

The present sequence encodes a human secreted and transmembrane polypeptide. The specification describes human polypeptides, designated PRO186, PRO444, PRO183, PRO185, PRO210, PRO215, PRO217, PRO242, PRO288, PRO365, PRO1361, PRO1308, PRO1183, PRO1272, PRO1419, PRO4999, PRO7170, PRO348, PRO353, PRO1318, PRO1600, PRO5940, PRO533, PRO301, PRO187, PRO337, PRO1411, PRO4356, PRO246, PRO265, PRO10996, PRO6003, PRO6004, PRO350, PRO2630 and PRO6309. The biological activity of cells can be modulated with agents that bind to these polypeptides, resulting in the death of the cells. The polynucleotides encoding these polypeptides are useful in the recombinant production of the polypeptides, as a hybridisation probe to screen libraries to isolate homologous sequences, or to map the gene. They may also be used for analysing genetic disorders, and to produce transgenic animals which are useful for the development and screening of therapeutically useful reagents. The polynucleotides can also be used in gene therapy e.g. to replace a defective gene.

Sequence 1734 BP; 503 A; 397 C; 580 G; 254 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	147	Length:	1734
Score:	8.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	5.63%	Indels:	0
DB:	4	Gaps:	0

US-09-690-825-34 (1-142) x AAC87038 (1-1734)

OY 1 MetGlyAlaProthrleuProPro 8

DB 1534 ATGGAGCCCCCAGCTCCTCTCT 1557

RESULT 43

AAS46025 ID AAS46025 standard; cDNA; 1734 BP.

XX AAS46025;

AC AAS46025;

XX AAS46025;

XX AAS46025;

XX AAS46025;

XX AAS46025;

XX AAS46025;

XX AAS46025;

XX AAS46025;

XX AAS46025;

XX AAS46025;

XX AAS46025;

XX AAS46025;

XX AAS46025;

XX AAS46025;

XX AAS46025;

XX AAS46025;

XX AAS46025;

XX AAS46025;

28-MAR-2000; 2000US-0192655P.
29-MAR-2000; 2000US-0193032P.
29-MAR-2000; 2000US-0193053P.
30-MAR-2000; 2000US-0194043P.
04-APR-2000; 2000US-0194449P.
04-APR-2000; 2000US-0194647P.
11-APR-2000; 2000US-0195975P.
11-APR-2000; 2000US-0196000P.
11-APR-2000; 2000US-0196187P.
11-APR-2000; 2000US-0196690P.
11-APR-2000; 2000US-0196820P.
18-APR-2000; 2000US-0198121P.
18-APR-2000; 2000US-0198585P.
25-APR-2000; 2000US-0199397P.
25-APR-2000; 2000US-0199509P.
25-APR-2000; 2000US-0199654P.
03-MAY-2000; 2000US-0201516P.
17-MAY-2000; 2000US-0201570S.
22-MAY-2000; 2000US-02014042.
30-MAY-2000; 2000US-02014941.
02-JUN-2000; 2000US-02015264.
05-JUN-2000; 2000US-0209832P.
26-JUN-2000; 2000US-02020710.
22-AUG-2000; 2000US-00544848.
24-AUG-2000; 2000US-02023328.
PR 08-NOV-2000; 2000US-02030952.
PR 01-DEC-2000; 2000US-02032678.
PR 20-DEC-2000; 2000US-02034956.

(GENTH) GENENTECH INC.

Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;

Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;

WPI; 2001-602746/68.

P-PSDB; AAU29124.

XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the

PT presence of tumors, such as prostate and breast tumors, in mammals and to

PT screen for modulators of the compounds.

XX Claim 2; Fig 201; 774pp; English.

Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR primers for PRO polypeptides of the invention. The sequences of the invention can be used to detect the presence of a tumour in a mammal by comparing the level of expression of a PRO polypeptide in a test sample of cells from the animal and a control sample of normal cells, whereby a higher level of expression in the test sample indicates the presence of a tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats and rabbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor (TNF) alpha release from human blood. When contacted with it, a specific polypeptide can be used to stimulate the proliferation or differentiation of chondrocyte cells. The PRO proteins can be used to determine the presence of tumours and also susceptibility to tumour development, particularly adrenal, lung, colon, breast, prostate, rectal, cervical, or liver tumours, in mammalian subjects. The oligonucleotide probes specific for the PRO nucleic acids can be used for genetic analysis of individuals with genetic disorders

Alignment Scores:

Pred. No.:	147	Length:	1734
Score:	8.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	5.63%	Indels:	0
DB:	4	Gaps:	0

US-09-690-825-34 (1-142) x AAS46025 (1-1734)

OY 1 MetGlyAlaProthrleuProPro 8

Db 1534 ATGGAGCCCCCACACTCCTCCT 1557

RESULT 44

AAF92083

AAF92083

15-MAY-2001 (first entry)

Human PRO:411 cDNA.

Human; PRO protein; mapping; ss.

Homo sapiens.

WO200116318-A2.

08-MAR-2001.

24-AUG-2000; 2000WO-US023328.

01-SEP-1999; 99WO-US020111.

15-SEP-1999; 99WO-US021030.

07-DEC-1999; 99US-0169495P.

09-DEC-1999; 99US-0170262P.

11-JAN-2000; 2000US-0175481P.

18-FEB-2000; 2000WO-US004341.

18-FEB-2000; 2000WO-US004342.

22-FEB-2000; 2000WO-US004343.

01-MAR-2000; 2000WO-US005601.

21-MAR-2000; 2000US-0187107P.

30-MAR-2000; 2000WO-US008439.

25-APR-2000; 2000US-0199397P.

22-MAY-2000; 2000WO-US014042.

05-JUN-2000; 2000US-0209832P.

(GETH) GENENTECH INC.

Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ,

Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;

WPI; 2001-183260/18.

P-PSDB; AAB87551.

Eighty four nucleic acids encoding PRO polypeptides, useful in molecular

biology, including use as hybridization probes, and in chromosome and

gene mapping.

Claim 2; Fig 51; 278pp; English.

The present sequence is the coding sequence for a human PRO polypeptide

(secreted and transmembrane). The PRO protein, and PRO agonists, PRO

antagonists or anti-PRO antibodies are useful for preparation of a

medicament useful in the treatment of a condition which is responsive to

the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO

protein may also be employed as molecular weight markers for protein

electrophoresis. The PRO coding sequence has applications in molecular

biology, including use as hybridisation probes, and in chromosome and

gene mapping

Sequence 1734 BP; 503 A; 397 C; 580 G; 254 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 147

Score: 8.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 5.63%

DB: 4

Length: 1734

Matches: 8

Conservative: 0

Mismatches: 0

Indels: 0

Gaps: 0

US-09-690-825-34 (1-142) x AAF92083 (1-1734)

Qy 1 MetGlyAlaProThrLeuProPro 8

Db 1534 ATGGAGCCCCCACACTCCTCCT 1557

RESULT 45

ABK33613

ABK33613

08-MAY-2002 (first entry)

CDNA encoding human PRO protein, Seq ID No 155.

Human; secreted protein; PRO; tumour; lung cancer; colon cancer;

breast cancer; prostate tumour; rectal tumour; liver tumour;

pericyte cell proliferation; chondrocyte cell proliferation;

tumour necrosis factor-alpha; gene; ss.

Homo sapiens.

WO200208288-A2.

31-JAN-2002.

29-JUN-2001; 2001WO-US021066.

20-JUL-2000; 2000US-0219556P.

25-JUL-2000; 2000US-0220585P.

25-JUL-2000; 2000US-0220605P.

25-JUL-2000; 2000US-0220607P.

25-JUL-2000; 2000US-0220624P.

25-JUL-2000; 2000US-0220638P.

25-JUL-2000; 2000US-0220664P.

25-JUL-2000; 2000US-0220666P.

26-JUL-2000; 2000US-0220839P.

28-JUL-2000; 2000WO-US020710.

01-AUG-2000; 2000US-0222425P.

22-AUG-2000; 2000US-0227133P.

23-AUG-2000; 2000WO-US023522.

24-AUG-2000; 2000WO-US023328.

10-NOV-2000; 2000WO-US030873.

28-NOV-2000; 2000US-0253646P.

01-DEC-2000; 2000WO-US032678.

20-DEC-2000; 2000US-00747259.

20-DEC-2000; 2000WO-US034956.

28-FEB-2001; 2001WO-US006520.

01-MAR-2001; 2001WO-US006666.

22-MAR-2001; 2001US-00816744.

10-MAY-2001; 2001US-00854208.

10-MAY-2001; 2001US-00854280.

25-MAY-2001; 2001WO-US017092.

(GETH) GENENTECH INC.

Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;

Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;

WPI; 2002-172001/22.

P-PSDB; AAB83669.

One hundred and twenty two nucleic acids encoding PRO polypeptides,

useful for treating a PRO related disorder and for diagnosing tumors such

as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor

or liver tumor.

Claim 2; Fig 155; 359pp; English.

The invention relates to one hundred and twenty two nucleic acids

encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides

encode human secreted proteins. The PRO nucleic acids, polypeptides,

CC agonists and antagonists are useful for treating a PRO related disorder.
CC The PRO polypeptides are useful for diagnosing tumours, especially lung
CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
CC liver tumour. The PRO polypeptides are useful for stimulating the
CC proliferation of, or gene expression, in pericyte cells, for stimulating
CC the proliferation or differentiation of chondrocyte cells, for
CC stimulating the release of tumour necrosis factor-alpha from human blood,
CC for stimulating or inhibiting the proliferation of normal human dermal
CC fibroblast cells. The PRO polypeptide may also be used as molecular
CC weight markers and for tissue typing. The PRO nucleic acids have
CC applications in molecular biology, including use as hybridisation probes,
CC and in chromosome and gene mapping. ABK3536-ABK3657 represent human PRO
CC protein coding sequences of the invention
XX
SQ Sequence 1734 BP; 503 A; 397 C; 580 G; 254 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 147 Length: 1734
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.63% Indels: 0
DB: 6 Gaps: 0

US-09-690-825-34 (1-142) x ABK3536 (1-1734)
QY 1 MetGlyAlaProThreupPro 8
Db 1534 ATGGAGCCGCCACACTCCCTCCT 1557

RESULT 46
ABK74403
ID ABK74403 standard; CDNA; 1734 BP.
AC ABK74403;
XX
XX 10-DEC-2002 (first entry)
DT
XX Human cDNA encoding secreted/transmembrane protein PRO1411.
DE
XX
XX Human; ss; gene; secreted protein; transmembrane protein; antirheumatic;
KM antiarthritic; osteopathic; sports-related joint problem;
KM articular cartilage defect; osteoarthritis; rheumatoid arthritis.
XX
OS Homo sapiens.
XX
XX US2002119130-A1.
PN
XX 29-AUG-2002.
PD
XX
PF 06-DEC-2001; 2001US-00006867.
XX
XX 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0064215P.
PR 22-APR-1998; 98US-0082797P.
PR 29-APR-1998; 98US-0083495P.
PR 15-MAY-1998; 98US-0085579P.
PR 02-JUN-1998; 98US-0087759P.
PR 04-JUN-1998; 98US-0088621P.
PR 04-JUN-1998; 98US-0088629P.
PR 04-JUN-1998; 98US-0088630P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088740P.
PR 10-JUN-1998; 98US-0088811P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088825P.
PR 11-JUN-1998; 98US-0088833P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089653P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090346P.
PR 24-JUN-1998; 98US-0090444P.

PR 25-JUN-1998; 98US-0090688P.
PR 25-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-0090862P.
PR 02-JUL-1998; 98US-0091628P.
PR 10-AUG-1998; 98US-0096012P.
PR 17-AUG-1998; 98US-0096757P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096959P.
PR 25-AUG-1998; 98US-0097654P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097979P.
PR 01-SEP-1998; 98US-0098749P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099792P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98US-0099815P.
PR 16-SEP-1998; 98US-0100627P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100683P.
PR 16-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100930P.
PR 22-SEP-1998; 98US-0101279P.
PR 23-SEP-1998; 98US-0101475P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101916P.
PR 30-SEP-1998; 98US-0102570P.
PR 06-OCT-1998; 98US-0103449P.
PR 08-MAR-1999; 99MO-US005028.
PR 14-MAY-1999; 99MO-US010733.
PR 02-JUN-1999; 99MO-US012252.
PR 01-SEP-1999; 99MO-US020111.
PR 15-SEP-1999; 99MO-US021090.
PR 15-SEP-1999; 99MO-US021194.
PR 22-DEC-1999; 99MO-US030720.
PR 18-FEB-2000; 2000MO-US004341.
PR 18-FEB-2000; 2000MO-US004342.
PR 22-FEB-2000; 2000MO-US004414.
PR 01-MAR-2000; 2000MO-US005601.
PR 30-MAR-2000; 2000MO-US008439.
PR 22-MAY-2000; 2000MO-US014042.
PR 02-JUN-2000; 2000MO-US015264.
PR 23-AUG-2000; 2000MO-US023522.
PR 24-AUG-2000; 2000MO-US023528.
PR 10-NOV-2000; 2000MO-US030873.
PR 01-DEC-2000; 2000MO-US033378.
PR 20-DEC-2000; 2000MO-US034956.
PR 28-FEB-2001; 2001MO-US006520.
PR 01-MAR-2001; 2001MO-US006666.
PR 30-MAY-2001; 2001MO-US017443.
PR 01-JUN-2001; 2001MO-US017800.
PR 20-JUN-2001; 2001MO-US016992.
PR 29-JUN-2001; 2001MO-US021066.
PR 09-JUL-2001; 2001MO-US021735.
XX
XX (GENTH) GENENTECH INC.
XX
XX Baton DL, Filvarcoff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
XX WPI: 2002-731348/79.
DR P-PSDB; ABG95876.
XX
XX New isolated secreted and transmembrane PRO polypeptide useful for
PT modulating biological activity of a cell, or for treating sports-related
PT joint problems, osteoarthritis or rheumatoid arthritis.
XX
XX Claim 2; Fig 51; 399pp; English.
XX
XX The invention relates to an isolated secreted and transmembrane PRO
CC polypeptide having 80 % sequence identity to a sequence appearing as

ABG95851-ABG95934 or their associated signal peptide, or a sequence of an extracellular domain of the proteins with their associated signal peptide or lacking its associated signal peptide. Also included are the nucleic acids encoding the proteins, vectors, host cells, fusion proteins and antibodies which specifically bind to the proteins. The proteins are useful for detecting a polypeptide designated as A, B, C or D in a sample suspected of containing an A, B, C or D polypeptide, by contacting the sample with a polypeptide designated as E, F, G, H or I (or vice versa) and determining the formation of A/E, B/F, G/G, C/H or D/I polypeptide conjugate in the sample, where the formation of the conjugate is indicative of the presence of an A, B, C or D polypeptide in the sample, where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO05601 polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G, H or I polypeptide is labeled with a detectable label or is attached to a solid support. The proteins are useful for linking a bioactive molecule to a cell expressing a polypeptide designated as A, B, C or D or E, F, G, H or I. The bioactive molecule is a toxin, a radiolabel or an antibody. The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H, or I, or antibodies against them are useful for modulating a biological activity of a cell expressing a polypeptide designated as A, B, C or D or E, F, G, H, or I. The cell is killed. The proteins are useful for identifying agonists or antagonists, for the preparation of a medicament useful in the treatment of a condition which is responsive to the proteins, as molecular weight markers for protein electrophoresis purposes, and as therapeutic agents for treating sports-related joint problems, articular cartilage defects, osteoarthritis or rheumatoid arthritis. Nucleic acids encoding the proteins are useful as hybridisation probes, in chromosome and gene mapping, in the generation of anti-sense RNA and DNA, for the preparation of the proteins, to generate transgenic or knockout animals which are useful in the development and screening of therapeutic useful reagents, for chromosome identification, and in gene therapy. The antibody is useful as a therapeutic agent, in a diagnostic assay and for affinity purification of the protein from recombinant cell culture natural sources. The present sequence encodes a novel secreted or transmembrane protein of the invention.

SEQ Sequence 1734 BP; 503 A; 397 C; 580 G; 254 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	147	Length:	1734
Score:	8.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	5.63%	Indels:	0
DB:	6	Gaps:	0

US-09-690-825-34 (1-142) * ABG74403 (1-1734)

QY 1 MetGlyAlaProThLeuProPro 8
1534 ATGGAGCCCCCAGCTCCCTCCT 1557

RESULT 47
ABL95635
ID ABL95635 standard; cDNA; 1734 BP.
XX
AC ABL95635;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human angiogenesis related cDNA PRO1411 SEQ ID NO: 149.
XX
KM Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
KM atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KM cardiatic; cytostatic; antiangiogenic; hypotensive; vulnerary;
KM antiarteriosclerotic; gene; ss.
XX
OS Homo sapiens.
XX

PN WO200208284-A2.
XX
PD 31-JAN-2002.
XX
PF 09-JUL-2001; 2001WO-US021735.
XX
PR 20-JUL-2000; 2000US-0219556P.
PR 25-JUL-2000; 2000US-0220624P.
PR 25-JUL-2000; 2000US-0220646P.
PR 28-JUL-2000; 2000WO-US020710.
PR 02-AUG-2000; 2000US-0222695P.
PR 17-AUG-2000; 2000US-00643657.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 07-SEP-2000; 2000US-0230978P.
PR 18-SEP-2000; 2000US-0064610.
PR 16-SEP-2000; 2000US-00665350.
PR 24-OCT-2000; 2000US-0242922P.
PR 08-NOV-2000; 2000US-00709238.
PR 10-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 22-JAN-2001; 2001US-00767609.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 30-MAY-2001; 2001US-00870574.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
XX
XX (CETH) GENENTECH INC.
XX (BAKE) BAKER K P.
XX (FERA) FERRARA N.
XX (GERB) GERBER H.
XX (GERR) GERRITSEN M E.
XX (GODD) GODDARD A.
XX (GODD) GODDARD P J.
XX (GURN) GURNEY A L.
XX (HILL) HILLAN K J.
XX (MARS) MARSTERS S A.
XX (PANT) PAN J.
XX (PAON) PAONI N F.
XX (SREP) STEPHAN J F.
XX (WATA) WATANABE C K.
XX (WILL) WILLIAMS P M.
XX (WOOD) WOOD W I.
XX
XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,
XX Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,
XX Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W,
XX WPI, 2002-171999/22.
XX P-PDS; ABB95497.
XX
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
XX useful in diagnosis and treatment of cardiovascular (e.g. myocardial
XX infarction), endothelial or angiogenic disorders in a mammal.
XX Claim 1, Fig 149; 567pp; English.
XX
XX The present invention provides the protein and coding sequences of human

CC PRO proteins. These are useful for treating or diagnosing a
CC cardiovascular, endometrial or angiogenic disorder, including cardiac
CC hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The present sequence is a coding sequence of the invention
XX

Sequence 1734 BP, 503 A, 397 C, 580 G, 254 T, 0 U, 0 Other;

Alignment Scores:

Pred. No.:	147	Length:	1734
Score:	8.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best local Similarity:	100.00%	Mismatches:	0
Query Match:	5.63%	Indels:	0
DB:	6	Gaps:	0

US-09-690-825-34 (1-142) x ABL95635 (1-1734)

Oy 1 MetGlyAlaProthrinProPro 8

Db 1534 ATGGAGCCCCCACCTCCTCT 1557

RESULT 48

ABX78628

ID ABX78628 standard; cDNA; 1734 BP.

XX

AC ABX78628;

XX

DT 15-APR-2003 (first entry)

XX

DE Human PRO polynucleotide #101.

XX

XX Human: PRO; gene; ss; cytosolic; tumour; cancer; breast; lung; stomach;
KM liver; dog; cat; cow; horse; sheep; pig; goat; rabbit; ADBPT;
KM antibody-dependent enzyme mediated prodng therapy.

XX

OS Homo sapiens.

XX

PN US2003027272-A1.

XX

PD 06-FEB-2003.

XX

PF 21-JUN-2002; 2002US-00176492.

XX

PR 18-SEP-1997; 97US-0059263P.

PR 18-SEP-1997; 97US-0059266P.

PR 17-OCT-1997; 97US-0062250P.

PR 21-OCT-1997; 97US-0063486P.

PR 24-OCT-1997; 97US-0063120P.

PR 24-OCT-1997; 97US-0063121P.

PR 28-OCT-1997; 97US-0063540P.

PR 28-OCT-1997; 97US-0063541P.

PR 28-OCT-1997; 97US-0063544P.

PR 28-OCT-1997; 97US-0063564P.

PR 29-OCT-1997; 97US-0063734P.

PR 31-OCT-1997; 97US-0063707P.

PR 31-OCT-1997; 97US-0064103P.

PR 13-NOV-1997; 97US-0065111P.

PR 21-NOV-1997; 97US-0066120P.

PR 24-NOV-1997; 97US-0066466P.

PR 24-NOV-1997; 97US-0066772P.

PR 11-DEC-1997; 97US-0069335P.

PR 12-DEC-1997; 97US-0069425P.

PR 17-DEC-1997; 97US-0069670P.

PR 18-DEC-1997; 97US-0068017P.

PR 10-MAR-1998; 98US-0077450P.

PR 11-MAR-1998; 98US-0077632P.

PR 11-MAR-1998; 98US-0077649P.

PR 20-MAR-1998; 98US-0078865P.

PR 20-MAR-1998; 98US-0078935P.

PR 27-MAR-1998; 98US-0079664P.

PR 27-MAR-1998; 98US-0079786P.

PR 31-MAR-1998; 98US-0080107P.

PR 01-APR-1998; 98US-0080194P.

PR 01-APR-1998; 98US-0080337P.

PR 08-APR-1998; 98US-0080333P.

PR 08-APR-1998; 98US-0081049P.

PR 08-APR-1998; 98US-0081070P.

PR 09-APR-1998; 98US-0081195P.

PR 15-APR-1998; 98US-0081838P.

PR 21-APR-1998; 98US-0082568P.

PR 21-APR-1998; 98US-0082569P.

PR 22-APR-1998; 98US-0082704P.

PR 22-APR-1998; 98US-0082797P.

PR 28-APR-1998; 98US-0083172P.

PR 29-APR-1998; 98US-0083455P.

PR 29-APR-1998; 98US-0083496P.

PR 29-APR-1998; 98US-0083499P.

PR 29-APR-1998; 98US-0083559P.

PR 29-APR-1998; 98US-0083566P.

PR 05-MAY-1998; 98US-0084366P.

PR 06-MAY-1998; 98US-0084414P.

PR 07-MAY-1998; 98US-0084639P.

PR 07-MAY-1998; 98US-0084640P.

PR 07-MAY-1998; 98US-0084643P.

PR 15-MAY-1998; 98US-0085579P.

PR 15-MAY-1998; 98US-0085580P.

PR 15-MAY-1998; 98US-0085582P.

PR 15-MAY-1998; 98US-0085700P.

PR 18-MAY-1998; 98US-0086023P.

PR 22-MAY-1998; 98US-0086392P.

PR 22-MAY-1998; 98US-0086486P.

PR 28-MAY-1998; 98US-0087098P.

PR 28-MAY-1998; 98US-0087208P.

PR 02-JUN-1998; 98US-0087609P.

PR 02-JUN-1998; 98US-0087759P.

PR 03-JUN-1998; 98US-0087827P.

PR 04-JUN-1998; 98US-0088025P.

PR 04-JUN-1998; 98US-0088028P.

PR 04-JUN-1998; 98US-0088029P.

PR 04-JUN-1998; 98US-0088033P.

PR 04-JUN-1998; 98US-0088326P.

PR 05-JUN-1998; 98US-0088167P.

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PR 05-JUN-1998; 98US-0088217P.

PR 09-JUN-1998; 98US-0088655P.

PR 10-JUN-1998; 98US-0088722P.

PR 10-JUN-1998; 98US-0088738P.

PR 10-JUN-1998; 98US-0088811P.

PR 10-JUN-1998; 98US-0088824P.

PR 10-JUN-1998; 98US-0088825P.

PR 10-JUN-1998; 98US-0088826P.

PR 11-JUN-1998; 98US-0088861P.

PR 11-JUN-1998; 98US-0088863P.

PR 11-JUN-1998; 98US-0088876P.

PR 12-JUN-1998; 98US-0089090P.

PR 12-JUN-1998; 98US-0089105P.

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PR 16-JUN-1998; 98US-0089514P.

PR 17-JUN-1998; 98US-0089518P.

PR 17-JUN-1998; 98US-0089598P.

PR 17-JUN-1998; 98US-0089653P.

PR 18-JUN-1998; 98US-0089658P.

PR 18-JUN-1998; 98US-0089908P.

PR 19-JUN-1998; 98US-0089952P.

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PR 22-JUN-1998; 98US-0090252P.

PR 22-JUN-1998; 98US-0090254P.

PR 24-JUN-1998; 98US-0090429P.

PR 24-JUN-1998; 98US-0090435P.

PR 24-JUN-1998; 98US-0090444P.

PR 24-JUN-1998; 98US-0090461P.

PR 24-JUN-1998; 98US-0090535P.

PR 24-JUN-1998; 98US-0090540P.

```
PR 25-JUN-1998; 98US-0090676P.
PR 25-JUN-1998; 98US-0090678P.
PR 25-JUN-1998; 98US-0090688P.
PR 25-JUN-1998; 98US-0090690P.
PR 25-JUN-1998; 98US-0090694P.
PR 25-JUN-1998; 98US-0090695P.
PR 25-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-00105413.
PR 26-JUN-1998; 98US-0090862P.
PR 26-JUN-1998; 98US-0090863P.
PR 26-JUN-1998; 98US-0091010P.
PR 01-JUL-1998; 98US-0091359P.
PR 01-JUL-1998; 98US-0091544P.
PR 02-JUL-1998; 98US-0091478P.
PR 02-JUL-1998; 98US-0091486P.
PR 02-JUL-1998; 98US-0091626P.
PR 02-JUL-1998; 98US-0091628P.
PR 02-JUL-1998; 98US-0091632P.
PR 24-JUL-1998; 98US-0094006P.
PR 04-AUG-1998; 98US-0095282P.
PR 10-AUG-1998; 98US-0095988P.
PR 10-AUG-1998; 98US-0096012P.
PR 17-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096766P.
PR 17-AUG-1998; 98US-0096867P.
PR 17-AUG-1998; 98US-0096891P.
PR 17-AUG-1998; 98US-0096897P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096955P.
PR 18-AUG-1998; 98US-0097022P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0098014P.
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0099602P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099812P.
PR 15-SEP-1998; 98US-0100388P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100664P.
PR 16-SEP-1998; 98US-0101751P.
PR 16-SEP-1998; 98US-01019330.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.
PR 18-SEP-1998; 98US-0100849P.
PR 18-SEP-1998; 98US-0101014P.
PR 18-SEP-1998; 98US-0101068P.
PR 23-SEP-1998; 98US-0101471P.
PR 23-SEP-1998; 98US-0101472P.
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QY 1 MetGlyAlaProThrLeuPro 8
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DT 07-JUL-2003 (first entry)
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KW tumour necrosis factor-alpha release; TNF-alpha release;
KW chondrocyte proliferation; chondrocyte differentiation; tumour;
KW adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour; gene; ss.
XX Homo sapiens.
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Alignment Scores:

Pred. No.:	147	Length:	1734
Score:	8.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
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US-09-690-825-34 (1-142) x ACA75600 (1-1734)

QY 1 MetGlyAlaProThrLeuPro 8

Db 1534 ATGGAGCCCCCACATCTCTCT 1557

RESULT 50

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ID ACA71080 standard; cDNA; 1734 BP.

AC ACA71080;

XX 02-AUG-2003 (first entry)

DE Human secreted/transmembrane protein (PRO) cDNA #101.

XX Human; Gene; ss; secreted and transmembrane protein; PRO; TNF-alpha;
 KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
 KW tissue typing.

XX Homo sapiens.

XX US2003032112-A1.

XX 13-FEB-2003.

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Alignment Scores:
Pred. No.: 147
Score: 8.00
Percent Similarity: 100.00%
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DB 1534 ATGGGAGCCCCACACTCCCTCT 1557

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KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnery; gene therapy; gene; ss.
OS Homo sapiens.
XX
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KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnary; gene therapy; gene; ss.
XX OS
XX Homo sapiens.
XX XX
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KW chromosome mapping; gene mapping; cytostatic; gene therapy; gene; ss.

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XX PN US2003032113-A1.

XX PD 13-FEB-2003.

XX PF 20-JUN-2002; 2002US-00176911.

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KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnery; gene therapy; gene; ss.
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XX chondrocyte proliferation; chondrocyte differentiation;
XX tumor necrosis factor-alpha release stimulator; gene; ss.
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DT 18-JUL-2003 (first entry)
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DE Human secreted/transmembrane protein (PRO) cDNA #101.
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KW Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;
KW proliferation; differentiation; chondrocyte cell; TNF-alpha;
KW tumour necrosis factor-alpha; gene therapy.
XX
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XX
PD 20-FEB-2003.
XX
PF 02-JUL-2002; 2002US-00187746.
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RESULT 60

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AC ACA66918;
XX 23-JUN-2003 (first entry)
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DE Human; PRO polypeptide; secreted and transmembrane protein;
KW anti-PRO antibody; diagnostic assay; gene expression; tumour; cytostatic;
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XX Homo sapiens.
XX US2003036635-A1.
XX 20-FEB-2003.
XX 28-AUG-2002; 2002US-00230163.
XX 25-JUL-2000; 2000US-0220638P.
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PR 29-JUN-2001; 2001WO-US021066.
PR 09-APR-2002; 2002US-00119480.
XX (GETH ) GENENTECH INC.
XX Baker KP, Deenoyers L, Gerritsen WE, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX WPI; 2003-342045/32.
DR P-PSDB; ABU80816.
XX One hundred and twenty two nucleic acids encoding PRO polypeptides.
PT useful for the manufacture of a medicament for diagnosing or treating
PT tumor.
XX Claim 2; Fig 155; 314pp; English.
XX The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides and polynucleotides are useful for preparing a medicament
CC useful in the diagnosis and treatment of tumours. Anti-PRO antibodies are
CC useful in diagnostic assays for PRO, by detecting its expression in
CC specific cells, tissues or serum, and for affinity purification of PRO
CC from recombinant cell culture or natural sources. ACA66918-ACA66962
CC represent cDNA sequences encoding the human PRO polypeptides of the
CC invention. Note: The sequence data for this patent was obtained in
CC electronic format directly from the USPTO web site at
CC seqdata.uspto.gov/paipsdIDentry.html
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Alignment Scores:
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Conservative: 0
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ID ACD08863 standard; cDNA; 1734 BP.

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XX tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
XX tissue typing; adrenal tumour; lung tumour; colon tumour; breast tumour;
XX prostate tumour; rectal tumour; cervical tumour; liver tumour.
XX Homo sapiens.
XX US2003040062-A1.
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US-09-690-825-34 (1-142) x ACD08863 (1-1734)

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KW immune response; inflammation; mononuclear cell infiltration;
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PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US008520.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 15-NOV-2001; 2001US-00002796.
XX
XX (GETH) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL,
PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A,
PI Godowski PJ, Gurney AL, Kljavin LJ, Mather JP, Napier MA, Pan J,
PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM,
PI Wood WI, Zhang Z;
XX
XX WPI; 2003-503396/47.
XX P-PSDB; ABO25176.
XX
XX New secreted and transmembrane PRO polypeptides, useful for treating
PT diabetes, retinal disorders and stimulating an immune response.
XX
XX Claim 2; Fig 53; 254pp; English.
XX
XX The invention describes an isolated polypeptide (1) having at least 80 %
CC amino acid sequence identity to 30 secreted and transmembrane
CC polypeptides. PRO polypeptides are also useful for stimulating
CC hypertrophy of adult heart, for inhibiting vascular endothelial growth
CC factor stimulated proliferation of endothelial cells, stimulating
CC proliferation of stimulated T-lymphocytes and for inducing proliferation
CC of PD812 pancreatic ductal cells and are thus useful in the treatment of
CC disorders which involve protein secretion by the pancreas, including
CC diabetes. PRO polypeptides are useful for inducing vascular permeability
CC and in enhancing survival of retinal neurons cells and are thus useful
CC for the treatment of retinal disorders. PRO polypeptides are also useful
CC for stimulating an immune response and inducing inflammation by inducing
CC mononuclear cell and eosinophil infiltration at the site of infection of
CC an animal. The PRO polypeptides are further useful for inducing apoptosis
CC in endothelial cells for inhibiting neoplastic growth. This sequence
CC encodes a novel human secreted and transmembrane PRO polypeptide
XX
XX Sequence 1734 BP; 503 A; 397 C; 580 G; 254 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 147 Length: 1734
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.63% Indels: 0
DB: 7 Gaps: 0
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QY 1 MetGlyAlaProThrLeuProPro 8
DB 1534 ATGGAGGCCCCACACTCCCTCCT 1557
RESULT 65
ACD68670
ID ACD68670 standard; cDNA; 1734 BP.
XX

ACD68670;
17-SEP-2003 (first entry)
Novel human secreted and transmembrane protein PRO1411 cDNA.
Human; secreted and transmembrane protein; PRO; cytostatic;
antiarthritic; osteopathic; gene therapy; TNF-Agonist-Alpha;
chondrocyte stimulator; pericyte stimulator; fibroblast modulator;
pharmaceutical; diagnostic; biosensor; bio-reactor; lung tumour;
colon tumour; breast tumour; prostate tumour; rectal tumour;
liver tumour; bone disorder; cartilage disorder; sports injury;
arthritis; wound; gene; ss.
Homo sapiens.
US2003045687-A1.
06-MAR-2003.
12-AUG-2002; 2002US-00218631.
01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
(GETH) GENENTECH INC.
Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ,
Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
WPI; 2003-512315/48.
P-PSDB; ABO33782.
New genes, and its encoded secreted and transmembrane polypeptides,
useful for stimulating Tumor Necrosis Factor alpha, or chondrocyte or
pericyte proliferation, especially for treating lung tumors, arthritis or
wounds in a mammal.
Claim 2; Fig 155; 314pp; English.
The invention describes an isolated nucleic acid molecule comprising a
sequence with at least 80% identity to: (a) a nucleotide encoding any of
122 PRO (secreted and transmembrane) polypeptides whose sequences are
fully defined in the specification; or (b) any of 122 nucleotide
sequences having e.g. 4834, 2504 or 1759 bp fully defined in the
specification; or the full length coding sequence of any these 122
nucleotide sequences. The PRO polypeptides or polynucleotides are useful
as pharmaceuticals, diagnostics, biosensors or bioreactors. These are
particularly useful for detecting tumors (e.g. lung tumour, colon
tumour, breast tumour, prostate tumour, rectal tumour, or liver tumour)
in a mammal, for stimulating the release of TNF-alpha from human blood,
for stimulating the proliferation or differentiation of chondrocyte
cells, for stimulating proliferation of pericyte cells, or for modulating
normal human dermal fibroblast proliferation. The PRO nucleic acid or
polypeptide is also useful for treating tumors or various bone and/or
cartilage disorders (e.g. sports injuries or arthritis), or wounds. The
PRO polypeptides are useful in drug screening, particularly as targets
for therapeutic intervention in these diseases, and in the diagnostic
determination of the presence of these diseases. The PRO polypeptides are
also useful as molecular weight markers, or for chromosome
identification. The PRO genes are useful as hybridisation probes, or for
screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may
also be used in gene therapy, particularly for replacing a defective
gene. This sequence encodes a novel human secreted and transmembrane PRO
polypeptide
SQ Sequence 1734 BP; 503 A; 397 C; 580 G; 254 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 147 Length: 1734
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.63% Indels: 0
DB: 7 Gaps: 0
US-09-690-825-34 (1-142) x ACD68670 (1-1734)
Qy 1 MetGlyValapProThreLeuProPro 8
Db 1534 ATGGGAGCCCCCACACTCCCTCT 1557
RESULT 66
ACA72871
ID ACA72871 standard; cDNA; 1734 BP.
XX
XX ACA72871;
AC
XX
DT 02-JUL-2003 (first entry)
XX
DE Human PRO polynucleotide #101.
XX
KW Human; PRO; Gene; ss; secreted polypeptide; transmembrane polypeptide;
tumour necrosis factor alpha; TNF-alpha; chondrocyte cell; tumour;
cytostatic.
KW
XX
OS Homo sapiens.
XX
PN US2003036140-A1.
XX
PD 20-FEB-2003.
XX
PF 01-JUL-2002; 2002US-00187588.
XX
XX 26-JUN-1998; 98US-00105413.
PR 16-SEP-1998; 98WO-US019330.
PR 07-OCT-1998; 98US-00168978.
PR 06-OCT-1998; 98WO-US021141.
PR 06-NOV-1998; 98US-00187388.
PR 01-DEC-1998; 98WO-US025108.
PR 07-DEC-1998; 98US-00202054.
PR 03-MAR-1999; 99US-00254311.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 25-AUG-1999; 99US-00380142.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99US-00423844.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028551.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 22-AUG-2000; 2000US-0064848.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.

PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-03908827.
PR 30-JUL-2001; 2001US-03918588.
PR 06-AUG-2001; 2001US-03924419.
PR 13-AUG-2001; 2001US-00929404.
PR 16-AUG-2001; 2001US-00931836.
PR 28-AUG-2001; 2001US-00941992.
PR 29-AUG-2001; 2001WO-US027099.
PR 04-SEP-2001; 2001US-00946374.
PR 15-JAN-2002; 2002US-0002586.
XX
PA (GETH) GENENTECH INC.
XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2003-332028/31.
DR P-PSDB; ABU85678.
PT Three hundred and five nucleic acids encoding PRO polypeptides, useful
PT for the manufacture of a medicament for diagnosing or treating tumor.
XX
XX Claim 2; Fig 201; 707pp; English.
XX
CC The invention relates to human PRO polypeptides (secreted and
CC transmembrane polypeptides) and the PRO polynucleotides encoding them.
CC The invention also relates to a method for stimulating the release of
CC tumor necrosis factor alpha (TNF-alpha) from human blood by contacting
CC the blood with a sequence of the invention, a method for stimulating the
CC proliferation or differentiation of chondrocyte cells by contacting the
CC cells with a PRO polypeptide and a method for detecting the presence of a
CC tumour in a mammal. The polypeptides and polynucleotides are useful for
CC the manufacture of a medicament for diagnosing or treating a tumour in a
CC mammal. Sequences ACA72771-ACA73075 represent human PRO polynucleotides
CC of the invention. Note: The sequence data for this patent is also
CC available in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
SQ Sequence 1734 BP; 503 A; 397 C; 580 G; 254 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 147 Length: 1734
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.63% Indels: 0
DB: 7 Gaps: 0

US-09-690-825-34 (1-142) x ACA72871 (1-1734)

Qy 1 MetGlyAlaProThrLeuProPro 8
Db 1534 ATGGGAGCCCCCACACCTCCCT 1557
RESULT 67
ACD03043
ID ACD03043 standard; cDNA; 1734 BP.
XX
AC ACD03043;

XX 01-AUG-2003 (first entry)
XX Novel human secreted and transmembrane protein PRO1411 cDNA.
DE
XX Human; secreted and transmembrane protein; PRO; cytostatic; gene therapy;
KW chondrocyte stimulator; tumour; adrenal tumour; lung tumour;
KW colon tumour; breast tumour; prostate tumour; rectal tumour;
KW cervical tumour; liver tumour; TNF-alpha release;
KW tumour necrosis factor alpha release; chondrocyte cell proliferation;
KW chondrocyte cell differentiation; pharmaceutical; diagnostic; biosensor;
KW bioreactor; gene; ss.
XX
XX Homo sapiens.
XX
XX US2003013153-A1.
XX
XX 16-JAN-2003.
XX
XX 19-JUN-2002; 2002US-00175737.
XX
XX 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
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PR 18-DEC-1997; 97US-0068017P.
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PR 15-MAY-1998; 98US-0085580P.

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PR 17-JUN-1998; 98US-0089663P.
PR 18-JUN-1998; 98US-0089908P.
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PR 22-JUN-1998; 98US-0090246P.
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PR 26-JUN-1998; 98US-00105413.
PR 26-JUN-1998; 98US-0090862P.
PR 26-JUN-1998; 98US-0090863P.
PR 26-JUN-1998; 98US-0091010P.
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PR 04-AUG-1998; 98US-0095282P.
PR 10-AUG-1998; 98US-0095988P.
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PR 17-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096766P.
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PR 17-AUG-1998; 98US-0096891P.
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PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0097022P.
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PR 09-SEP-1998; 98US-0099602P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
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PR 15-SEP-1998; 98US-0100388P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100664P.
PR 16-SEP-1998; 98US-0101751P.
PR 16-SEP-1998; 98US-0101753P.
PR 17-SEP-1998; 98US-0100684P.
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PR 18-SEP-1998; 98US-0100849P.
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Alignment Scores:
Pred. No.: 147
Score: 8.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 5.63%
DB: 7

Length: 1734
Matches: 8
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-09-690-825-34 (1-142) x ACD03043 (1-1734)
QY 1 MetGlyAlaProThrLeuProPro 8
DB 1534 ATGGAGCCCCCACACTCCCTCT 1557

RESULT 68
ACD01858
ID ACD01858 standard; cDNA; 1734 BP.
XX
AC ACD01858;
XX
DT 30-JUL-2003 (first entry)
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XX Novel human secreted and transmembrane protein PRO1411 cDNA.
DE Human; secreted and transmembrane protein; PRO; cytostatic; gene therapy;
XX Chondrocyte stimulator; tumour; adrenal tumour; lung tumour;
KW colon tumour; breast tumour; prostate tumour; rectal tumour;
KW cervical tumour; liver tumour; chromosome identification; gene; ss.
XX Homo sapiens.
OS
XX
XX US2003017544-A1.
PD
XX
XX 23-JAN-2003.
XX
XX 21-JUN-2002; 2002US-00176915.
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
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PR 28-APR-1998; 98US-0083495P.
PR 28-APR-1998; 98US-0083496P.
PR 28-APR-1998; 98US-0083499P.
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PR 05-MAY-1998; 98US-0084366P.
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PR 07-MAY-1998; 98US-0084639P.
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DT 09-JUL-2003 (first entry)

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KW prostate; rectal; cervical; liver; cancer; TNF-alpha;
KW tumour necrosis factor-alpha; proliferation; differentiation;
KW chondrocyte cell; bone disorder; cartilage disorder; sports injury;
KW arthritis; cytostatic; antiarthritic; osteopathic; gene therapy; gene
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XX US2003036141-A1.

XX 20-FEB-2003.

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PR 26-JUN-1998; 98US-00105413.
PR 26-JUN-1998; 98US-0090862P.
PR 26-JUN-1998; 98US-0090863P.
PR 26-JUN-1998; 98US-0091010P.
PR 01-JUL-1998; 98US-0091359P.
PR 01-JUL-1998; 98US-0091544P.
PR 02-JUL-1998; 98US-0091478P.
PR 02-JUL-1998; 98US-0091486P.
PR 02-JUL-1998; 98US-0091626P.
PR 02-JUL-1998; 98US-0091628P.
PR 02-JUL-1998; 98US-0091632P.
PR 24-JUL-1998; 98US-0094006P.
PR 04-AUG-1998; 98US-0095282P.
PR 10-AUG-1998; 98US-0095998P.
PR 10-AUG-1998; 98US-0096012P.
PR 17-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096766P.
PR 17-AUG-1998; 98US-0096867P.
PR 17-AUG-1998; 98US-0096891P.
PR 17-AUG-1998; 98US-0096897P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0097022P.
PR 26-AUG-1998; 98US-0097952P.

[illegible]

PR 15-JAN-2002; 2002US-00052586.
 XX (GETH) GENENTECH INC.
 XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
 PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
 XX WPI; 2003-332034/31.
 DR P-PSDB; AB086293.
 XX
 XX Three hundred and five nucleic acids encoding PRO polypeptides, useful in
 PT gene therapy, chromosome identification, tissue typing, and for detecting
 PT the presence of tumor in a mammal.
 XX
 XX Claim 2; Fig 201; 707pp; English.
 PS
 XX The invention relates to three hundred and five nucleic acids encoding
 CC PRO polypeptides (secreted and transmembrane), sequences 80% identical to
 CC them, or encoding a PRO polypeptide lacking its associated signal peptide
 CC or an extracellular domain of the PRO polypeptide, with or lacking its
 CC associated signal peptide. Also included are the encoded PRO proteins,
 CC PRO expression vectors, host cells transformed with the vector (used to
 CC produce PRO proteins), a chimeric molecule comprising the PRO
 CC polypeptide fused to a heterologous amino acid sequence, an anti-PRO
 CC antibody, a method for stimulating the release of tumor necrosis factor
 CC alpha (TNF-alpha) from human blood (by contacting the blood with PRO1079,
 CC PRO827, PRO791, PRO1131, PRO1183, PRO1343, PRO1760, PRO1567 or
 CC PRO4333), a method for stimulating the proliferation or differentiation
 CC of chondrocyte cells by contacting the cells with a PRO6029 polypeptide,
 CC a method for detecting the presence of tumor in a mammal and an
 CC oligonucleotide probe derived from any of the nucleotide sequences cited
 CC above. The PRO polypeptide or anti-PRO antibody is useful for preparing a
 CC medicament for treating a condition that is responsive to the PRO
 CC polypeptide or anti-PRO antibody. The PRO nucleotide sequences are useful
 CC as hybridisation probes in chromosome and gene mapping, or in generating
 CC antisense RNA and DNA. PRO nucleic acids are also useful in preparing PRO
 CC polypeptides, in assays to identify other proteins or molecules involved
 CC in a binding reaction, to generate transgenic animals or knockout
 CC animals, which in turn are useful in the development and screening of
 CC therapeutically useful reagents, for chromosome identification, and
 CC tissue typing. The PRO polypeptides and nucleic acid molecules are also
 CC useful for detecting the presence of a tumour in a mammal, stimulating
 CC proliferation or differentiation of chondrocyte cells, stimulating the
 CC release of tumour necrosis factor-alpha from human blood, in gene
 CC therapy, or as molecular weight markers for protein electrophoresis
 CC purposes. The anti-PRO antibodies may be used in diagnostic assays for
 CC PRO, or for the affinity purification of PRO from recombinant cell
 CC culture or natural sources. The present sequence is a cDNA encoding a PRO
 CC protein
 XX
 SQ Sequence 1734 BP; 503 A; 397 C; 580 G; 254 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 147 Length: 1734
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 5.63% Indels: 0
 DB: 7 Gaps: 0
 US-09-690-825-34 (1-142) x ACA73485 (1-1734)
 QV 1 MetGlyAlaProThrLeuProPro 8
 Db 1534 ATGGAGCCCCACACTCCCTCT 1557
 RESULT 72
 ID ACA05800
 AC ACA05800 standard; cDNA; 1734 BP.
 XX
 AC ACA05800;
 XX
 XX 29-MAY-2003 (first entry)
 DT

XX
 DE
 XX
 KW Human secreted/transmembrane protein (PRO) cDNA #101.
 KW Human; gene; ss; secreted and transmembrane protein; PRO; TNF-alpha;
 KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
 XX tissue typing.
 OS Homo sapiens.
 XX
 PN US2003036162-A1.
 XX
 PD 20-FEB-2003.
 XX
 XX 12-JUL-2002; 2002US-00194423.
 XX
 XX 26-JUN-1998; 98US-00105413.
 PR 16-SEP-1998; 98WO-US019330.
 PR 07-OCT-1998; 98US-00168978.
 PR 07-OCT-1998; 98WO-US021141.
 PR 06-NOV-1998; 98US-00187368.
 PR 01-DEC-1998; 98WO-US025108.
 PR 07-DEC-1998; 98US-00202054.
 PR 03-MAR-1999; 98US-00254311.
 PR 08-MAR-1999; 98WO-US005028.
 PR 14-MAY-1999; 98US-00311832.
 PR 14-MAY-1999; 98WO-US010733.
 PR 02-JUN-1999; 98US-0012252.
 PR 25-AUG-1999; 98US-00380137.
 PR 25-AUG-1999; 98US-00380138.
 PR 25-AUG-1999; 98US-00380139.
 PR 25-AUG-1999; 98US-00380142.
 PR 01-SEP-1999; 98WO-US020111.
 PR 15-SEP-1999; 98WO-US021090.
 PR 18-OCT-1999; 98US-00403297.
 PR 12-NOV-1999; 98US-00423844.
 PR 01-DEC-1999; 98WO-US028301.
 PR 02-DEC-1999; 98WO-US028551.
 PR 30-DEC-1999; 98WO-US031274.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 22-FEB-2000; 2000WO-US004342.
 PR 24-FEB-2000; 2000WO-US004414.
 PR 01-MAR-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 22-AUG-2000; 2000US-00544848.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 18-SEP-2000; 2000US-00664610.
 PR 18-SEP-2000; 2000US-00665350.
 PR 08-NOV-2000; 2000US-00709238.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 22-MAR-2001; 2001US-00816744.
 PR 10-MAY-2001; 2001US-00854208.
 PR 10-MAY-2001; 2001US-00854280.
 PR 25-MAY-2001; 2001US-00866028.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 05-JUN-2001; 2001US-00874503.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 18-JUL-2001; 2001US-00908827.
 PR 30-JUL-2001; 2001US-00918585.

PR 06-AUG-2001; 2001US-00924419.
PR 13-AUG-2001; 2001US-00929404.
PR 16-AUG-2001; 2001US-00931836.
PR 28-AUG-2001; 2001US-00941992.
PR 29-AUG-2001; 2001WO-US027099.
PR 04-SEP-2001; 2001US-00946374.
PR 15-JAN-2002; 2002US-00052586.
XX
PA (GETH) GENENTECH INC.
XX
XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
PI
XX WPI; 2003-332039/31.
DR P-PSDB; ABU67506.
XX
XX PT New secreted and transmembrane PRO polypeptides and nucleic acids, useful
PT in gene therapy, in chromosome and gene mapping, as chromosome markers,
PT in tissue typing, and in chromosome identification.
XX
PS Claim 2; Fig 201; 706pp; English.
XX
CC The invention discloses human nucleic acids encoding secreted and
CC transmembrane (PRO) polypeptides. Also disclosed is an antibody that
CC specifically binds to the PRO polypeptide, a method for stimulating the
CC release of tumour necrosis factor alpha (TNF-alpha) from human blood by
CC contacting the blood a PRO polypeptide, a method for stimulating the
CC proliferation or differentiation of chondrocyte cells by contacting the
CC cells with a PRO polypeptide, a method for detecting the presence of a
CC tumour in a mammal and an oligonucleotide probe derived from any of the
CC PRO nucleotide sequences. The nucleotide sequences are useful as probes,
CC in chromosome and gene mapping, in generating antisense RNA and DNA, in
CC preparing PRO polypeptides by recombinant techniques and in gene therapy
CC (e.g. for replacement of defective gene). The PRO polypeptides are useful
CC as molecular weight markers for protein electrophoresis purposes, for
CC chromosome identification, as chromosome markers, as therapeutic agents,
CC for stimulating the release of TNF-alpha from human blood, for
CC stimulating the proliferation or differentiation of chondrocytes and
CC detecting the presence of a tumour. The PRO polypeptides and nucleic
CC acids may also be used diagnostically for tissue typing. The sequences
CC presented in ACA05700-ACA06004 are the cDNAs encoding the PRO
CC polypeptides of the invention
XX
SQ Sequence 1734 BP; 503 A; 397 C; 580 G; 254 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 147 Length: 1734
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.63% Indels: 0
DB: 7 Gaps: 0
US-09-690-825-34 (1-142) x ACA05800 (1-1734)
QY 1 MetGlyAlaProHrLeuPro 8
Db 1534 ATGGAGGCCCCACATCCCTCT 1557
RESULT 73
ACA66634
ID ACA66634 standard; cDNA; 1734 BP.
XX
AC ACA66634;
XX
DT 23-JUN-2003 (first entry)
XX cDNA encoding human PRO protein #101.
XX Human; tumour; adrenal; lung; colon; breast; prostate; rectal; cervical;
KW liver; PRO; gene therapy; gene; ss.
XX
OS Homo sapiens.

XX US2003036137-A1.
PN
XX 20-FEB-2003.
PD
XX
XX 27-JUN-2002; 2002US-00184640.
PF
XX
PR 26-JUN-1998; 98US-00105413.
PR 16-SEP-1998; 98WO-US019330.
PR 07-OCT-1998; 98US-00168978.
PR 07-OCT-1998; 98WO-US021141.
PR 06-NOV-1998; 98US-00187368.
PR 01-DEC-1998; 98WO-US025108.
PR 07-DEC-1998; 98US-00202054.
PR 03-MAR-1999; 99US-00254311.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 25-AUG-1999; 99US-00380142.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99US-00423844.
PR 01-DEC-1999; 99WO-US028301.
PR 30-DEC-1999; 99WO-US028551.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005601.
PR 15-MAR-2000; 2000WO-US005841.
PR 30-MAR-2000; 2000WO-US006884.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014842.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00664610.
PR 08-NOV-2000; 2000US-00665350.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 25-MAY-2001; 2001US-00854280.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 30-JUL-2001; 2001US-00918585.
PR 06-AUG-2001; 2001US-00924419.
PR 13-AUG-2001; 2001US-00929404.
PR 16-AUG-2001; 2001US-00931836.
PR 28-AUG-2001; 2001WO-US027099.
PR 29-AUG-2001; 2001US-00946374.
PR 04-SEP-2001; 2001US-00946374.
PR 15-JAN-2002; 2002US-00052586.
XX

PA (GETH) GENENTECH INC.
 XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
 PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
 XX WPI; 2003-342038/32.
 DR P-PSDB; ABU0534.
 XX
 DR Three hundred and five nucleic acids encoding secreted and transmembrane
 PT PRO polypeptides, useful for the diagnosis, prevention and/or treatment
 PT of tumors, such as adrenal, lung, colon, breast, prostate, rectal,
 PT cervical or liver tumors.
 XX
 XX Claim 2; Fig 201; 708pp; English.
 PS
 XX The invention relates to three hundred and five nucleic acids encoding
 CC PRO polypeptides (secreted and transmembrane). Methods and compositions
 CC of the present invention are useful for the diagnosis, prevention and/or
 CC treatment of tumors, such as adrenal, lung, colon, breast, prostate,
 CC rectal, cervical or liver tumors. The PRO polypeptides are also useful
 CC as molecular weight markers, or for chromosome identification. The PRO
 CC genes are useful as hybridisation probes, or for screening libraries of
 CC human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene
 CC therapy, particularly for replacing a defective gene. The present
 CC sequence represents a cDNA encoding a human PRO polypeptide of the
 CC invention
 XX
 SQ Sequence 1734 BP; 503 A; 397 C; 580 G; 254 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 147 Length: 1734
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 5.63% Indels: 0
 DB: 7 Gaps: 0
 US-09-690-825-34 (1-142) x ACA66534 (1-1734)
 QY 1 MetGlyAlaProThrLeuProPro 8
 DB 1534 ATGGAGGCCCCACACTCCCTCCT 1557
 RESULT 74
 ID ACA91189 standard; cDNA; 1734 BP.
 AC ACA91189;
 XX 11-JUL-2003 (first entry)
 DT
 XX Novel human secreted and transmembrane protein PRO1411 cDNA.
 DE
 XX Human; secreted and transmembrane protein; PRO; antibody therapy;
 KW pharmaceutical; diagnostic; biosensor; bioreactor; gene; ss.
 XX Homo sapiens.
 OS
 XX US2003018173-A1.
 FN
 XX 23-JAN-2003.
 FD
 XX 01-MAY-2002; 2002US-00063515.
 PF
 XX 06-DEC-2001; 2001US-00006867.
 PR
 XX (GETH) GENENTECH INC.
 FA
 XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
 PI WPI; 2003-401702/38.
 XX P-PSDB; ABU90501.
 DR

XX New antibody useful for identifying PRO polypeptides, for affinity
 PT purification of PRO polypeptides, and for preparing a medicament for
 PT diagnosing or treating conditions responsive to the antibody or PRO
 PT polypeptide.
 XX
 XX Disclosure; Fig 51; 345pp; English.
 PS
 XX The invention describes an antibody that specifically binds to a PRO
 CC polypeptide having a fully defined amino acid sequence given in the
 CC specification. The antibody is useful in identifying PRO polypeptides
 CC useful for various industrial applications, including pharmaceuticals,
 CC diagnostics, biosensors and bioreactors. The antibody is also used for
 CC affinity purification of PRO polypeptides from recombinant cell culture
 CC or natural sources. The antibody, PRO polypeptide, or its agonists or
 CC antagonists, may be used for preparing a medicament for diagnosing or
 CC treating a condition responsive to the antibody, PRO polypeptide, or its
 CC agonists or antagonists. This sequence encodes a novel human secreted and
 CC transmembrane PRO polypeptide
 XX
 SQ Sequence 1734 BP; 503 A; 397 C; 580 G; 254 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 147 Length: 1734
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 5.63% Indels: 0
 DB: 7 Gaps: 0
 US-09-690-825-34 (1-142) x ACA91189 (1-1734)
 QY 1 MetGlyAlaProThrLeuProPro 8
 DB 1534 ATGGAGGCCCCACACTCCCTCCT 1557
 RESULT 75
 ID ACD81566
 XX ACD81566 standard; cDNA; 1734 BP.
 AC ACD81566;
 XX 18-SEP-2003 (first entry)
 DT
 XX Human cDNA encoding secreted/transmembrane protein PRO411.
 DE
 XX Human; ss; gene; secreted/transmembrane protein; PRO; tumour; cancer;
 KW cytostatic.
 XX Homo sapiens.
 OS
 XX US2003009013-A1.
 FN
 XX 09-JAN-2003.
 PD
 XX 01-MAY-2002; 2002US-00063519.
 PF
 XX 30-DEC-1998; 98KR-00062142.
 PR 08-MAR-1999; 99WO-US005028.
 PR 14-MAY-1999; 99US-00311832.
 PR 14-MAY-1999; 99WO-US010733.
 PR 25-AUG-1999; 99US-00380137.
 PR 25-AUG-1999; 99US-00380138.
 PR 25-AUG-1999; 99US-00380139.
 PR 25-AUG-1999; 99US-00380142.
 PR 15-SEP-1999; 99US-00397342.
 PR 18-OCT-1999; 99US-00403297.
 PR 12-NOV-1999; 99US-00423844.
 PR 30-DEC-1999; 99WO-US031274.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 21-MAR-2000; 2000WO-US007532.


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PR 22-MAY-2000; 2000WC-US014042.
PR 02-JUN-2000; 2000WC-US015264.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WC-US023328.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 10-NOV-2000; 2000WC-US030873.
PR 01-DEC-2000; 2000WC-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WC-US034956.
PR 28-FEB-2001; 2001WC-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 30-MAY-2001; 2001US-00854280.
PR 01-JUN-2001; 2001WC-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 29-JUN-2001; 2001US-00869599.
PR 18-JUL-2001; 2001US-00908827.
PR 06-DEC-2001; 2001US-00006867.
XX
XX (GETH ) GENENTECH INC.
XX
XX Paton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
XX WPI; 2003-447354/42.
XX P-PSDB; ABO33950.
XX
XX PT New isolated antibody specifically binding a PRO polypeptide, useful for
XX PT the preparation of a medicament for treating disorders with the aberrant
XX PT expression or activity of the PRO polypeptide, such as tumor conditions
XX PT and cancer.
XX
XX PS Disclosure; Fig 51; 223pp; English.
XX
XX CC The invention relates to an antibody that binds to a secreted or
XX CC transmembrane protein designated PRO1446 appearing as ABO33941. The
XX CC protein is one of 84 PRO polypeptides which (along with their encoding
XX CC nucleic acids) are disclosed in the specification. The methods and
XX CC compositions of the present invention are useful for the preparation of a
XX CC medicament for the treatment of disorders associated with the aberrant
XX CC expression or activity of the PRO polypeptide, such as tumour conditions
XX CC and cancer. They can also be used to generate transgenic or knockout
XX CC animals useful in the development and screening of therapeutically useful
XX CC reagents. The PRO polypeptides and encoding nucleic acids can be used as
XX CC molecular weight markers for protein electrophoresis, chromosome
XX CC identification and tissue typing. The antibodies may be used in various
XX CC diagnostic, competitive binding and/or immunoprecipitation assays. The
XX CC present sequence encodes a PRO polypeptide
XX
XX SQ Sequence 1734 BP; 503 A; 397 C; 580 G; 254 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 147 Length: 1734
XX Score: 8.00 Matches: 8
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 5.63% Indels: 0
XX DB: 7 Gaps: 0
XX
XX US-09-690-825-34 (1-142) x ACD81566 (1-1734)
XX
XX QY 1 MetGlyAlaProThrieuProPro 8
XX
XX Db 1534 ATGGAGCCCCCACACTCCCTCT 1557
XX
XX Search completed: August 16, 2004, 01:35:39
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Run on: August 16, 2004, 02:47:05 ; Search time 1465 Seconds

(without alignments)
475.589 Million cell updates/sec

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12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:
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15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:
16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:
17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:
18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:
19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Match Length DB ID Description

1	142	100.0	429	17	US-10-665-975-1	Sequence 1, Appli
2	142	100.0	1619	9	US-09-918-186A-97	Sequence 97, Appl
3	142	100.0	1619	13	US-10-342-887-566	Sequence 566, App
4	142	100.0	1619	13	US-10-172-118-566	Sequence 566, App
5	142	100.0	1619	13	US-10-181-316-97	Sequence 97, Appl
6	142	100.0	1619	13	US-10-388-360-324	Sequence 324, App
7	142	100.0	1619	17	US-10-283-975A-445	Sequence 445, App
8	142	100.0	2404	14	US-10-071-766-109	Sequence 109, App
9	142	100.0	2404	15	US-10-084-817-285	Sequence 285, App
10	93	65.5	740	16	US-10-305-720-918	Sequence 918, App
11	41	28.9	955	9	US-09-918-186A-10	Sequence 10, Appl
12	41	28.9	955	13	US-10-181-316-10	Sequence 10, Appl
13	40	28.2	121	15	US-10-179-730-33	Sequence 33, Appl
14	39	27.5	14795	13	US-10-181-316-3	Sequence 3, Appl
15	39	27.5	14796	9	US-09-954-456-973	Sequence 973, App
16	39	27.5	14796	9	US-09-954-456-1636	Sequence 1636, Ap
17	39	27.5	14796	9	US-09-918-186A-3	Sequence 3, Appli
18	39	27.5	14796	9	US-09-850-107-3421	Sequence 3421, Ap
19	39	27.5	14796	12	US-09-968-007A-522	Sequence 522, App
20	39	27.5	14796	15	US-10-138-618-35	Sequence 35, Appl
21	36	25.4	120	15	US-10-029-386-23672	Sequence 23672, A
22	36	25.4	555	15	US-10-029-386-9972	Sequence 9972, Ap
23	36	25.4	1100	15	US-10-108-877-2	Sequence 2, Appli
24	14	9.9	332	9	US-09-833-381-1331	Sequence 1331, Ap
25	9	6.3	30	15	US-10-400-382-265	Sequence 265, App
26	9	6.3	30	17	US-10-636-065-199	Sequence 199, App
27	8	5.6	26	9	US-09-918-186A-13	Sequence 13, Appl
28	8	5.6	26	13	US-10-181-316-13	Sequence 13, Appl
29	8	5.6	281	9	US-09-833-381-1330	Sequence 1330, Ap
30	8	5.6	420	13	US-10-027-632-65868	Sequence 65868, A
31	8	5.6	420	13	US-10-027-632-65870	Sequence 65870, A
32	8	5.6	420	13	US-10-027-632-65870	Sequence 65870, A
33	8	5.6	420	16	US-10-027-632-65868	Sequence 65868, A
34	8	5.6	420	16	US-10-027-632-65869	Sequence 65869, A
35	8	5.6	420	16	US-10-027-632-65870	Sequence 65870, A
36	8	5.6	454	13	US-10-424-599-114486	Sequence 114486, A
37	8	5.6	515	13	US-09-918-186A-231	Sequence 231, App
38	8	5.6	515	13	US-10-181-316-231	Sequence 231, App
39	8	5.6	587	10	US-09-918-995-15078	Sequence 15078, A
40	8	5.6	1224	16	US-10-369-493-35886	Sequence 35886, A
41	8	5.6	1441	15	US-10-050-704-14	Sequence 14, Appl
42	8	5.6	1441	17	US-10-798-512-14	Sequence 14, Appl
43	8	5.6	1734	10	US-09-946-374-51	Sequence 51, Appl
44	8	5.6	1734	12	US-10-015-395A-51	Sequence 51, Appl
45	8	5.6	1734	13	US-10-206-915-201	Sequence 201, App
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47	8	5.6	1734	13	US-10-201-858-201	Sequence 201, App
48	8	5.6	1734	13	US-10-081-056-149	Sequence 149, App
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53	8	5.6	1734	13	US-10-201-853-201	Sequence 201, App
54	8	5.6	1734	13	US-10-063-745-51	Sequence 51, Appl
55	8	5.6	1734	13	US-10-063-512-51	Sequence 51, Appl
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60	8	5.6	1734	13	US-10-063-551-51	Sequence 51, Appl
61	8	5.6	1734	13	US-10-174-581-201	Sequence 201, App
62	8	5.6	1734	13	US-10-176-483-201	Sequence 201, App
63	8	5.6	1734	13	US-10-176-749-201	Sequence 201, App
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65	8	5.6	1734	13	US-10-176-915-201	Sequence 201, App
66	8	5.6	1734	13	US-10-006-485A-51	Sequence 51, Appl
67	8	5.6	1734	13	US-10-013-907A-51	Sequence 51, Appl
68	8	5.6	1734	13	US-10-015-499A-51	Sequence 51, Appl
69	8	5.6	1734	13	US-10-063-555-51	Sequence 51, Appl
70	8	5.6	1734	13	US-10-063-563-51	Sequence 51, Appl
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73      8      5.6      1734      13      US-10-063-554-51      Sequence 51, App
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75      8      5.6      1734      13      US-10-180-550-201      Sequence 201, App
76      8      5.6      1734      13      US-10-183-014-201      Sequence 201, App
77      8      5.6      1734      13      US-10-187-738-201      Sequence 201, App
78      8      5.6      1734      13      US-10-187-740-201      Sequence 201, App
79      8      5.6      1734      13      US-10-187-883-201      Sequence 201, App
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81      8      5.6      1734      13      US-10-194-460-201      Sequence 201, App
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87      8      5.6      1734      13      US-10-196-755-201      Sequence 201, App
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91      8      5.6      1734      13      US-10-198-758-201      Sequence 201, App
92      8      5.6      1734      13      US-10-198-766-201      Sequence 201, App
93      8      5.6      1734      13      US-10-199-304-201      Sequence 201, App
94      8      5.6      1734      13      US-10-199-309-201      Sequence 201, App
95      8      5.6      1734      13      US-10-199-313-201      Sequence 201, App
96      8      5.6      1734      13      US-10-199-456-201      Sequence 201, App
97      8      5.6      1734      13      US-10-201-329-201      Sequence 201, App
98      8      5.6      1734      13      US-10-202-412-201      Sequence 201, App
99      8      5.6      1734      13      US-10-206-919-201      Sequence 201, App
100     8      5.6      1734      13      US-10-206-922-201      Sequence 201, App

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ALIGNMENTS

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RESULT 1
US-10-665-975-1
; Sequence 1, Application US/10665975
; Publication No. US20040138119A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Tamm, Ingo
; TITLE OF INVENTION: USE OF HEPATITIS VIRUS B X-INTERACTING
; TITLE OF INVENTION: PROTEIN (HEXIP) IN MODULATION OF APOPTOSIS
; FILE REFERENCE: BURNHAM.005A
; CURRENT APPLICATION NUMBER: US/10/665.975
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: 60/412,109
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 429
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-665-975-1

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Alignment Scores:
Pred. No.: 7.45e-146      Length: 429
Score: 142.00      Matches: 142
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%      Indels: 0
DB: 17      Gaps: 0

US-09-690-825-34 (1-142) x US-10-665-975-1 (1-429)
QY      1      MetGlyAlaProThrLeuProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
Db      1      ATGGGTGCCCCGAGCTTGCCCTGCGCTGGCAGCCCTTCTCAAGGACCACCGCATCTCT 60
QY      21      ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
Db      61      ACATTCAGAACTGGCCCTTCTTGAGGGCTGCGCCCTGCACCCCGGAGCGGATGGCGGAG 120
QY      41      AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPheCys 60

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Db      121      GCTGGCTTCATCACTGCCCACTGAGAACGAGCAGACTTGCCCACTGTTCTTCTGC 180
QY      61      PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHisLysLysHis 80
Db      181      TTCAGGAGCTGAAGGCTGGGAGCCAGATGACGACCCCATAGAGGAACATAAAGCAT 240
QY      81      SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
Db      241      TCGTCGGTGGCGCTTCCTTCTCTCAAGAAAGCAGTTTGAAGAATTAACTCCCTGGTGA 300
QY      101      PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
Db      301      TTTTGAACCTGACAGAGAGAGCCCAAGACAAATTTGCAAGAAACCAACAATAAG 360
QY      121      LysLysGluPheGluGluThrAlaLysLysValArgAlaIleGluGlnLeuAla 140
Db      361      AAGAAAGAAATTTGAGGAAACTCGAAGAAAGTGCCTGCGCATCGAGCGCTGCTGCC 420
QY      141      MetAsp 142
Db      421      ATGGAT 426

RESULT 2
US-09-918-186A-97
; Sequence 97, Application US/09918186A
; Patent No. US20020137708A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Eric E. Swayze
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: ISPH-0585
; CURRENT APPLICATION NUMBER: US/09/918,186A
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 09/496,694
; PRIOR FILING DATE: 2000-02-02
; PRIOR APPLICATION NUMBER: 09/286,407
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 09/163,162
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 250
; SEQ ID NO 97
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-186A-97

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Pred. No.: 2.54e-145      Length: 1619
Score: 142.00      Matches: 142
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%      Indels: 0
DB: 9      Gaps: 0

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Db      50      ATGGGTGCCCCGAGCTTGCCCTGCGCTGGCAGCCCTTCTCAAGGACCACCGCATCTCT 109
QY      21      ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
Db      110      ACATTCAGAACTGGCCCTTCTTGAGGGCTGCGCCCTGCACCCCGGAGCGGATGGCGGAG 169
QY      41      AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPheCys 60
Db      170      GCTGGCTTCATCACTGCCCACTGAGAACGAGCAGACTTGCCCACTGTTCTTCTTCTGC 229
QY      61      PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHisLysLysHis 80

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Db 230 TTCAAGGAGCTGGAAGGCTGGGAGCGCAGATGACGACCCCATAGAGAAACATAAAAGCAT 289
Qy 81 SerSerGlyCysAlaPheLeuSerVallysLysGlnPheGluGluLeuThrLeuGlyGlu 100
Db 290 TCGTCCGGTGGCTTTCTCTGTCAGAGAGCAGTTTGAAGAAATTAACCTTGGTGA 349
Qy 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysLysAlaLysGluThrAsnAsnLys 120
Db 350 TTTTGAAGAACTGGACAGAGAAAGCCCAAGAAACAAAATTCGAAAGGAAACCAACAATAAG 409
Qy 121 LysLysGluPheGluGluThrAlaLysLysValArgAlaLysGluThrLeuAlaAla 140
Db 410 AAGAAAGAAATTTGAGGAAACTGCGAGAAAGTGGCGGTCGCCATCGACAGCTGGCTGCC 469
Qy 141 MetAsp 142
Db 470 ATGGAT 475
RESULT 3
US-10-342-887-566
; Sequence 566, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 566
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-566
Alignment Scores:
Pred. No.: 2,54e-145 Length: 1619
Score: 142.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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US-09-690-825-34 (1-142) x US-10-342-887-566 (1-1619)
Qy 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
Db 50 ATGGGTGCCCGCAGTGTGCCCTGCTGGCAGCCCTTTCTCAAGACCAACCGCATCTCT 109
Qy 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
Db 110 ACATTCAAGAACTGGCCCTTTCTGGAGGGCTGGCCCTGCACCCCGGAGCGGATGGCCGAG 169
Qy 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
Db 170 GCTGGCTTCATCCACTGCCCTCTTGGAGGGCTGGCCCTGCACCCCGGAGCGGATGGCCGAG 229
Qy 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHisLysLysHis 80
Db 230 TTCAAGGAGCTGGAGAGCTGGGAGCCAGATGACGACCCCATAGAGAAACATAAAAGCAT 289

Qy 81 SerSerGlyCysAlaPheLeuSerVallysLysGlnPheGluGluLeuThrLeuGlyGlu 100
Db 290 TCGTCCGGTGGCTTTCTCTGTCAGAGAGCAGTTTGAAGAAATTAACCTTGGTGA 349
Qy 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysLysAlaLysGluThrAsnAsnLys 120
Db 350 TTTTGAAGAACTGGACAGAGAAAGCCCAAGAAACAAAATTCGAAAGGAAACCAACAATAAG 409
Qy 121 LysLysGluPheGluGluThrAlaLysLysValArgAlaLysGluThrLeuAlaAla 140
Db 410 AAGAAAGAAATTTGAGGAAACTGCGAGAAAGTGGCGGTCGCCATCGACAGCTGGCTGCC 469
Qy 141 MetAsp 142
Db 470 ATGGAT 475
RESULT 4
US-10-172-118-566
; Sequence 566, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 566
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_001168
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-566
Alignment Scores:
Pred. No.: 2,54e-145 Length: 1619
Score: 142.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0
US-09-690-825-34 (1-142) x US-10-172-118-566 (1-1619)
Qy 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
Db 50 ATGGGTGCCCGCAGTGTGCCCTGCTGGCAGCCCTTTCTCAAGACCAACCGCATCTCT 109
Qy 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
Db 110 ACATTCAAGAACTGGCCCTTTCTGGAGGGCTGGCCCTGCACCCCGGAGCGGATGGCCGAG 169
Qy 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
Db 170 GCTGGCTTCATCCACTGCCCTCTTGGAGGGCTGGCCCTGCACCCCGGAGCGGATGGCTTCTG 229
Qy 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHisLysLysHis 80
Db 230 TTCAAGGAGCTGGAGAGCTGGGAGCCAGATGACGACCCCATAGAGAAACATAAAAGCAT 289
Qy 81 SerSerGlyCysAlaPheLeuSerVallysLysGlnPheGluGluLeuThrLeuGlyGlu 100

Db 290 TCGTCCGGTTGGCTTTCTCTCTCAAGAGCAGTTTGAAGAAATTAACCCCTTGGTGAA 349
 QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
 Db 350 TTTTGTAAACTGGACAGAGAAAGAGCCCAAGAAATAATTCAGAGGAAACCAACAATAAG 409
 QY 121 LysLysGluPheGluGluThrAlaLysLysValArgAlaIleGluGlnLeuAlaA 140
 Db 410 AAGAAGAAATTTGAGAAACTGCGAAGAAAGTGCCCGTGCCATCGAGCAGCTGGCTGCC 469
 QY 141 MetAsp 142
 Db 470 ATGGAT 475

RESULT 5

US-10-181-316-97
 ; Sequence 97, Application US/10181316
 ; Publication No. US20030211607A1
 ; GENERAL INFORMATION:
 ; APPLICANT: C. Frank Bennett
 ; APPLICANT: Elizabeth J. Ackermann
 ; APPLICANT: Eric E. Swayze
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
 ; FILE REFERENCE: ISPH-0650
 ; CURRENT APPLICATION NUMBER: US/10181,316
 ; PRIOR FILING DATE: 2002-07-15
 ; PRIOR APPLICATION NUMBER: PCT/US01/02939
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: 09/496,694
 ; PRIOR FILING DATE: 2000-02-02
 ; PRIOR APPLICATION NUMBER: 09/286,407
 ; PRIOR FILING DATE: 1999-04-05
 ; PRIOR APPLICATION NUMBER: 09/163,162
 ; PRIOR FILING DATE: 1998-09-29
 ; NUMBER OF SEQ ID NOS: 249
 ; SEQ ID NO 97
 ; LENGTH: 1619
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-181-316-97

Alignment Scores:
 Pred. No.: 2,54e-145 Length: 1619
 Score: 142.00 Matches: 142
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 13 Gaps: 0

US-09-690-825-34 (1-142) x US-10-181-316-97 (1-1619)

QY 1 MetGlyAlaProThrLeuProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
 Db 50 ATGGGTGCCCCGACGTTTGCCTTCTGGAGGCTTCTCAAGGACCCACCGCATCTCT 109
 QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
 Db 110 ACATTCAAGAACTGGCCCTTCTTGAGGGCTGCGCCTGCACCCCGGAGCGGATGGCCGAG 169
 QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
 Db 170 GCTGGCTTCATCCACTGCCCACTGAGAACGAGCCAGACTTGGCCCACTGTTTCTTCTGC 229
 QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHisLysLysHis 80
 Db 230 TTCAGGAGCTGGAAGGCTGGAGCCAGATGACGACCCCATAGAGGAACATAAAGCAT 289
 QY 81 SerSerGlyCysAlaPheLeuSerValLysGlnPheGluGluHisLysLysHis 100
 Db 290 TCGTCCGGTTGGCTTTCTCTCTCAAGAGCAGTTTGAAGAAATTAACCCCTTGGTGAA 349

QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
 Db 350 TTTTGTAAACTGGACAGAGAAAGAGCCCAAGAAATAATTCAGAGGAAACCAACAATAAG 409
 QY 121 LysLysGluPheGluGluThrAlaLysLysValArgAlaIleGluGlnLeuAlaA 140
 Db 410 AAGAAGAAATTTGAGAAACTGCGAAGAAAGTGCCCGTGCCATCGAGCAGCTGGCTGCC 469
 QY 141 MetAsp 142
 Db 470 ATGGAT 475

RESULT 6

US-10-388-360-324
 ; Sequence 324, Application US/10388360
 ; Publication No. US2003022528A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GENOMIC HEALTH
 ; APPLICANT: Baker, Joffrey B.
 ; APPLICANT: Cronin, Maureen T.
 ; APPLICANT: Kiefer, Michael C.
 ; APPLICANT: Shak, Steve
 ; APPLICANT: Walker, Michael Graham
 ; TITLE OF INVENTION: GENE EXPRESSION PROFILING IN BIOPSIED TUMOR TISSUES
 ; FILE REFERENCE: 39740-0001US
 ; CURRENT APPLICATION NUMBER: US/10/388,360
 ; CURRENT FILING DATE: 2003-03-12
 ; PRIOR FILING DATE: 2002-09-18
 ; PRIOR APPLICATION NUMBER: US 60/412,049
 ; PRIOR FILING DATE: 2002-03-13
 ; PRIOR APPLICATION NUMBER: US 60/364,890
 ; NUMBER OF SEQ ID NOS: 384
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 324
 ; LENGTH: 1619
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-388-360-324

Alignment Scores:
 Pred. No.: 2,54e-145 Length: 1619
 Score: 142.00 Matches: 142
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 13 Gaps: 0

US-09-690-825-34 (1-142) x US-10-388-360-324 (1-1619)

QY 1 MetGlyAlaProThrLeuProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
 Db 50 ATGGGTGCCCCGACGTTTGCCTTCTGGAGGCTTCTCAAGGACCCACCGCATCTCT 109
 QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
 Db 110 ACATTCAAGAACTGGCCCTTCTTGAGGGCTGCGCCTGCACCCCGGAGCGGATGGCCGAG 169
 QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
 Db 170 GCTGGCTTCATCCACTGCCCACTGAGAACGAGCCAGACTTGGCCCACTGTTTCTTCTGC 229
 QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHisLysLysHis 80
 Db 230 TTCAGGAGCTGGAAGGCTGGAGCCAGATGACGACCCCATAGAGGAACATAAAGCAT 289
 QY 81 SerSerGlyCysAlaPheLeuSerValLysGlnPheGluGluHisLysLysHis 100
 Db 290 TCGTCCGGTTGGCTTTCTCTCTCAAGAGCAGTTTGAAGAAATTAACCCCTTGGTGAA 349
 QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
 Db 350 TTTTGTAAACTGGACAGAGAAAGAGCCCAAGAAATAATTCAGAGGAAACCAACAATAAG 409

QY 121 LysLysGluPheGluGluThrAlaLysLysValArgAlaAlaGluGluLeuAlaAla 140
 DB 410 AAGAAGAAATTTGAGGAAGTGGAGAAAGTGGCCCGTGGCATCGAGCAGCTGGCTGCC 469
 QY 141 MetAsp 142
 DB 470 ATGGAT 475

RESULT 7

US-10-283-975A-445
 ; Sequence 445, Application US/10283975A
 ; Publication No. US20040110792A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ortho-Clinical Diagnostics, Inc.
 ; TITLE OF INVENTION: Methods For Assessing and Treating Leukemia
 ; FILE REFERENCE: CDS 293 PCT
 ; CURRENT APPLICATION NUMBER: US/10/283,975A
 ; CURRENT FILING DATE: 2002-10-30
 ; PRIOR APPLICATION NUMBER: 60/340,938
 ; PRIOR FILING DATE: 2001-10-30
 ; PRIOR APPLICATION NUMBER: 60/338,997
 ; PRIOR FILING DATE: 2001-10-30
 ; PRIOR APPLICATION NUMBER: 60/340,081
 ; PRIOR FILING DATE: 2001-10-30
 ; PRIOR APPLICATION NUMBER: 60/341,012
 ; PRIOR FILING DATE: 2001-10-30
 ; NUMBER OF SEQ ID NOS: 900
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 445
 ; LENGTH: 1619
 ; TYPE: DNA
 ; ORGANISM: HUMAN
 US-10-283-975A-445

Alignment Scores:
 Pred. No.: 2,54e-145 Length: 1619
 Score: 142.00 Matches: 142
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 17 Gaps: 0

US-09-690-825-34 (1-142) x US-10-283-975A-445 (1-1619)

QY 1 MetGlyAlaProThrLeuProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
 DB 50 ATGGGTGCCCCGACGTGGCCCCCTGCTGGCAGCCCTTTCTCAAGGACCACCGCATCTCT 109
 QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
 DB 110 ACATTCAGAACTGGCCCTTCTTGGAGGCTGGCCTGCACCCCGAGCGGATGGCCGAG 169
 QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPheCys 60
 DB 170 GCTGGCTTTCATCCACTGCCCTCTTGGAGGCTGGCCTGCACCCCGAGCGGATGGCCGAG 229
 QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluHisLysLysHis 80
 DB 230 TTCAGAGCTGGAGGCTGGAGCCAGATGACGACCCCATGAGAGAACTTAAAGACAT 289
 QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluLeuThrLeuGlyGlu 100
 DB 290 TCGTCCGCTTTCCTTCTCTGTCAGAAAGCAGTTTGAAGATTAACCCCTTGGTGAA 349
 QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120
 DB 350 TTTTGAACCTGACAGAGAAAGAGCCAGAAACAAATTCGAAAGGAAACCAACATAAG 409
 QY 121 LysLysGluPheGluGluThrAlaLysLysValArgAlaIleGluGlnLeuAlaAla 140
 DB 410 AAGAAGAAATTTGAGGAAGTGGAGAAAGTGGCCCGTGGCATCGAGCAGCTGGCTGCC 469
 QY 141 MetAsp 142

DB 470 ATGGAT 475

RESULT 8

US-10-071-766-109
 ; Sequence 109, Application US/10071766
 ; Publication No. US20020192678A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Huei-Mei Chen
 ; TITLE OF INVENTION: GENES EXPRESSED IN SENESENCE
 ; FILE REFERENCE: PA-0043 US
 ; CURRENT APPLICATION NUMBER: US/10/071,766
 ; CURRENT FILING DATE: 2002-02-07
 ; NUMBER OF SEQ ID NOS: 144
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 109
 ; LENGTH: 2404
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. US20020192678A1 251651.4
 ; NAME/KEY: unsure
 ; LOCATION: 710, 717, 724, 982-1007
 ; OTHER INFORMATION: a, t, c, g, or other
 US-10-071-766-109

Alignment Scores:
 Pred. No.: 3,66e-145 Length: 2404
 Score: 142.00 Matches: 142
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 14 Gaps: 0

US-09-690-825-34 (1-142) x US-10-071-766-109 (1-2404)

QY 1 MetGlyAlaProThrLeuProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
 DB 56 ATGGGTGCCCCGACGTGGCCCCCTGCTGGCAGCCCTTTCTCAAGGACCACCGCATCTCT 115
 QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
 DB 116 ACATTCAGAACTGGCCCTTCTTGGAGGCTGGCCTGCACCCCGAGCGGATGGCCGAG 175
 QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPheCys 60
 DB 176 GCTGGCTTTCATCCACTGCCCTCTTGGAGGCTGGCCTGCACCCCGAGCGGATGGCCGAG 235
 QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluHisLysLysHis 80
 DB 236 TTCAGAGCTGGAGGCTGGAGCCAGATGACGACCCCATAGAGGAACATAAAAGCAT 295
 QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluLeuThrLeuGlyGlu 100
 DB 296 TCGTCCGCTTTCCTTCTCTGTCAGAAAGCAGTTTGAAGATTAACCCCTTGGTGAA 355
 QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120
 DB 356 TTTTGAACCTGACAGAGAAAGAGCCAGAAACAAATTCGAAAGGAAACCAACATAAG 415
 QY 121 LysLysGluPheGluGluThrAlaLysLysValArgAlaIleGluGlnLeuAlaAla 140
 DB 416 AAGAAGAAATTTGAGGAAGTGGAGAAAGTGGCCCGTGGCATCGAGCAGCTGGCTGCC 475
 QY 141 MetAsp 142
 DB 476 ATGGAT 481

RESULT 9

US-10-084-817-285
 ; Sequence 285, Application US/10084817
 ; Publication No. US20030119009A1

GENERAL INFORMATION:
; APPLICANT: Susan Stuart
; APPLICANT: Jed G. Nuchtern
; APPLICANT: Sharon E. Plon
; APPLICANT: Jason M. Shohet
; TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION
; FILE REFERENCE: PA-0046 US
; CURRENT APPLICATION NUMBER: US/10/084,817
; CURRENT FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 60/270,784
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 365
; SOFTWARE: PERL Program
; SEQ ID NO 285
; LENGTH: 2404
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030119009A1 251651.4
; NAME/KEY: unsure
; LOCATION: 710, 717, 724
; OTHER INFORMATION: a, t, c, g, or other
US-10-084-817-285

Alignment Scores:
Pred. No.: 3,66e-145 Length: 2404
Score: 142.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-09-690-825-34 (1-142) x US-10-084-817-285 (1-2404)

QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
DB 56 ATGGTGGCCCGAGCTTCCCTCCCTGCTGGAGCCCTTCTCAAGGACCCAGCATCTCT 115
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 116 ACATTCAAGAACTGGCCCTTCTTGGAGGCTGCCTGCACCCCGAGCGATGGCCGAG 175
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
DB 176 GCTGCTTCATCCACTGCCCCACCTGAGAACGAGCCAGCTTGGCCCCAGTGTCTTCTTC 235
QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHisLysLysHis 80
DB 236 TTCAAGGAGCTGGAAGGCTGGAGCCAGATGACGACCCCATAGAGGAACATAAAAGCAT 295
QY 81 SerSerGlyCysAlaPheLeuSerValLysGlnPheGluGluLeuThrLeuGlyGlu 100
DB 296 TCGTCCCGGTGCGCTTCCCTTCTGTCAAGAGCAGATTGAAGAAATTAACCCCTTGGTGA 355
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
DB 356 TTTTGAACCTGGACAGAGAAGAGCCAGAACAAATTTCAAGAGGAACCAACATAAG 415
QY 121 LysLysGluPheGluGluThrAlaLysLysValArgAlaIleGluGlnLeuAlaAla 140
DB 416 AAGAAAGAAATTGAGGAACATCGAAGAAAGTGGCGGTGCCATCGACGAGCTGGCTGCC 475
QY 141 MetAsp 142
DB 476 ATGGAT 481

RESULT 10
US-10-305-720-918
; Sequence 918, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.

; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305,720
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016,434
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO 918
; LENGTH: 740
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040010136A1 752848
; NAME/KEY: unsure
; LOCATION: (1).... (740)
; OTHER INFORMATION: a, t, c, g, or other
US-10-305-720-918

Alignment Scores:
Pred. No.: 4,74e-92 Length: 740
Score: 93.00 Matches: 130
Percent Similarity: 98.48% Conservative: 0
Best Local Similarity: 98.48% Mismatches: 1
Query Match: 65.49% Indels: 2
DB: 16 Gaps: 0

US-09-690-825-34 (1-142) x US-10-305-720-918 (1-740)

QY 12 PropheLeuLysAspHisArgIleSerThrPheLysAsnTrpProPheLeuGluGlyCys 31
DB 51 CCGCTTCTCAAGGACCCAGCATCTCTACATTCAGAACTGGCCCTTCTTGGAGGGCTGC 110
QY 32 AlaCysThrProGluArgMetAlaGluAlaGlyPheIleHisCysProThrGlu-AsnGl 51
DB 111 GCGTCACCCCGAGCGATGGCCGAGCTGGCTTCATCCACTGCCCATGA-NAACGA 169
QY 51 uProAspLeuAlaGlnCysPhePheCysPheLysGluLeuGluGlyTrpGluProAspAs 71
DB 170 GCACAGACTTGGCCAGTGTCTTCTTCTGTCTCAAGAGCTGGAAGCTGGGAGCCAGATGA 229
QY 71 pAspProIleGluGluHisLysLysHisSerSerGlyCysAlaPheLeuSerValLysLy 91
DB 230 CGACCCCATAGAGGAACATTAAGAGCATTCGTCGGTTCGCTTTCCTTCTGTCAAGAA 289
QY 91 sGlnPheGluGluLeuThrLeuGlyGluPheLeuLysLeuAspArgGluArgAlaLysAs 111
DB 290 GCAGTTTGAAGAAATTAACCTTGGTGAATTTTGAACCTGGACAGAGAAAGACCAAGAA 349
QY 111 nLysIleAlaLysGluThrAsnAsnLysLysLysGluPheGluGluThrAlaLysLysVa 131
DB 350 CAAAATTCGAAGGAACCAACAATAAGAAAGAAATTTGAGGAACCTGCAAGAAAGT 409
QY 131 lArgArgAlaIleGluGlnLeuAlaAlaMetAsp 142
DB 410 GCGCGGTGCCATCGAGCAGCTGGCTGCCATGGAT 443

RESULT 11
US-09-918-186A-10
; Sequence 10, Application US/09918186A
; Patent No. US20020137708A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Eric E. Swayze
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: ISPH-0585
; CURRENT APPLICATION NUMBER: US/09/918,186A
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 09/496,694


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; PRIOR FILING DATE: 2000-02-02
; PRIOR APPLICATION NUMBER: 09/286,407
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 09/163,162
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 250
; SEQ ID NO 10
; LENGTH: 955
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (109)...(531)
US-09-918-186A-10

Alignment Scores:
Pred. No.: 4.4e-35 Length: 955
Score: 41.00 Matches: 41
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 28.87% Indels: 0
DB: 9 Gaps: 0

US-09-690-825-34 (1-142) x US-09-918-186A-10 (1-955)
QY 31 CysAlaCysThrProGluArgMetAlaGluAlaGlyPheIleHisCysProThrGluAsn 50
Db 199 TGGCCTGCACCCAGAGCGAATGGCGGAGGCTGGCTTCATCCACTGCCCTACCGAGAAC 258
QY 51 GluProAspLeuAlaGlnCysPhePheCysPheLysGluLeuGluGlyTrpGluProAsp 70
Db 259 GAGCCTGATTGGCCCACTGTTTTCTGCTTTAAGGAATTGGAAGGCTGGGAACCCGAT 318
QY 71 Asp 71
Db 319 GAC 321

RESULT 12
US-10-181-316-10
; Sequence 10, Application US/10181316
; Publication No. US20030211607A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Eric E. Swayze
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: ISPH-0650
; CURRENT APPLICATION NUMBER: US/10/181,316
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: PCT/US01/02939
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 09/496,694
; PRIOR FILING DATE: 2000-02-02
; PRIOR APPLICATION NUMBER: 09/286,407
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 09/163,162
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 249
; SEQ ID NO 10
; LENGTH: 955
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (109)...(531)
US-10-181-316-10

Alignment Scores:
Pred. No.: 4.4e-35 Length: 955
Score: 41.00 Matches: 41
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 28.87% Indels: 0
DB: 9 Gaps: 0

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Query Match: 28.87% Indels: 0
DB: 13 Gaps: 0

US-09-690-825-34 (1-142) x US-10-181-316-10 (1-955)
QY 31 CysAlaCysThrProGluArgMetAlaGluAlaGlyPheIleHisCysProThrGluAsn 50
Db 199 TGGCCTGCACCCAGAGCGAATGGCGGAGGCTGGCTTCATCCACTGCCCTACCGAGAAC 258
QY 51 GluProAspLeuAlaGlnCysPhePheCysPheLysGluLeuGluGlyTrpGluProAsp 70
Db 259 GAGCCTGATTGGCCCACTGTTTTCTGCTTTAAGGAATTGGAAGGCTGGGAACCCGAT 318
QY 71 Asp 71
Db 319 GAC 321

RESULT 13
US-10-179-730-33
; Sequence 33, Application US/10179730
; Publication No. US20030129611A1
; GENERAL INFORMATION:
; APPLICANT: BAQ, GANG
; APPLICANT: TSOURKAS, ANDREW
; APPLICANT: XU, YANGQING
; TITLE OF INVENTION: DUAL RESONANCE ENERGY TRANSFER NUCLEIC ACID PROBES
; FILE REFERENCE: 17625-0037
; CURRENT APPLICATION NUMBER: US/10/179,730
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: 60/300,672
; PRIOR FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: 60/303,258
; PRIOR FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 121
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-179-730-33

Alignment Scores:
Pred. No.: 8.09e-35 Length: 121
Score: 40.00 Matches: 40
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 28.17% Indels: 0
DB: 15 Gaps: 0

US-09-690-825-34 (1-142) x US-10-179-730-33 (1-121)
QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
Db 1 ATGGGTGCCCGACGTTGCCCTGCTGGCAGCCCTTCTCAAGGACCCACCGCATCTCT 60
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
Db 61 ACATTCAGAACTGCCCTTCTTGGAGGCTGCCCTTGCACCCCGAGCGGATGGCCGAG 120

RESULT 14
US-10-181-316-3
; Sequence 3, Application US/10181316
; Publication No. US20030211607A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Eric E. Swayze
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: ISPH-0650
; CURRENT APPLICATION NUMBER: US/10/181,316
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: PCT/US01/02939

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; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: 09/496,694
 ; PRIOR FILING DATE: 2000-02-02
 ; PRIOR FILING DATE: 2000-02-02
 ; PRIOR APPLICATION NUMBER: 09/286,407
 ; PRIOR FILING DATE: 1999-04-05
 ; PRIOR APPLICATION NUMBER: 09/163,162
 ; PRIOR FILING DATE: 1998-09-29
 ; NUMBER OF SEQ ID NOS: 249
 ; SEQ ID NO 3
 ; LENGTH: 14795
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (2811)...(2921)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (3174)...(3283)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (5158)...(5275)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (11955)...(12044)
 ; LOCATION: (11955)...(12044)
 ; US-10-181-316-3

Alignment Scores:
 Pred. No.: 8,5e-32 Length: 14795
 Score: 39.00 Matches: 39
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Mismatches: 0
 Query Match: 27.46%
 Indels: 0
 DB: 13 Gaps: 0

US-09-690-825-34 (1-142) x US-10-181-316-3 (1-14795)

QY 75 GluGluHisLysLysHisSerSerGlyCysAlaPheLeuSerValLysLysGlnPheGlu 94
 |||||
 Db 5158 GAGGAACATATAAAGCATTCGCGTTGCGTTCTTCTGTCAGAGCAGTTTGA 5217
 |||||
 QY 95 GluLeuThrLeuGlyGluPheLeuLysLeuAspArgGluArgAlaLysAsnLysIle 113
 |||||
 Db 5218 GAATTAACCCCTTGGTGAATTTTGAAACTGGACAGAGAAAGAGCCAAACAAAT 5274
 |||||

RESULT 15
 US-09-954-456-973
 ; Sequence 973, Application US/09954456
 ; Patent No. US20020115057A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Young, Paul
 ; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cance
 ; FILE REFERENCE: 689290-76
 ; CURRENT APPLICATION NUMBER: US/09/954,456
 ; CURRENT FILING DATE: 2001-09-18
 ; PRIOR APPLICATION NUMBER: US/60/233,617
 ; PRIOR FILING DATE: 2000-09-18
 ; PRIOR APPLICATION NUMBER: US/60/234,052
 ; PRIOR FILING DATE: 2000-09-20
 ; PRIOR APPLICATION NUMBER: US/60/235,923
 ; PRIOR FILING DATE: 2000-09-25
 ; PRIOR APPLICATION NUMBER: US/60/235,134
 ; PRIOR FILING DATE: 2000-09-25
 ; PRIOR APPLICATION NUMBER: US/60/235,637
 ; PRIOR FILING DATE: 2000-09-26
 ; PRIOR APPLICATION NUMBER: US/60/235,638
 ; PRIOR FILING DATE: 2000-09-26
 ; PRIOR APPLICATION NUMBER: US/60/235,711
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: US/60/235,720
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: US/60/235,840
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: US/60/235,863
 ; PRIOR FILING DATE: 2000-09-27
 ; NUMBER OF SEQ ID NOS: 2276
 ; SOFTWARE: Patent in version 3.0
 ; SEQ ID NO 1636
 ; LENGTH: 14796
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-954-456-1636

Alignment Scores:
 Pred. No.: 8,5e-32 Length: 14796
 Score: 39.00 Matches: 39
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Mismatches: 0
 Query Match: 27.46%
 Indels: 0

; PRIOR APPLICATION NUMBER: US/60/235,863
 ; PRIOR FILING DATE: 2000-09-27
 ; NUMBER OF SEQ ID NOS: 2276
 ; SOFTWARE: Patent in version 3.0
 ; SEQ ID NO 973
 ; LENGTH: 14796
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-954-456-973

Alignment Scores:
 Pred. No.: 8,5e-32 Length: 14796
 Score: 39.00 Matches: 39
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Mismatches: 0
 Query Match: 27.46%
 Indels: 0
 DB: 9 Gaps: 0

US-09-690-825-34 (1-142) x US-09-954-456-973 (1-14796)

QY 75 GluGluHisLysLysHisSerSerGlyCysAlaPheLeuSerValLysLysGlnPheGlu 94
 |||||
 Db 5159 GAGGAACATATAAAGCATTCGCGTTGCGTTCTTCTGTCAGAGCAGTTTGA 5218
 |||||
 QY 95 GluLeuThrLeuGlyGluPheLeuLysLeuAspArgGluArgAlaLysAsnLysIle 113
 |||||
 Db 5219 GAATTAACCCCTTGGTGAATTTTGAAACTGGACAGAGAAAGAGCCAAACAAAT 5275
 |||||

RESULT 16
 US-09-954-456-1636
 ; Sequence 1636, Application US/09954456
 ; Patent No. US20020115057A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Young, Paul
 ; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cance

; FILE REFERENCE: 689290-76
 ; CURRENT APPLICATION NUMBER: US/09/954,456
 ; CURRENT FILING DATE: 2001-09-18
 ; PRIOR APPLICATION NUMBER: US/60/233,617
 ; PRIOR FILING DATE: 2000-09-18
 ; PRIOR APPLICATION NUMBER: US/60/234,052
 ; PRIOR FILING DATE: 2000-09-20
 ; PRIOR APPLICATION NUMBER: US/60/234,923
 ; PRIOR FILING DATE: 2000-09-25
 ; PRIOR APPLICATION NUMBER: US/60/235,134
 ; PRIOR FILING DATE: 2000-09-25
 ; PRIOR APPLICATION NUMBER: US/60/235,637
 ; PRIOR FILING DATE: 2000-09-26
 ; PRIOR APPLICATION NUMBER: US/60/235,638
 ; PRIOR FILING DATE: 2000-09-26
 ; PRIOR APPLICATION NUMBER: US/60/235,711
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: US/60/235,720
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: US/60/235,840
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: US/60/235,863
 ; PRIOR FILING DATE: 2000-09-27
 ; NUMBER OF SEQ ID NOS: 2276
 ; SOFTWARE: Patent in version 3.0
 ; SEQ ID NO 1636
 ; LENGTH: 14796
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-954-456-1636

Alignment Scores:
 Pred. No.: 8,5e-32 Length: 14796
 Score: 39.00 Matches: 39
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Mismatches: 0
 Query Match: 27.46%
 Indels: 0

```

; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3421
; LENGTH: 14796
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 U75285
US-09-880-107-3421

Alignment Scores:
Pred. No.: 8,5e-32 Length: 14796
Score: 39.00 Matches: 39
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 27.48% Indels: 0
DB: Gaps: 0

US-09-690-825-34 (1-142) x US-09-880-107-3421 (1-14796)
QY 75 GluGluHisLysLysHisSerSerGlyCysAlaPheLeuSerVallyLysGlnPheGlu 94
Db 5159 GAGGGAACATATAAAGCAATTCGTCGGCTTCGCTTCCTTCCTCTCAAGAGACAGTTTGA 5218
QY 95 GluLeuThrLeuGlyGluPheLeuLysLeuAspArgGluArgAlaLysAsnLysIle 113
Db 5219 GAATTAACCTTTGGTGAATTTTGTGAACCTGGACAGAGAAGAGCAAGAACAAATT 5275

RESULT 19
US-09-968-007A-522
; Sequence 522, Application US/09968007A
; Publication No. US20040115625A1
; GENERAL INFORMATION:
; APPLICANT: Eber, Reinhard
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; FILE REFERENCE: 689290-71
; CURRENT APPLICATION NUMBER: US/09/968,007A
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/60/237,172
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,173
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,278
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,294
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,295
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,316
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 1001
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 522
; LENGTH: 14796
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-968-007A-522

Alignment Scores:
Pred. No.: 8,5e-32 Length: 14796
Score: 39.00 Matches: 39
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

```

Query Match: 27.46% Indels: 0
DB: 12 Gaps: 0

US-09-690-825-34 (1-142) x US-09-968-007A-522 (1-14796)

Qy 75 GluGluHisLysLysHisSerGlyCysAlaPheLeuSerValLysLysGlnPheGlu 94
|||
Db 5159 GAGGAACATAAAAGCATTGCGGTTGCCGCTTCTCTGTCAGAGCAGTTTGAA 5218
|||
Qy 95 GluLeuThrLeuGlyGluPheLeuLysLeuAspArgGluArgAlaLysAsnLysile 113
|||
Db 5219 GAATTAACCCCTGGTGAATTTTGAACACTGGACAGAGAAAGAGCCAGACAAATT 5275
|||

RESULT 20

US-10-138-618-35
; Sequence 35, Application US/10138618
; Publication No. US20030100525A1
; GENERAL INFORMATION:
; APPLICANT: Altieri, Dario C.
; TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
; CELLULAR APOPTOSIS, AND ITS MODULATION

NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/138,618
FILING DATE: 06-May-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/975,080
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: US 60/031,435
FILING DATE: 20-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176

INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 14796 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 35:

US-10-138-618-35

Alignment Scores:
Pred. No.: 8.5e-32 Length: 14796
Score: 39.00 Matches: 39
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 27.46% Indels: 0
DB: 15 Gaps: 0

US-09-690-825-34 (1-142) x US-10-138-618-35 (1-14796)

Qy 75 GluGluHisLysLysHisSerGlyCysAlaPheLeuSerValLysLysGlnPheGlu 94
|||
Db 5159 GAGGAACATAAAAGCATTGCGGTTGCCGCTTCTCTGTCAGAGCAGTTTGAA 5218
|||

Qy 95 GluLeuThrLeuGlyGluPheLeuLysLeuAspArgGluArgAlaLysAsnLysile 113
|||
Db 5219 GAATTAACCCCTGGTGAATTTTGAACACTGGACAGAGAAAGAGCCAGACAAATT 5275
|||

RESULT 21

US-10-029-386-23672/c
; Sequence 23672, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GE
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 23672
; LENGTH: 120
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR17.3
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.66
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.52
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
; OTHER INFORMATION: NT HIT: U75285.1, EVALUE 2.00e-61
; OTHER INFORMATION: EST HUMAN HIT: AA994786.1, EVALUE 5.00e-60
; OTHER INFORMATION: SWISSPROT HIT: O15392, EVALUE 2.00e-18

US-10-029-386-23672
Alignment Scores:
Pred. No.: 1.9e-30 Length: 120
Score: 36.00 Matches: 36
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 25.35% Indels: 0
DB: 15 Gaps: 0

US-09-690-825-34 (1-142) x US-10-029-386-23672 (1-120)

Qy 38 MetaGluAlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCys 57
|||
Db 117 ATGGCCGAGGCTGGCTTCATCCACTGCCCACTGAGACGAGCCAGACTTGGCCCATGT 58
|||
Qy 58 PhePheCysPheLysGluLeuGlyTrpGluProAspAspPro 73
|||
Db 57 TTCTTCTGCTTCAAGGAGCTGGAAGGCTGGAGCCAGATGACGACCCC 10
|||

RESULT 22

US-10-029-386-9972/c
; Sequence 9972, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GE
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 9972
; LENGTH: 555
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR17.3

US-10-029-386-9972/c
Alignment Scores:
Pred. No.: 8.5e-32 Length: 14796
Score: 39.00 Matches: 39
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 27.46% Indels: 0
DB: 15 Gaps: 0

US-09-690-825-34 (1-142) x US-10-138-618-35 (1-14796)

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.66
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.52
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
OTHER INFORMATION: EST_HUMAN HIT: AA954786.1, EVALUATE 1.00e-122
OTHER INFORMATION: SWISSPROT HIT: O15392, EVALUATE 4.00e-19
OTHER INFORMATION: NT HIT: U75285.1, EVALUATE 0.00e+00
NAME/KEY: unsure
LOCATION: 320
US-10-029-386-9972

Alignment Scores:
Pred. No.: 7,82e-30 Length: 555
Score: 36.00 Matches: 36
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 25.35% Indels: 0
DB: 15 Gaps: 0

US-09-690-825-34 (1-142) x US-10-029-386-9972 (1-555)

QY 38 MetalagluAlaglyPheileHisCysProThrGluAsnGluProAspLeuAlaGlnCys 57
DB 222 ATGGCGAGGCTGGCTTCATCCACTGCCCACTGAGAACGAGCCAGACTTGGCCAGGT 163
QY 58 PhePheCysPheGluLeuGluGlyTrpGluProAspAspPro 73
DB 162 TTCCTTCTGCTCAAGAGCTGGAAGCTGGAGCGGAGCAGATGAGACCCC 115

RESULT 23

US-10-108-877-2
Sequence 2, Application US/10108877
Publication No. US20030083482A1
GENERAL INFORMATION:
APPLICANT: Fox Chase Cancer Center
APPLICANT: Murphy, Maureen E.
TITLE OF INVENTION: Compositions and Methods for
TITLE OF INVENTION: P53-Mediated Repression of Gene Expression
FILE REFERENCE: FCCC 99-03
CURRENT APPLICATION NUMBER: US/10/108,877
CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: PCT/US00/27078
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 60/157,171
PRIOR FILING DATE: 1999-09-30
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 1100
TYPE: DNA
ORGANISM: murine
US-10-108-877-2

Alignment Scores:
Pred. No.: 1.47e-29 Length: 1100
Score: 36.00 Matches: 36
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 25.35% Indels: 0
DB: 15 Gaps: 0

US-09-690-825-34 (1-142) x US-10-108-877-2 (1-1100)

QY 1 MetGlyAlaProThrLeuProAlaTrpGlnProPheLeuIysAspHisArgIleSer 20
DB 991 ATGGTGCCCGAGCGTGGCCCTGCTGGCAGCCCTTCTCAAGACCCAGCATCTCT 1050
QY 21 ThrPheIysAsnTrpPropheLeuGluGlyCysAlaCysThrProGlu 36
DB 1051 ACATTCAAGAACTGGCCCTTCTGGAGGCTGGCCTGCACCCCGGAG 1098

RESULT 24

US-09-833-381-1331

Sequence 1331, Application US/09833381
Patent No. US20020132090A1
GENERAL INFORMATION:
APPLICANT: Robison, Keith E.
TITLE OF INVENTION: No. US20020132090A1 Nucleic Acid and Protein Homologs
FILE REFERENCE: 5800-119
CURRENT APPLICATION NUMBER: US/09/833,381
CURRENT FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 09/516,448
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 2050
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1331
LENGTH: 332
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(332)
OTHER INFORMATION: n = A,T,C or G
US-09-833-381-1331

Alignment Scores:
Pred. No.: 5.57e-06 Length: 332
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.86% Indels: 0
DB: 9 Gaps: 0

US-09-690-825-34 (1-142) x US-09-833-381-1331 (1-332)

QY 68 GluProAspAspProIleGluGluHisIleIysHisSer 81
DB 240 GAGCCAGATGACGACCCNATAGAGACATATAAAGCATTCG 281

RESULT 25

US-10-400-382-265
Sequence 265, Application US/10400382
Publication No. US20030190659A1
GENERAL INFORMATION:
APPLICANT: Lacasse, Eric
APPLICANT: McManus, Daniel
APPLICANT: Durkin, Jonathan P.
TITLE OF INVENTION: Antisense IAP Nucleobase Oligomers and
TITLE OF INVENTION: Uses Thereof
FILE REFERENCE: 07891/025004
CURRENT APPLICATION NUMBER: US/10/400,382
CURRENT FILING DATE: 2003-03-27
PRIOR APPLICATION NUMBER: US 60/367,853
PRIOR FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 460
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 265
LENGTH: 30
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: based on Homo sapiens.
US-10-400-382-265

Alignment Scores:
Pred. No.: 0.177 Length: 30
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 6.34% Indels: 0
DB: 15 Gaps: 0

US-09-690-825-34 (1-142) x US-10-400-382-265 (1-30)

QY 69 ProAspAspProIleGluHis 77
|||||

Db 3 CCAGATGACGACCCCATAGAGGAACAT 29

RESULT 26

US-10-636-065-199
; Sequence 199, Application US/10636065
; Publication No. US20040127694A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: LaCasse, Eric
; APPLICANT: Baird, Stephen
; APPLICANT: Holcik, Martin
; APPLICANT: Young, Sean
; TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses
; FILE REFERENCE: 07891/025005
; CURRENT APPLICATION NUMBER: US/10/636,065
; CURRENT FILING DATE: 2003-08-07
; PRIOR APPLICATION NUMBER: 09/672,717
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 199
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: based on Homo sapiens
US-10-636-065-199

Alignment Scores:

Pred. No.:	0.177	Length:	30
Score:	9.00	Matches:	9
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	6.34%	Indels:	0
DB:	17	Gaps:	0

US-09-690-825-34 (1-142) x US-10-636-065-199 (1-30)

Qy 69 ProAspAspProfileGluGluHis 77

Db 3 CCAGATGACGACCCCATAGAGGAACAT 29

RESULT 27

US-09-918-186A-13
; Sequence 13, Application US/09918186A
; Patent No. US20020137708A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Eric E. Swayze
; APPLICANT: Lex M. Cowsert
; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: ISFH-0585
; CURRENT APPLICATION NUMBER: US/09/918,186A
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 09/496,694
; PRIOR FILING DATE: 2000-02-02
; PRIOR APPLICATION NUMBER: 09/286,407
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 09/163,162
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 250
; SEQ ID NO 13
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Probe
US-09-918-186A-13

Alignment Scores:

Pred. No.:	1.93	Length:	26
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Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.63% Indels: 0
DB: 9 Gaps: 0

US-09-690-825-34 (1-142) x US-09-918-186A-13 (1-26)

Qy 62 LysGluLeuGluGlyTTPGluPro 69

Db 2 AAGGAATTGGAAGCTGGGAACCC 25

RESULT 28

US-10-181-316-13
; Sequence 13, Application US/10181316
; Publication No. US20030211607A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Eric E. Swayze
; APPLICANT: Lex M. Cowsert
; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: ISFH-0650
; CURRENT APPLICATION NUMBER: US/10/181,316
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: PCT/US01/02939
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 09/496,694
; PRIOR FILING DATE: 2000-02-02
; PRIOR APPLICATION NUMBER: 09/286,407
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 09/163,162
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 249
; SEQ ID NO 13
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Probe
US-10-181-316-13

Alignment Scores:

Pred. No.:	1.93	Length:	26
Score:	8.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	5.63%	Indels:	0
DB:	13	Gaps:	0

US-09-690-825-34 (1-142) x US-10-181-316-13 (1-26)

Qy 62 LysGluLeuGluGlyTTPGluPro 69

Db 2 AAGGAATTGGAAGCTGGGAACCC 25

RESULT 29

US-09-833-381-1330
; Sequence 1330, Application US/09833381
; Patent No. US20020132090A1
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. US20020132090A1el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1330
; LENGTH: 281
; TYPE: DNA

```

; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(281)
; OTHER INFORMATION: n = A,T,C or G
US-09-833-381-1330

Alignment Scores:
Pred. No.: 17.4 Length: 281
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.63% Indels: 0
DB: 9 Gaps: 0

US-09-690-825-34 (1-142) x US-09-833-381-1330 (1-281)

QY 60 CysPheIysGluLeuGluGlyTyr 67
DB 258 TCCTTCAGGAGCTGGAGGCTGG 281

RESULT 30
US-10-027-632-65868
; Sequence 65868, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65868
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-65868

Alignment Scores:
Pred. No.: 25.2 Length: 420
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.63% Indels: 0
DB: 13 Gaps: 0

US-09-690-825-34 (1-142) x US-10-027-632-65868 (1-420)

QY 79 LysHisSerSerGlyCysAlaphe 86
DB 21 AAACATAGTTCAGGCTGTGCATT 44

RESULT 31
US-10-027-632-65869
; Sequence 65869, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:

```

```
US-10-027-632-65870
Alignment Scores:
Pred. No.: 25.2 Length: 420
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.63% Indels: 0
DB: 13 Gaps: 0

US-09-690-825-34 (1-142) x US-10-027-632-65870 (1-420)
QY 79 LysHisSerSerGlyCysAlaphe 86
DB 21 AAACATAGTTGAGGCTGTGCATT 44

RESULT 33
US-10-027-632-65868
; Sequence 65868, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR FILING DATE: 2000-04-20
; PRIOR FILING DATE: 2000-03-29
; PRIOR FILING DATE: 1999-09-28
; PRIOR FILING DATE: 2000-02-24
; PRIOR FILING DATE: 1999-11-23
; PRIOR FILING DATE: 2000-03-29
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65868
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-65868
Alignment Scores:
Pred. No.: 25.2 Length: 420
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.63% Indels: 0
DB: 16 Gaps: 0

US-09-690-825-34 (1-142) x US-10-027-632-65868 (1-420)
QY 79 LysHisSerSerGlyCysAlaphe 86
DB 21 AAACATAGTTGAGGCTGTGCATT 44

RESULT 34
US-10-027-632-65869
; Sequence 65869, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR FILING DATE: 2000-04-20
; PRIOR FILING DATE: 2000-03-29
; PRIOR FILING DATE: 1999-09-28
; PRIOR FILING DATE: 2000-02-24
; PRIOR FILING DATE: 1999-11-23
; PRIOR FILING DATE: 2000-03-29
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65869
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-65869
Alignment Scores:
Pred. No.: 25.2 Length: 420
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.63% Indels: 0
DB: 16 Gaps: 0

US-09-690-825-34 (1-142) x US-10-027-632-65869 (1-420)
QY 79 LysHisSerSerGlyCysAlaphe 86
DB 21 AAACATAGTTGAGGCTGTGCATT 44

RESULT 35
US-10-027-632-65870
; Sequence 65870, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR FILING DATE: 2000-04-20
; PRIOR FILING DATE: 2000-03-29
; PRIOR FILING DATE: 1999-09-28
; PRIOR FILING DATE: 2000-02-24
; PRIOR FILING DATE: 1999-11-23
; PRIOR FILING DATE: 2000-03-29
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65870
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-65870
Alignment Scores:
Pred. No.: 25.2 Length: 420
Score: 8.00 Matches: 8
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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.63% Indels: 0
DB: 16 Gaps: 0

US-09-690-825-34 (1-142) x US-10-027-632-65870 (1-420)

QY 79 LysHisSerGlyCysAlaPhe 86
DB 21 AAACATAGTTCAGGCTGTCATT 44

RESULT 36

US-10-424-599-114486
; Sequence 114486, Application US/10424599
; Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Kovalic David X

APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53223)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 114486

LENGTH: 454

TYPE: DNA

ORGANISM: Glycine max

FEATURE:

OTHER INFORMATION: Clone ID: PAT_MRT3847_7438C.1

US-10-424-599-114486

Alignment Scores: 27.1 Length: 454
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.63% Indels: 0
DB: 13 Gaps: 0

US-09-690-825-34 (1-142) x US-10-424-599-114486 (1-454)

QY 2 GlyAlaProThrLeuProPheAla 9
DB 271 GGTGCCCCGACCTTCCCGGCT 294

RESULT 37

US-09-918-186A-231
; Sequence 231, Application US/09918186A
; Patent No. US20020137708A1

GENERAL INFORMATION:

APPLICANT: C. Frank Bennett

APPLICANT: Elizabeth J. Ackermann

APPLICANT: Eric B. Swayze

APPLICANT: Lex M. Cowsett

TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION

FILE REFERENCE: ISPH-0585

CURRENT APPLICATION NUMBER: US/09/918,186A

CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: 09/496,694

PRIOR FILING DATE: 2000-02-02

PRIOR APPLICATION NUMBER: 09/286,407

PRIOR FILING DATE: 1999-04-05

PRIOR APPLICATION NUMBER: 09/163,162

PRIOR FILING DATE: 1998-09-29

NUMBER OF SEQ ID NOS: 250

SEQ ID NO 231

LENGTH: 515

TYPE: DNA

ORGANISM: Mus musculus

FEATURE:

OTHER INFORMATION: Application US/09918995

; NAME/KEY: unsure
; LOCATION: 266
; OTHER INFORMATION: unknown
; NAME/KEY: CDS
; LOCATION: (301)...(384)
US-09-918-186A-231

Alignment Scores:

Pred. No.: 30.4 Length: 515
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.63% Indels: 0
DB: 9 Gaps: 0

US-09-690-825-34 (1-142) x US-09-918-186A-231 (1-515)

QY 122 LysGluPheGluThrAlaLys 129
DB 325 AAAGAGTTTGAGAGACTGCAAG 348

RESULT 38

US-10-181-316-231

; Sequence 231, Application US/10181316

; Publication No. US20030211607A1

GENERAL INFORMATION:

APPLICANT: C. Frank Bennett

APPLICANT: Elizabeth J. Ackermann

APPLICANT: Eric E. Swayze

APPLICANT: Lex M. Cowsett

TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION

FILE REFERENCE: ISPH-0650

CURRENT APPLICATION NUMBER: US/10/181,316

CURRENT FILING DATE: 2002-07-16

PRIOR APPLICATION NUMBER: PCT/US01/02939

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: 09/496,694

PRIOR FILING DATE: 2000-02-02

PRIOR APPLICATION NUMBER: 09/286,407

PRIOR FILING DATE: 1999-04-05

PRIOR APPLICATION NUMBER: 09/163,162

PRIOR FILING DATE: 1998-09-29

NUMBER OF SEQ ID NOS: 249

SEQ ID NO 231

LENGTH: 515

TYPE: DNA

ORGANISM: Mus musculus

FEATURE:

NAME/KEY: unsure

LOCATION: 266

OTHER INFORMATION: unknown

FEATURE:

NAME/KEY: CDS

LOCATION: (301)...(384)

US-10-181-316-231

Alignment Scores:

Pred. No.: 30.4 Length: 515
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.63% Indels: 0
DB: 13 Gaps: 0

US-09-690-825-34 (1-142) x US-10-181-316-231 (1-515)

QY 122 LysGluPheGluThrAlaLys 129
DB 325 AAAGAGTTTGAGAGACTGCAAG 348

RESULT 39

US-09-918-995-15078

; Sequence 15078, Application US/09918995

Publication No. US20030073623A1
 GENERAL INFORMATION:
 APPLICANT: Hyseq, Inc.
 TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
 FILE REFERENCE: 20411-756
 CURRENT APPLICATION NUMBER: US/09/918,995
 PRIOR FILING DATE: 2001-07-30
 PRIOR APPLICATION NUMBER: US/09/235,076
 PRIOR FILING DATE: 1999-01-20
 NUMBER OF SEQ ID NOS: 38054
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 15078
 LENGTH: 587
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1)...(587)
 OTHER INFORMATION: n = A,T,C or G
 US-09-918-995-15078

Alignment Scores:
 Pred. No.: 34.3 Length: 587
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 5.63% Indels: 0
 DB: 10 Gaps: 0

US-09-690-825-34 (1-142) x US-09-918-995-15078 (1-587)

QY 1 MetGlyAlaProThrLeuProPro 8
 DB 367 ATGGGAGCCCCACACTCCCTCCT 390

RESULT 40

US-10-369-493-35886/c
 Sequence 35886, Application US/10369493
 Publication No. US20030233675A1
 GENERAL INFORMATION:
 APPLICANT: Cao, Yongwei
 APPLICANT: Hinkle, Gregory J.
 APPLICANT: Slater, Steven C.
 APPLICANT: Goldman, Barry S.
 APPLICANT: Chen, Xianfeng
 TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 FILE REFERENCE: 38-10(52052)B
 CURRENT APPLICATION NUMBER: US/10/369,493
 CURRENT FILING DATE: 2003-02-28
 PRIOR APPLICATION NUMBER: US 60/360,039
 PRIOR FILING DATE: 2002-02-21
 NUMBER OF SEQ ID NOS: 47374
 SEQ ID NO 35886
 LENGTH: 1224
 TYPE: DNA
 ORGANISM: Mesorhizobium loti
 US-10-369-493-35886

Alignment Scores:
 Pred. No.: 67.6 Length: 1224
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 5.63% Indels: 0
 DB: 16 Gaps: 0

US-09-690-825-34 (1-142) x US-10-369-493-35886 (1-1224)

QY 94 GluGluLeuThrLeuGlyGluPhe 101
 DB 351 GAGGAGTTCGTTGGTGAATTT 328

RESULT 41
 US-10-050-704-14
 Sequence 14, Application US/10050704
 Publication No. US20030050442A1
 GENERAL INFORMATION:
 APPLICANT: Ruben et al.
 TITLE OF INVENTION: 62 Human Secreted Proteins
 FILE REFERENCE: P2039P1
 CURRENT APPLICATION NUMBER: US/10/050,704
 CURRENT FILING DATE: 2002-01-18
 PRIOR APPLICATION NUMBER: 09/684,524
 PRIOR FILING DATE: 2000-10-10
 PRIOR APPLICATION NUMBER: PCT/US00/08979
 PRIOR FILING DATE: 2000-04-06
 PRIOR APPLICATION NUMBER: 60/128,693
 PRIOR FILING DATE: 1999-04-09
 PRIOR APPLICATION NUMBER: 60/130,991
 PRIOR FILING DATE: 1999-04-26
 NUMBER OF SEQ ID NOS: 344
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 14
 LENGTH: 1441
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: SITE
 LOCATION: (1436)
 OTHER INFORMATION: n equals a,t,g, or c
 NAME/KEY: SITE
 LOCATION: (1438)
 OTHER INFORMATION: n equals a,t,g, or c
 US-10-050-704-14

Alignment Scores:
 Pred. No.: 78.7 Length: 1441
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 5.63% Indels: 0
 DB: 15 Gaps: 0

US-09-690-825-34 (1-142) x US-10-050-704-14 (1-1441)

QY 1 MetGlyAlaProThrLeuProPro 8
 DB 1343 ATGGGAGCCCCACACTCCCTCCT 1366

RESULT 42

US-10-798-512-14
 Sequence 14, Application US/10798512
 Publication No. US20040152164A1
 GENERAL INFORMATION:
 APPLICANT: Ruben et al.
 TITLE OF INVENTION: 62 Human Secreted Proteins
 FILE REFERENCE: P2039P1
 CURRENT APPLICATION NUMBER: US/10/798,512
 CURRENT FILING DATE: 2004-03-12
 PRIOR APPLICATION NUMBER: US/09/684,524
 PRIOR FILING DATE: 2000-10-10
 PRIOR APPLICATION NUMBER: PCT/US00/08979
 PRIOR FILING DATE: 2000-04-06
 PRIOR APPLICATION NUMBER: 60/128,693
 PRIOR FILING DATE: 1999-04-09
 PRIOR APPLICATION NUMBER: 60/130,991
 PRIOR FILING DATE: 1999-04-26
 NUMBER OF SEQ ID NOS: 344
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 14
 LENGTH: 1441
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:

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; NAME/KEY: SITE
; LOCATION: (1436)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1438)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-798-512-14

Alignment Scores:
Pred. No.:      78.7      Length:      1441
Score:          8.00      Matches:      8
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      5.63%      Indels:      0
DB:              17      Gaps:      0

US-09-690-825-34 (1-142) x US-10-798-512-14 (1-1441)
QY      1 MetGlyAlaProThreuProPro 8
Db      1343 ATGGGAGCCCCACACTCCCTCT 1366

RESULT 43
US-09-946-374-51
; Sequence 51, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830PICI
; CURRENT APPLICATION NUMBER: US/09/946,374
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099602
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099642
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099741
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099754
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099763
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099792
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099808
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099815
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100388
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100584
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100661
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100662
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100664
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100683
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100684
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100710
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100711
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100849
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100930
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101014
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101068
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101071
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101279
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: 60/101471
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101472
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101474
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101475
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101476
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
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; PRIOR APPLICATION NUMBER: 60/101479
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101743
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101915
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/102207
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102240
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102307
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102330
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102331
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102484
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102487
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102570
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102571
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102684
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102687
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102965
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 60/103258
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103314
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103315
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103328
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103395
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103396
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103401
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103449
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103633
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103678
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103679
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103711
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/104257
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266

; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807
Alignment Scores:
Pred. No.: 93.3 Length: 1734
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.63% Indels: 0
DB: 10 Gaps: 0
US-09-690-825-34 (1-142) x US-09-946-374-51 (1-1734)
QY 1 MetGlyAlaProThrLeuProPro 8
DB 1534 ATGGAGCCCCCACACTCCCTCCT 1557
RESULT 44
US-10-015-395A-51
; Sequence 51, Application US/10015395A
; Publication No. US20040073015A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830PIC57
; CURRENT APPLICATION NUMBER: US/10/015,395A
; CURRENT FILING DATE: 2001-12-12
; Prior application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 51
; LENGTH: 1734
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-015-395A-51
Alignment Scores:
Pred. No.: 93.3 Length: 1734
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.63% Indels: 0
DB: 12 Gaps: 0
US-09-690-825-34 (1-142) x US-10-015-395A-51 (1-1734)
QY 1 MetGlyAlaProThrLeuProPro 8
DB 1534 ATGGAGCCCCCACACTCCCTCCT 1557
RESULT 45
US-10-206-915-201
; Sequence 201, Application US/10206915
; Publication No. US20040029221A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.

APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C464
CURRENT APPLICATION NUMBER: US/10/206,915
CURRENT FILING DATE: 2002-07-26
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063541
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063544
PRIOR FILING DATE: 1997-10-28
Prior Application data removed - See File Wrapper or PALM.
SEQ ID NO 201
LENGTH: 1734
TYPE: DNA
ORGANISM: Homo Sapien
US-10-206-915-201
Alignment Scores:
Pred. No.: 93.3 Length: 1734
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.63% Indels: 0
DB: 13 Gaps: 0
US-09-690-825-34 (1-142) x US-10-206-915-201 (1-1734)
QY 1 MetGlyAlaProThrLeuProPro 8
DB 1534 ATGGAGCCCCCACACTCCCTCCT 1557
RESULT 46
US-10-199-670-201
Sequence 201, Application US/10/199670
Publication No. US20040033560A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C464
CURRENT APPLICATION NUMBER: US/10/201,858
CURRENT FILING DATE: 2002-07-23
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266

APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C401
CURRENT APPLICATION NUMBER: US/10/199,670
CURRENT FILING DATE: 2002-07-19
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063544
PRIOR FILING DATE: 1997-10-28
Prior Application data removed - See File Wrapper or PALM.
SEQ ID NO 201
LENGTH: 1734
TYPE: DNA
ORGANISM: Homo Sapien
US-10-199-670-201
Alignment Scores:
Pred. No.: 93.3 Length: 1734
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.63% Indels: 0
DB: 13 Gaps: 0
US-09-690-825-34 (1-142) x US-10-199-670-201 (1-1734)
QY 1 MetGlyAlaProThrLeuProPro 8
DB 1534 ATGGAGCCCCCACACTCCCTCCT 1557
RESULT 47
US-10-201-858-201
Sequence 201, Application US/10201858
Publication No. US2004003837A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C464
CURRENT APPLICATION NUMBER: US/10/201,858
CURRENT FILING DATE: 2002-07-23
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266

```

; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 201
; LENGTH: 1734
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-201-858-201

```

```

Alignment Scores:
Pred. No.: 93.3 Length: 1734
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best local Similarity: 100.00% Mismatches: 0
Query Match: 5.63% Indels: 0
DB: 13 Gaps: 0

```

US-09-690-825-34 (1-142) x US-10-201-858-201 (1-1734)

QY 1 MetGlyAlaProThrLeuProPro 8

DB 1534 ATGGAGGCCCCACACTCCCTCT 1557

RESULT 48

```

US-10-081-056-149
; Sequence 149, Application US/10081056
; Publication No. US20040043927A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Masters, Scott A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P.Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: F3235F1C1
; CURRENT APPLICATION NUMBER: US/10/081,056
; CURRENT FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28

```

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; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/230,978
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/000,000
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 09/664,610
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 60/242,922
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 09/709,238
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: PCT/US00/30952
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 09/747,259
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/34956
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 09/767,609
; PRIOR FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: US 09/796,498
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/06666
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: US 09/802,706
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: US 09/808,689
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 09/816,744
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US 09/828,366
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 09/854,208
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 09/854,280
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 09/866,034
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: PCT/US01/17092
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 09/870,574
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: PCT/US01/17443
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/00000
; PRIOR FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 149
; LENGTH: 1734
; TYPE: DNA
; ORGANISM: Homosapiens
US-10-081-056-149

```

Alignment Scores:
 Pred. No.: 93.3 Length: 1734
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 5.63% Indels: 0
 DB: 13 Gaps: 0

US-09-690-825-34 (1-142) x US-10-081-056-149 (1-1734)

QY 1 MetGlyAlaProThrLeuProPro 8
 DB 1534 ATGGAGCCCCCACACTCCCTCCT 1557

RESULT 49

US-10-219-535-155

; Sequence 155, Application US/10219555

; Publication No. US20040044179A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Desnoyers, Luc

; APPLICANT: Gerritsen, Mary

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Smith, Victoria

; APPLICANT: Stephan, Jean-Philippe F.

; APPLICANT: Watanabe, Colin L.

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3530P1C103

; CURRENT APPLICATION NUMBER: US/10/219,535

; CURRENT FILING DATE: 2002-08-14

; PRIOR APPLICATION NUMBER: 10/119,480

; PRIOR FILING DATE: 2002-04-09

; PRIOR APPLICATION NUMBER: 60/059113

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/062287

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/063549

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/064103

; PRIOR FILING DATE: 1997-10-31

; PRIOR APPLICATION NUMBER: 60/069873

; PRIOR FILING DATE: 1997-12-17

; PRIOR APPLICATION NUMBER: 60/078910

; PRIOR FILING DATE: 1998-03-20

; PRIOR APPLICATION NUMBER: 60/079294

; PRIOR FILING DATE: 1998-03-25

; PRIOR APPLICATION NUMBER: 60/079656

; PRIOR FILING DATE: 1998-03-26

; PRIOR APPLICATION NUMBER: 60/079728

; PRIOR FILING DATE: 1998-03-27

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 246

; SEQ ID NO 155

; LENGTH: 1734

; TYPE: DNA

; ORGANISM: Homo Sapien

US-10-219-535-155

Alignment Scores:

Pred. No.: 93.3 Length: 1734

Score: 8.00 Matches: 8

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 5.63% Indels: 0

DB: 13 Gaps: 0

US-09-690-825-34 (1-142) x US-10-219-535-155 (1-1734)

QY 1 MetGlyAlaProThrLeuProPro 8

DB 1534 ATGGAGCCCCCACACTCCCTCCT 1557

RESULT 51

US-10-205-890-201

; Sequence 201, Application US/10205890

; Publication No. US20040048334A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

QY 1 MetGlyAlaProThrLeuProPro 8
 DB 1534 ATGGAGCCCCCACACTCCCTCCT 1557

RESULT 50

US-10-232-230-155

; Sequence 155, Application US/10232230

; Publication No. US20040044180A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Desnoyers, Luc

; APPLICANT: Gerritsen, Mary

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Smith, Victoria

; APPLICANT: Stephan, Jean-Philippe F.

; APPLICANT: Watanabe, Colin L.

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3530P1C103

; CURRENT APPLICATION NUMBER: US/10/232,230

; CURRENT FILING DATE: 2002-08-29

; PRIOR APPLICATION NUMBER: 10/119,480

; PRIOR FILING DATE: 2002-04-09

; PRIOR APPLICATION NUMBER: 60/059113

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/062287

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/063549

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/064103

; PRIOR FILING DATE: 1997-10-31

; PRIOR APPLICATION NUMBER: 60/069873

; PRIOR FILING DATE: 1997-12-17

; PRIOR APPLICATION NUMBER: 60/078910

; PRIOR FILING DATE: 1998-03-20

; PRIOR APPLICATION NUMBER: 60/079294

; PRIOR FILING DATE: 1998-03-25

; PRIOR APPLICATION NUMBER: 60/079656

; PRIOR FILING DATE: 1998-03-26

; PRIOR APPLICATION NUMBER: 60/079728

; PRIOR FILING DATE: 1998-03-27

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 246

; SEQ ID NO 155

; LENGTH: 1734

; TYPE: DNA

; ORGANISM: Homo Sapien

US-10-232-230-155

Alignment Scores:

Pred. No.: 93.3 Length: 1734

Score: 8.00 Matches: 8

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 5.63% Indels: 0

DB: 13 Gaps: 0

US-09-690-825-34 (1-142) x US-10-232-230-155 (1-1734)

QY 1 MetGlyAlaProThrLeuProPro 8

DB 1534 ATGGAGCCCCCACACTCCCTCCT 1557

RESULT 51

US-10-205-890-201

; Sequence 201, Application US/10205890

; Publication No. US20040048334A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

```

; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C519
; CURRENT APPLICATION NUMBER: US/10/205,890
; CURRENT FILING DATE: 2002-07-26
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 201
; LENGTH: 1734
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-205-890-201

Alignment Scores:
Pred. No.: 93.3 Length: 1734
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.63% Indels: 0
DB: 13 Gaps: 0

US-09-690-825-34 (1-142) x US-10-205-890-201 (1-1734)

QY 1 MetGlyAlaProThrLeuProPro 8
Db 1534 ATGGAGCCCCCACACTCCCTCCT 1557

RESULT 52
US-10-208-024-201
; Sequence 201, Application US/10208024
; Publication No US20040048335A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C465
; CURRENT APPLICATION NUMBER: US/10/201,853
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266

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; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C538
; CURRENT APPLICATION NUMBER: US/10/208,024
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 201
; LENGTH: 1734
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-208-024-201

Alignment Scores:
Pred. No.: 93.3 Length: 1734
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.63% Indels: 0
DB: 13 Gaps: 0

US-09-690-825-34 (1-142) x US-10-208-024-201 (1-1734)

QY 1 MetGlyAlaProThrLeuProPro 8
Db 1534 ATGGAGCCCCCACACTCCCTCCT 1557

RESULT 53
US-10-201-853-201
; Sequence 201, Application US/10201853
; Publication No. US20040053358A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C465
; CURRENT APPLICATION NUMBER: US/10/201,853
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266

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; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 201
; LENGTH: 1734
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-201-853-201

Alignment Scores:
Pred. No.: 93.3 Length: 1734
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.63% Indels: 0
DB: 13 Gaps: 0

US-09-690-825-34 (1-142) x US-10-201-853-201 (1-1734)

QY 1 MetGlyAlaProThrLeuProPro 8
Db 1534 ATGGGAGCCCCCACACTCCCTCCT 1557

RESULT 54
US-10-063-745-51
; Sequence 51, Application US/10063745
; Publication No. US20040059411A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT FILING DATE: 2002-05-09
; PRIOR APPLICATION removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 51
; LENGTH: 1734
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-745-51

Alignment Scores:
Pred. No.: 93.3 Length: 1734
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.63% Indels: 0
DB: 13 Gaps: 0

US-09-690-825-34 (1-142) x US-10-063-745-51 (1-1734)
```

```
QY 1 MetGlyAlaProThrLeuProPro 8
Db 1534 ATGGGAGCCCCCACACTCCCTCCT 1557

RESULT 55
US-10-063-512-51
; Sequence 51, Application US/10063512
; Publication No. US20030018183A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT FILING DATE: 2002-05-01
; PRIOR APPLICATION removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 51
; LENGTH: 1734
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-512-51

Alignment Scores:
Pred. No.: 93.3 Length: 1734
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.63% Indels: 0
DB: 13 Gaps: 0

US-09-690-825-34 (1-142) x US-10-063-512-51 (1-1734)

QY 1 MetGlyAlaProThrLeuProPro 8
Db 1534 ATGGGAGCCCCCACACTCCCTCCT 1557

RESULT 56
US-10-053-513-51
; Sequence 51, Application US/10063513
; Publication No. US20030018172A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT FILING DATE: 2002-05-01
; PRIOR APPLICATION removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 51
; LENGTH: 1734
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-053-513-51
```

Alignment Scores:
Pred. No.: 93.3 Length: 1734
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.63% Indels: 0
DB: 13 Gaps: 0

US-09-690-825-34 (1-142) x US-10-063-513-51 (1-1734)

QY 1 MetGlyAlaProThrLeuProPro 8
Db 1534 ATGGGAGCCCCCACACTCCCTCCT 1557

RESULT 57

US-10-063-515-51
; Sequence 51, Application US/10063515
; Publication No. US20030018173A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,515
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 51
; LENGTH: 1734
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-515-51

Alignment Scores:
Pred. No.: 93.3 Length: 1734
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.63% Indels: 0
DB: 13 Gaps: 0

US-09-690-825-34 (1-142) x US-10-063-515-51 (1-1734)

QY 1 MetGlyAlaProThrLeuProPro 8
Db 1534 ATGGGAGCCCCCACACTCCCTCCT 1557

RESULT 58

US-10-063-549-51
; Sequence 51, Application US/10063549
; Publication No. US20030027986A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,549

; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 51
; LENGTH: 1734
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-549-51

Alignment Scores:
Pred. No.: 93.3 Length: 1734
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.63% Indels: 0
DB: 13 Gaps: 0

US-09-690-825-34 (1-142) x US-10-063-549-51 (1-1734)

QY 1 MetGlyAlaProThrLeuProPro 8
Db 1534 ATGGGAGCCCCCACACTCCCTCCT 1557

RESULT 59

US-10-063-569-51
; Sequence 51, Application US/10063569
; Publication No. US20030018168A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,569
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 51
; LENGTH: 1734
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-569-51

Alignment Scores:
Pred. No.: 93.3 Length: 1734
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.63% Indels: 0
DB: 13 Gaps: 0

US-09-690-825-34 (1-142) x US-10-063-569-51 (1-1734)

QY 1 MetGlyAlaProThrLeuProPro 8
Db 1534 ATGGGAGCCCCCACACTCCCTCCT 1557

RESULT 60

US-10-063-551-51
; Sequence 51, Application US/10063551
; Publication No. US20020183494A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey

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; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: US/10/063,551
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 51
; LENGTH: 1734
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-551-51

Alignment Scores:
Pred. No.: 93.3 Length: 1734
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.63% Indels: 0
DB: 13 Gaps: 0

US-09-690-825-34 (1-142) x US-10-063-551-51 (1-1734)

Qy 1 MetClyAlaProThrLeuProPro 8
Db 1534 ATGGGAGCCCCACACTCTCTCT 1557

RESULT 61
US-10-174-581-201
; Sequence 201, Application US/10174581
; Publication No. US20030017540A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C41
; CURRENT APPLICATION NUMBER: US/10/174,581
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/052250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063564
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063734
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063870
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066120
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/066466
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066772
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/069335
; PRIOR FILING DATE: 1997-12-11
; PRIOR APPLICATION NUMBER: 60/069425
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: 60/069870
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/068017
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079664
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079786
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/080107
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080333
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/081049
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081070
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081195
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081838
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082568
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082569
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082704
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/083495
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083496
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083499
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083559
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/084366
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; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084639
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086023
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/086392
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/086486
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087098
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087208
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088025
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088028
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088029
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088033
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088167
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088202
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088212
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088217
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088326
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088655
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/088722
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088738
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088740
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088811
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088824
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088825
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088826
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088861
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088863
; PRIOR FILING DATE: 1998-06-11

; PRIOR APPLICATION NUMBER: 60/088876
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/089090
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089512
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089514
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089598
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089653

Alignment Scores:

Pred. No.:	93.3	Length:	1734
Score:	8.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	5.63%	Indels:	0
DB:	13	Gaps:	0

US-09-690-825-34 (1-142) x US-10-174-581-201 (1-1734)

QY 1 MetGlyAlaProThrLeuProPro 8

Db 1534 ATGGAGGCCCCACACTCCCTCCT 1557

RESULT 62

US-10-176-483-201

; Sequence 201, Application US/10176483

; Publication No. US20030017541A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3430R1C68

; CURRENT APPLICATION NUMBER: US/10/176,483

; CURRENT FILING DATE: 2002-06-20

; Prior application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 201

; LENGTH: 1734

; TYPE: DNA

; ORGANISM: Homo Sapien

US-10-176-483-201

Alignment Scores:

Pred. No.:	93.3	Length:	1734
Score:	8.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	5.63%	Indels:	0
DB:	13	Gaps:	0

US-09-690-825-34 (1-142) x US-10-176-483-201 (1-1734)

QY 1 MetGlyAlaProThrLeuProPro 8

Db 1534 ATGGAGGCCCCACACTCCCTCCT 1557

RESULT 63

US-10-176-749-201
 ; Sequence 201, Application US/10176749
 ; Publication No. US20030017542A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3430R1C76
 ; CURRENT APPLICATION NUMBER: US/10/176,749
 ; CURRENT FILING DATE: 2002-06-20
 ; Prior application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 612
 ; SEQ ID NO 201
 ; LENGTH: 1734
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 US-10-176-749-201

Alignment Scores:

Pred. No.:	93.3	Length:	1734
Score:	8.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	5.63%	Indels:	0
DB:	13	Gaps:	0

US-09-690-825-34 (1-142) x US-10-176-749-201 (1-1734)

QY 1 MetGlyAlaProThrLeuPro 8
 DB 1534 ATGGAGCCCCCACCTCCCTCT 1557

RESULT 64

US-10-176-914-201
 ; Sequence 201, Application US/10176914
 ; Publication No. US20030017543A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3430R1C83
 ; CURRENT APPLICATION NUMBER: US/10/176,914
 ; CURRENT FILING DATE: 2002-06-20
 ; Prior application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 612
 ; SEQ ID NO 201
 ; LENGTH: 1734
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 US-10-176-914-201

Alignment Scores:

Pred. No.:	93.3	Length:	1734
Score:	8.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	5.63%	Indels:	0
DB:	13	Gaps:	0

Pred. No.:	93.3	Length:	1734
Score:	8.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	5.63%	Indels:	0
DB:	13	Gaps:	0

US-09-690-825-34 (1-142) x US-10-176-914-201 (1-1734)

QY 1 MetGlyAlaProThrLeuPro 8
 DB 1534 ATGGAGCCCCCACCTCCCTCT 1557

RESULT 65

US-10-176-915-201
 ; Sequence 201, Application US/10176915
 ; Publication No. US20030017544A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3430R1C110
 ; CURRENT APPLICATION NUMBER: US/10/176,915
 ; CURRENT FILING DATE: 2002-06-21
 ; Prior application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 612
 ; SEQ ID NO 201
 ; LENGTH: 1734
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 US-10-176-915-201

Alignment Scores:

Pred. No.:	93.3	Length:	1734
Score:	8.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	5.63%	Indels:	0
DB:	13	Gaps:	0

US-09-690-825-34 (1-142) x US-10-176-915-201 (1-1734)

QY 1 MetGlyAlaProThrLeuPro 8
 DB 1534 ATGGAGCCCCCACCTCCCTCT 1557

RESULT 66

US-10-006-485A-51
 ; Sequence 51, Application US/10006485A
 ; Publication No. US20030084062A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan I.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.

APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830PIC9
CURRENT APPLICATION NUMBER: US/10/006,485A
CURRENT FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: 60/098716
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098723
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098749
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098750
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098803
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/098821
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/098843
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/098536
PRIOR FILING DATE: 1998-09-03
PRIOR APPLICATION NUMBER: 60/098596
PRIOR FILING DATE: 1998-09-03
PRIOR APPLICATION NUMBER: 60/098598
PRIOR FILING DATE: 1998-09-03
PRIOR APPLICATION NUMBER: 60/098602
PRIOR FILING DATE: 1998-09-03
PRIOR APPLICATION NUMBER: 60/098642
PRIOR FILING DATE: 1998-09-03
PRIOR APPLICATION NUMBER: 60/098741
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/098754
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/098763
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/098792
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/098808
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/098812
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/098815
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/098816
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/100385
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/100388
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/100390
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/100584
PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/100627
PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/100661
PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/100662
PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/100664
PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/100683
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/100684
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/100710
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/100711
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/100846
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/100849
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/100919
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/100930
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/101014
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/101068
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/101071
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/101279
PRIOR FILING DATE: 1998-09-22
PRIOR APPLICATION NUMBER: 60/101471
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101472
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101474
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101475
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101476
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101477
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101479
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101738
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101741
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101743
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101915
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101916
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/102207
PRIOR FILING DATE: 1998-09-29
PRIOR APPLICATION NUMBER: 60/102240
PRIOR FILING DATE: 1998-09-29
PRIOR APPLICATION NUMBER: 60/102307
PRIOR FILING DATE: 1998-09-29
PRIOR APPLICATION NUMBER: 60/102330
PRIOR FILING DATE: 1998-09-29
PRIOR APPLICATION NUMBER: 60/102331
PRIOR FILING DATE: 1998-09-29
PRIOR APPLICATION NUMBER: 60/102484
PRIOR FILING DATE: 1998-09-30
PRIOR APPLICATION NUMBER: 60/102487
PRIOR FILING DATE: 1998-09-30
PRIOR APPLICATION NUMBER: 60/102570
PRIOR FILING DATE: 1998-09-30
PRIOR APPLICATION NUMBER: 60/102571
PRIOR FILING DATE: 1998-09-30
PRIOR APPLICATION NUMBER: 60/102684
PRIOR FILING DATE: 1998-10-01
PRIOR APPLICATION NUMBER: 60/102687
PRIOR FILING DATE: 1998-10-01
PRIOR APPLICATION NUMBER: 60/102965
PRIOR FILING DATE: 1998-10-02
PRIOR APPLICATION NUMBER: 60/103258
PRIOR FILING DATE: 1998-10-06
PRIOR APPLICATION NUMBER: 60/103314
PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: 60/103315
PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: 60/103328
PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: 60/103395
PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: 60/103396

;; PRIOR FILING DATE: 1998-10-07
;; PRIOR APPLICATION NUMBER: 60/103401
;; PRIOR FILING DATE: 1998-10-07
;; PRIOR APPLICATION NUMBER: 60/103449
;; PRIOR FILING DATE: 1998-10-06
;; PRIOR APPLICATION NUMBER: 60/103633
;; PRIOR FILING DATE: 1998-10-08
;; PRIOR APPLICATION NUMBER: 60/103678
;; PRIOR FILING DATE: 1998-10-08
;; PRIOR APPLICATION NUMBER: 60/103679
;; PRIOR FILING DATE: 1998-10-08
;; PRIOR APPLICATION NUMBER: 60/103711
;; PRIOR FILING DATE: 1998-10-08
;; PRIOR APPLICATION NUMBER: 60/104257
;; PRIOR FILING DATE: 1998-10-14
;; PRIOR APPLICATION NUMBER: 60/104987
;; PRIOR FILING DATE: 1998-10-20
;; PRIOR APPLICATION NUMBER: 60/105000
;; PRIOR FILING DATE: 1998-10-20
;; PRIOR APPLICATION NUMBER: 60/105002
;; PRIOR FILING DATE: 1998-10-20
;; PRIOR APPLICATION NUMBER: 60/105104
;; PRIOR FILING DATE: 1998-10-21
;; PRIOR APPLICATION NUMBER: 60/105169
;; PRIOR FILING DATE: 1998-10-22
;; PRIOR APPLICATION NUMBER: 60/105266
;; PRIOR FILING DATE: 1998-10-22
;; PRIOR APPLICATION NUMBER: 60/105693
;; PRIOR FILING DATE: 1998-10-26
;; PRIOR APPLICATION NUMBER: 60/105694
;; PRIOR FILING DATE: 1998-10-26
;; PRIOR APPLICATION NUMBER: 60/105807
;; PRIOR FILING DATE: 1998-10-27
;; PRIOR APPLICATION NUMBER: 60/105881
;; PRIOR FILING DATE: 1998-10-27
;; PRIOR APPLICATION NUMBER: 60/105882
;; PRIOR FILING DATE: 1998-10-27
;; PRIOR APPLICATION NUMBER: 60/106023
;; PRIOR FILING DATE: 1998-10-28

Alignment Scores:
Pred. No.: 93.3 Length: 1734
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.63% Indels: 0
DB: 13 Gaps: 0

US-09-690-825-34 (1-142) x US-10-006-485A-51 (1-1734)

Qy 1 MetGlyAlaProThrLeuPro 8
Db 1534 ATGGAGCCCCCACCCTCTCT 1557

RESULT 67

US-10-013-907A-51
; Sequence 51, Application US/10013907A
; Publication No. US20030064925A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.

;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2830PIC34
;; CURRENT APPLICATION NUMBER: US/10/013,907A
;; CURRENT FILING DATE: 2001-12-10
;; Prior Application removed - See File Wrapper or Palm
;; NUMBER OF SEQ ID NOS: 477
;; SEQ ID NO 51
;; LENGTH: 1734
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-013-907A-51

Alignment Scores:
Pred. No.: 93.3 Length: 1734
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.63% Indels: 0
DB: 13 Gaps: 0

US-09-690-825-34 (1-142) x US-10-013-907A-51 (1-1734)

Qy 1 MetGlyAlaProThrLeuPro 8
Db 1534 ATGGAGCCCCCACCCTCTCT 1557

RESULT 68

US-10-015-499A-51
; Sequence 51, Application US/10015499A
; Publication No. US20030065142A1
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.

;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2830PIC42
;; CURRENT APPLICATION NUMBER: US/10/015,499A
;; CURRENT FILING DATE: 2001-12-11
;; Prior Application removed - See File Wrapper or Palm
;; NUMBER OF SEQ ID NOS: 477
;; SEQ ID NO 51
;; LENGTH: 1734
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-015-499A-51

Alignment Scores:
Pred. No.: 93.3 Length: 1734
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.63% Indels: 0
DB: 13 Gaps: 0

US-09-690-825-34 (1-142) x US-10-015-499A-51 (1-1734)

Qy 1 MetGlyAlaProThrLeuPro 8
Db 1534 ATGGAGCCCCCACCCTCTCT 1557

```

RESULT 69
US-10-063-555-51
; Sequence 51, Application US/10063555
; Publication No. US20030065143A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,555
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 51
; LENGTH: 1734
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-555-51

Alignment Scores:
Pred. No.: 93.3 Length: 1734
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.63% Indels: 0
DB: 13 Gaps: 0

US-09-690-825-34 (1-142) x US-10-063-555-51 (1-1734)
QY 1 MetGlyAlaProThrLeuPro 8
Db 1534 ATGGGAGCCCCCACACTCCCTCT 1557

RESULT 70
US-10-063-563-51
; Sequence 51, Application US/10063563
; Publication No. US20030060602A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,563
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 51
; LENGTH: 1734
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-563-51

Alignment Scores:
Pred. No.: 93.3 Length: 1734
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.63% Indels: 0
DB: 13 Gaps: 0

US-09-690-825-34 (1-142) x US-10-063-563-51 (1-1734)
QY 1 MetGlyAlaProThrLeuPro 8
Db 1534 ATGGGAGCCCCCACACTCCCTCT 1557

RESULT 71
US-10-063-594-51
; Sequence 51, Application US/10063594
; Publication No. US20030065161A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,594
; CURRENT FILING DATE: 2002-05-30
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 51
; LENGTH: 1734
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-594-51

Alignment Scores:
Pred. No.: 93.3 Length: 1734
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.63% Indels: 0
DB: 13 Gaps: 0

US-09-690-825-34 (1-142) x US-10-063-594-51 (1-1734)
QY 1 MetGlyAlaProThrLeuPro 8
Db 1534 ATGGGAGCCCCCACACTCCCTCT 1557

RESULT 72
US-10-063-553-51
; Sequence 51, Application US/10063553
; Publication No. US20030045684A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,553
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 51
; LENGTH: 1734
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-553-51

Alignment Scores:
Pred. No.: 93.3 Length: 1734
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.63% Indels: 0
DB: 13 Gaps: 0

US-09-690-825-34 (1-142) x US-10-063-553-51 (1-1734)
QY 1 MetGlyAlaProThrLeuPro 8
Db 1534 ATGGGAGCCCCCACACTCCCTCT 1557

```

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Query Match: 5.63% Indels: 0
DB: 13 Gaps: 0

US-09-690-825-34 (1-142) x US-10-063-563-51 (1-1734)
QY 1 MetGlyAlaProThrLeuPro 8
Db 1534 ATGGGAGCCCCCACACTCCCTCT 1557

RESULT 71
US-10-063-594-51
; Sequence 51, Application US/10063594
; Publication No. US20030065161A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,594
; CURRENT FILING DATE: 2002-05-30
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 51
; LENGTH: 1734
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-594-51

Alignment Scores:
Pred. No.: 93.3 Length: 1734
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.63% Indels: 0
DB: 13 Gaps: 0

US-09-690-825-34 (1-142) x US-10-063-594-51 (1-1734)
QY 1 MetGlyAlaProThrLeuPro 8
Db 1534 ATGGGAGCCCCCACACTCCCTCT 1557

RESULT 72
US-10-063-553-51
; Sequence 51, Application US/10063553
; Publication No. US20030045684A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,553
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 51
; LENGTH: 1734
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-553-51

Alignment Scores:
Pred. No.: 93.3 Length: 1734
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.63% Indels: 0
DB: 13 Gaps: 0

US-09-690-825-34 (1-142) x US-10-063-553-51 (1-1734)
QY 1 MetGlyAlaProThrLeuPro 8
Db 1534 ATGGGAGCCCCCACACTCCCTCT 1557

```


; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C64
; CURRENT APPLICATION NUMBER: US/10/176,484
; CURRENT FILING DATE: 2002-06-20
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 201
; LENGTH: 1734
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-484-201

Alignment Scores:
Pred. No.: 93.3 Length: 1734
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.63% Indels: 0
DB: 13 Gaps: 0

US-09-690-825-34 (1-142) x US-10-176-484-201 (1-1734)

QY 1 MetGlyAlaProThrLeuProPro 8
DB 1534 ATGGGAGCCCCCACACTCCCTCCT 1557

RESULT 75

US-10-180-550-201
; Sequence 201, Application US/10180550
; Publication No. US2003006440A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C149
; CURRENT APPLICATION NUMBER: US/10/180,550
; CURRENT FILING DATE: 2002-06-25
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 201
; LENGTH: 1734
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-180-550-201

Alignment Scores:
Pred. No.: 93.3 Length: 1734
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.63% Indels: 0
DB: 13 Gaps: 0

US-09-690-825-34 (1-142) x US-10-180-550-201 (1-1734)

QY 1 MetGlyAlaProThrLeuProPro 8
DB 1534 ATGGGAGCCCCCACACTCCCTCCT 1557

; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-553-51
Alignment Scores:
Pred. No.: 93.3 Length: 1734
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.63% Indels: 0
DB: 13 Gaps: 0

US-09-690-825-34 (1-142) x US-10-063-553-51 (1-1734)

QY 1 MetGlyAlaProThrLeuProPro 8
DB 1534 ATGGGAGCCCCCACACTCCCTCCT 1557

RESULT 73

US-10-063-554-51
; Sequence 51, Application US/10063554
; Publication No. US20030040013A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,554
; CURRENT FILING DATE: 2002-05-02
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 51
; LENGTH: 1734
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-554-51

Alignment Scores:
Pred. No.: 93.3 Length: 1734
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.63% Indels: 0
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RESULT 74

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; Sequence 201, Application US/10176484
; Publication No. US20030059876A9
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.

Tue Aug 17 05:54:52 2004

us-09-690-825-34.oligo.rnpb

Page 32

Search completed: August 16, 2004, 05:21:35
Job time : 1494 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 16, 2004, 01:19:04 ; Search time 96 Seconds
(without alignments)
820.865 Million cell updates/sec

Title: US-09-690-825-34

Perfect score: 142

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Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Word size: 1

Total number of hits satisfying chosen parameters: 1360442

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

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Database :

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6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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2	142	100.0	1619	3	US-09-163-162-1
3	142	100.0	1619	3	US-09-286-407-1
4	142	100.0	1619	4	US-09-496-694B-97
5	107	75.4	1165	3	US-08-448-722A-1
6	107	75.4	1165	3	US-08-189-309B-1
7	93	55.5	740	4	US-09-016-434-918
8	41	28.9	955	4	US-09-496-694B-10
9	39	27.5	14796	3	US-08-975-080-35
10	39	27.5	14796	3	US-09-630-706-10
11	39	27.5	14796	4	US-09-496-694B-3
12	37	26.1	417	4	US-09-283-144-1

13	14	9.9	332	4	US-09-833-361-1331	Sequence 1331, Ap
14	9	6.3	30	4	US-09-672-717-199	Sequence 199, App
15	8	5.6	26	4	US-09-496-694B-13	Sequence 13, Appl
16	8	5.6	281	4	US-09-833-381-1330	Sequence 1330, Ap
17	8	5.6	293	4	US-09-621-976-13359	Sequence 13359, A
18	8	5.6	326	4	US-09-621-976-13398	Sequence 13398, A
19	8	5.6	337	4	US-09-621-976-13384	Sequence 13384, A
20	8	5.6	342	4	US-09-621-976-13367	Sequence 13367, A
21	8	5.6	346	4	US-09-621-976-13443	Sequence 13443, A
22	8	5.6	349	4	US-09-621-976-13375	Sequence 13375, A
23	8	5.6	351	4	US-09-621-976-13420	Sequence 13420, A
24	8	5.6	357	4	US-09-621-976-13407	Sequence 13407, A
25	8	5.6	361	4	US-09-621-976-13392	Sequence 13392, A
26	8	5.6	365	4	US-09-621-976-13428	Sequence 13428, A
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38	7	4.9	23	4	US-09-496-694B-6	Sequence 6, Appl
39	7	4.9	273	4	US-09-313-294A-1818	Sequence 1818, Ap
40	7	4.9	310	3	US-09-328-111-715	Sequence 715, App
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47	7	4.9	627	4	US-09-134-000C-912	Sequence 912, App
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49	7	4.9	777	4	US-09-134-000C-375	Sequence 375, App
50	7	4.9	924	4	US-09-252-991A-4263	Sequence 4263, Ap
51	7	4.9	939	4	US-09-352-991A-3424	Sequence 3424, Ap
52	7	4.9	942	3	US-09-475-316A-117	Sequence 117, App
53	7	4.9	942	4	US-09-704-640-117	Sequence 117, App
54	7	4.9	944	3	US-09-475-316A-119	Sequence 119, App
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57	7	4.9	993	3	US-08-969-644-21	Sequence 21, Appl
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76	7	4.9	1779	1	US-08-428-823-16	Sequence 16, Appl
77	7	4.9	2463	4	US-09-134-000C-3032	Sequence 3032, Ap
78	7	4.9	2517	1	US-07-906-930B-1	Sequence 1, Appl
79	7	4.9	2631	1	US-08-428-036-13	Sequence 13, Appl
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81	7	4.9	2939	1	US-07-906-930B-3	Sequence 3, Appl
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93	7	4, 9	9361	4	US-08-934-386-7	Sequence 7, Appl
94	7	4, 9	17417	4	US-09-648-004-27	Sequence 27, Appl
95	7	4, 9	30001	1	US-08-125-468-1	Sequence 1, Appl
96	7	4, 9	30001	2	US-08-474-933-1	Sequence 1, Appl
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98	7	4, 9	53266	3	US-08-658-136-2	Sequence 2, Appl
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ALIGNMENTS

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RESULT 1
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; Sequence 2, Application US/09283144
; Patent No. 6346389
; GENERAL INFORMATION:
; APPLICANT: Yale University
; TITLE OF INVENTION: Method for Selectively Modulating the Interactions
; TITLE OF INVENTION: between survivin and Tubulin
; FILE REFERENCE: 44574-5033-US
; CURRENT APPLICATION NUMBER: US/09/283,144
; CURRENT FILING DATE: 1999-04-01
; EARLIER APPLICATION NUMBER: US 60/080,288
; EARLIER FILING DATE: 1998-04-01
; EARLIER APPLICATION NUMBER: US 08/975,080
; EARLIER FILING DATE: 1997-11-20
; EARLIER APPLICATION NUMBER: PCT/US97/21880
; EARLIER FILING DATE: 1997-11-20
; EARLIER APPLICATION NUMBER: US 60/031,435
; EARLIER FILING DATE: 1996-11-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 426
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence of open reading frame encoding
US-09-283-144-2

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Qy	101	PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys	120
Db	301	TTTTTGAACCTGACAGAGAAAGGCCAAGAACAAAATTGCCAAGGAAACCAACAATAAG	360
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; Patent No. 607709			
; GENERAL INFORMATION:			
; APPLICANT: Bennett, C. Frank			
; APPLICANT: Ackermann, Elizabeth J.			
; APPLICANT: Swayze, Eric B.			
; APPLICANT: Cowert, Lex M.			
; TITLE OF INVENTION: ANTISENSE MODULATION OF Survivin EXPRESSION			
; FILE REFERENCE: RTS-0008			
; CURRENT APPLICATION NUMBER: US/09/163,162			
; CURRENT FILING DATE: 1998-09-29			
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Ddb	121	GTGGCTTTATCCACTGCCCCACTGAGAACGACCCAGACTTGGCCCGAGTGTCTTCTTCGC	180
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Db 470 ATGGAT 475
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; Sequence 1, Application US/09286407A
; Patent No. 6165788
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Ackermann, Elizabeth J.
; APPLICANT: Swayze, Eric E.
; APPLICANT: Cowsett, Lex M.
; TITLE OF INVENTION: ANTISENSE MODULATION OF Survivin EXPRESSION
; FILE REFERENCE: ISPH-0349
; CURRENT APPLICATION NUMBER: US/09/286,407A
; PRIOR FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 48
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; ORGANISM: Homo sapiens
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; NAME/KEY: CDS
; LOCATION: (50)...(478)
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QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
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Db 170 GCTGGCTTCATCCACTGCCCTGAGACGAGCCAGACTTGGCCCGAGTGTCTTCTGCC 229
QY 61 PheLysGluLeuGluGlyTrpGluProAspAspAspProIleGluGluHisLysHis 80
Db 230 TTCAGGAGCTGGAGGCTGGAGGCTGGAGGCTGGAGGCTGGAGGCTGGAGGCTGGAGGCT 289
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
Db 290 TCGTCCGGTTCGGCTTTCCTTCTGTCAAGAGGAGTTCAGAGAAATTAACCTTGGTGAA 349
QY 101 PheLysGluLeuAspArgGluArgAlaLysAsnLysLysLysLysLysLysLys 120
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Db 410 AAGAAAGAAATTTGAGGAACTGCGAGAAAGTGGCCCGTGCATCGACAGCTGGCTGCC 469
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Db 470 ATGGAT 475
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US-09-496-694B-97
; Sequence 97, Application US/09496694B
; Patent No. 6335194
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Eric E. Swayze
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: ISPH-0439
; CURRENT APPLICATION NUMBER: US/09/496,694B
; PRIOR FILING DATE: 2000-02-02
; PRIOR APPLICATION NUMBER: 09/286,407
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 09/163,162
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 249
; SEQ ID NO 97
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapiens
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Score: 142.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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Db 50 ATGGGTGCCCGACGTTGCCCTGCTGGCAGCCCTTTCTCAAGGACACCGCATCTCT 109
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
Db 110 ACATTCAAGAACTGGGCCCTTTCTGGAGGGCTGGCCCTGCACCCCGAGCGGATGGCCGAG 169
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Db 230 TTCAGGAGCTGGAGGCTGGAGGCTGGAGGCTGGAGGCTGGAGGCTGGAGGCTGGAGGCT 289
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
Db 290 TCGTCCGGTTCGGCTTTCCTTCTGTCAAGAGGAGTTCAGAGAAATTAACCTTGGTGAA 349
QY 101 PheLysLysLeuAspArgGluArgAlaLysAsnLysLysLysLysLysLysLys 120
Db 350 TTTTGAACCTGGACAGAGAAAGGCGCAAGAACAAAATTGCAAGAGAAACCAACAATAAG 409
QY 121 LysLysGluPheGluGluThrAlaLysLysValArgAlaLysGluGluGluLeuAlaAla 140
Db 410 AAGAAAGAAATTTGAGGAACTGCGAGAAAGTGGCCCGTGCATCGACAGCTGGCTGCC 469
QY 141 MetAsp 142
Db 470 ATGGAT 475
RESULT 5
US-09-448-722A-1/c
; Sequence 1, Application US/08448722A
; Patent No. 6072028
; GENERAL INFORMATION:

APPLICANT: Altieri, Dario C.
TITLE OF INVENTION: No. 6072028e1 Cell Surface Receptor, Antibody
COMPOSITIONS, and Methods of Using Same
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSER: Office of Patent Counsel, The Scripps
ADDRESSER: Research Institute
STREET: 10550 No. 6072028th Torrey Pines Road, TPC-8
CITY: La Jolla
STATE: CA
COUNTRY: US
ZIP: 92037

Db 875 TCGTCGGTTGCGCTTCTCTTCTGTCAGAGCAGATTGAGATTAAACCTTGGTGAA 816
Qy 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
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US-08-189-309B-1/C

; Sequence 1, Application US/08189309B

; Patent No. 6218875

; GENERAL INFORMATION:

; APPLICANT: Altieri, Dario C.

; TITLE OF INVENTION: Diagnostic Methods Useful in the Characterization of

; TITLE OF INVENTION: Lymphoproliferative Disease Characterized by Increased EPR-1

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Office of Patent Counsel, The Scripps

; ADDRESSEE: Research Institute

; STREET: 10550 No. 6238875th Torrey Pines Road, TPC-8

; CITY: La Jolla

; STATE: CA

; COUNTRY: US

; ZIP: 92037

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/189,309B

; FILING DATE: 28-JAN-1994

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/988,897

; FILING DATE: 10-DEC-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/667,957

; FILING DATE: 12-MAR-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Fitting, Thomas

; REGISTRATION NUMBER: 34,163

; REFERENCE/DOCKET NUMBER: 233.1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619) 784-2937

; TELEFAX: (619) 784-9399

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1165 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 37..1047

US-08-189-309B-1

Alignment Scores:

Pred. No.: 2,15e-103

Score: 107.00

Percent Similarity: 99.28%

Best Local Similarity: 99.28%

Query Match: 75.35%

DB: 3

Length: 1165

Matches: 138

Conservative: 0

Mismatches: 1

Indels: 1

Gaps: 0

US-09-690-825-34 (1-142) x US-08-189-309B-1 (1-1165)

Qy 1 MetGlyAlaProThrLeuProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20

Db 1114 ATGGGTGCCCCGAGTTGCCCCCTGCTGGAGCCCTTCTCAAGGACCAACCGCATCTCT 1055

Qy 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40

Db 1054 ACATTCAAGAACTGGCCCTCTTGGAGGCTGGCC-TGCACCCCGGAGCGATGGCCGAG 996

Qy 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60

Db 995 GCTGGCTTCATCCACTGCCCATCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 936

Qy 61 PheLysGluLeuGluGlyTyrGluProAspAspProIleGluGluHisLysLysHis 80

Db 935 TTCAAGGAGCTGGAAGCTGGAGCCAGATGACGACCCCATAGAGGAACATAAAGCAT 876

Qy 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100

Alignment Scores:

Pred. No.: 2,15e-103

Score: 107.00

Percent Similarity: 99.28%

Best Local Similarity: 99.28%

Query Match: 75.35%

DB: 3

Length: 1165

Matches: 138

Conservative: 0

Mismatches: 1

Indels: 1

Gaps: 0

US-09-690-825-34 (1-142) x US-08-448-722A-1 (1-1165)

Qy 1 MetGlyAlaProThrLeuProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20

Db 1114 ATGGGTGCCCCGAGTTGCCCCCTGCTGGAGCCCTTCTCAAGGACCAACCGCATCTCT 1055

Qy 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40

Db 1054 ACATTCAAGAACTGGCCCTCTTGGAGGCTGGCC-TGCACCCCGGAGCGATGGCCGAG 996

Qy 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60

Db 995 GCTGGCTTCATCCACTGCCCATCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 936

Qy 61 PheLysGluLeuGluGlyTyrGluProAspAspProIleGluGluHisLysLysHis 80

Db 935 TTCAAGGAGCTGGAAGCTGGAGCCAGATGACGACCCCATAGAGGAACATAAAGCAT 876

Qy 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100

QY 1 MetGlyAlaProThrLeuProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
Db 1114 ATGGGTGGCCGACGTTGCCCCCTGCTGGCAGCCCTTCTCAAGGACCCACCGCATCTCT 1055
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
Db 1054 ACATTCAAGAACTGGCCCTCTTGTGAGGGCTGCGC-TGCACCCCGGAGCGGATGGCCGAG 996
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
Db 995 GTGGCTTCATCCACTGCCCCACTGAGAACGACGAGCAGACTTGGCCCACTGTTCTTCGCG 936
QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHisIleLysHis 80
Db 935 TTCAGGAGCTGGAAGGCTGGAGCGCAGATGACGCCCCATAGAGAAACATAAAAGCAT 876
QY 81 SerSerGlyCysAlaPheLeuSerValIleLysGlnPheGluGluLeuThrIleuGlyGlu 100
Db 875 TCGTCGGTGGCTTCTCTGTCAGAGAGCAGTTTGAAGAATTAAACCTTGGTGAA 816
QY 101 PheLysLeuLysArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120
Db 815 TTTTGAAGTGGACAGAGAAAGCCAGCAACAAATTGCAAGGAAACCCACACANTAG 756
QY 121 LysLysGluPheGluThrAlaLysLysValArgAlaIleGluGluLeuAla 139
Db 755 AAGAAAGAAATTCAGGAAACTGGAAGAAAGTGGCGCGTCCATCGCAGCGTGGCC 699

RESULT 7

US-09-016-434-918
; Sequence 918, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 918:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 740 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BRAITUT01

CLONE: 752848
US-09-016-434-918
Alignment Scores:
Pred. No.: 7,26e-89 Length: 740
Score: 93.00 Matches: 130
Percent Similarity: 98.48% Conservative: 0
Best Local Similarity: 98.48% Mismatches: 1
Query Match: 65.49% Indels: 2
DB: 4 Gaps: 0

US-09-690-825-34 (1-142) x US-09-016-434-918 (1-740)

QY 12 ProPheLeuLysAspHisArgIleSerThrPheLysAsnTrpProPheLeuGluGlyCys 31
Db 51 CCCCCCTCAAGGACCCACCGCATCTCTACATTCAAGAACTGGCCCTTCTTGGAGGCTGC 110
QY 32 AlaCysThrProGluArgMetAlaGluAlaGlyPheIleHisCysProThrGlu-AsnGlu 51
Db 111 GCTGTCACCCCGGAGGATGGCGAGGCTGGCTTATCCACTGCCCATCTGA-NACGA 169
QY 51 uProAspLeuAlaGlnCysPhePheCysPheLysGluLeuGluGlyTrpGluProAspAs 71
Db 170 GCCAGACTTGGCCAGTGTCTTCTGCTTCAAGGAGCTGGAAGCTGGGAGCCAGATGA 229
QY 71 pAspProIleGluGluHisLysLysHisSerSerGlyCysAlaPheLeuSerValIleLys 91
Db 230 CGACCCCATAGAGAACATAAAAGCATTCGTCGGTGGCTTCTTCTTGTCAAGAA 289
QY 91 sGlnPheGluGluLeuThrLeuGlyGluPheLeuLysLeuAspArgGluArgAlaLysAs 111
Db 290 GCATTTGAAGAAATTAAACCTTGGTGAATTTTGAAGCTGCAGAGAAAGCCAAAGAA 349
QY 111 nLysIleAlaLysGluThrAsnLysLysLysGluPheGluGluThrAlaLysLysVa 131
Db 350 CAAATTTGAAAGGAAACCAACAAATAAGAAAGAAATTTGAGGAAACTCGGAAGAAAGT 409
QY 131 lArgArgAlaIleGluGlnLeuAlaAlaMetAsp 142
Db 410 GCGCGTGCATCGAGCAGCTGGCTGCCATGGAT 443

RESULT 8

US-09-496-694B-10
; Sequence 10, Application US/09496694B
; Patent No. 6335194
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Eric E. Swazy
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: ISPH-0439
; CURRENT APPLICATION NUMBER: US/09/496,694B
; CURRENT FILING DATE: 2000-02-02
; PRIOR APPLICATION NUMBER: 09/286,407
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 09/163,162
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 249
; SEQ ID NO 10
; LENGTH: 955
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (109)...(531)
US-09-496-694B-10

Alignment Scores:
Pred. No.: 4.04e-34 Length: 955
Score: 41.00 Matches: 41
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 28.87% Indels: 0
 DB: 4 Gaps: 0

US-09-690-825-34 (1-142) x US-09-496-694B-10 (1-955)

QY 31 CysAlaCysThrProGluArgMetAlaGluAlaGlyPheIleHisCysProThrGluAsn 50
 DB 199 TCGGCTGACCCAGAGCGAATGCGGAGGTGGCTTCATCCCTGCCCTACCGAGAAC 258
 QY 51 GluProAspLeuAlaGlnCysPheCysPheLysGluLeuGluGlyTTPGluProAsp 70
 DB 259 GAGCGTGAATTTGGCCAGTGTCTTTCTGCTTAAAGGATTTGAAGCTGGGACCCGAT 318
 QY 71 Asp 71
 DB 319 GAC 321

RESULT 9

US-08-975-080-35
 ; Sequence 35, Application US/08975080
 ; Patent No. 6245523

; GENERAL INFORMATION:
 ; APPLICANT: Altieri, Dario C.
 ; TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
 ; CELLULAR APOPTOSIS, AND ITS MODULATION
 ; NUMBER OF SEQUENCES: 35
 ; CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
 STREET: 1800 M Street, N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA

ZIP: 20036-5869

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/975,080
 ; FILING DATE: 20-NOV-1997
 ; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/031,435
 FILING DATE: 20-NOV-1996
 ATTORNEY/AGENT INFORMATION:

NAME: Adler, Reid G.

REGISTRATION NUMBER: 30,988

REFERENCE/DOCKET NUMBER: 044574-5022-01-WO

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-467-7000

TELEFAX: 202-467-7176

INFORMATION FOR SEQ ID NO: 35:

SEQUENCE CHARACTERISTICS:

LENGTH: 14796 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-975-080-35

Alignment Scores:

Pred. No.: 6,48e-31 Length: 14796
 Score: 39.00 Matches: 39
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 27.46% Indels: 0
 DB: 3 Gaps: 0

US-09-690-825-34 (1-142) x US-08-975-080-35 (1-14796)

QY 75 GluGluHisLysLysHisSerSerGlyCysAlaPheLeuSerValLysLysGlnPheGlu 94
 DB 5159 GAGGAACATAAAAGCATTCGTCGGTTGCGCTTCTTCTGTCAGAGAGCAGTTTGA 5218

QY 95 GluLeuThrLeuGlyGluPheLeuLysLeuAspArgGluArgAlaLysAsnLysIle 113
 DB 5219 GAATTAACCTTGGTGAATTTTGAACCTGGACAGAGAGAGCCAGACAAAT 5275

RESULT 10

US-09-630-706-10
 ; Sequence 10, Application US/09630706
 ; Patent No. 6277640

; GENERAL INFORMATION:

APPLICANT: C. Frank Bennett

APPLICANT: Lex M. Cowsett

FILE OF INVENTION: ANTISENSE MODULATION OF HER-3 EXPRESSION

FILE REFERENCE: RTS-0053

CURRENT APPLICATION NUMBER: US/09/630,706

CURRENT FILING DATE: 2000-08-01

NUMBER OF SEQ ID NOS: 94

SEQ ID NO 10

LENGTH: 14796

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (2811)...(2921)

NAME/KEY: CDS

LOCATION: (3174)...(3283)

NAME/KEY: CDS

LOCATION: (5158)...(5275)

NAME/KEY: CDS

LOCATION: (11955)...(12044)

US-09-630-706-10

Alignment Scores:

Pred. No.: 6,48e-31 Length: 14796
 Score: 39.00 Matches: 39
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 27.46% Indels: 0
 DB: 3 Gaps: 0

US-09-690-825-34 (1-142) x US-09-630-706-10 (1-14796)

QY 75 GluGluHisLysLysHisSerSerGlyCysAlaPheLeuSerValLysLysGlnPheGlu 94
 DB 5159 GAGGAACATAAAAGCATTCGTCGGTTGCGCTTCTTCTGTCAGAGAGCAGTTTGA 5218

QY 95 GluLeuThrLeuGlyGluPheLeuLysLeuAspArgGluArgAlaLysAsnLysIle 113
 DB 5219 GAATTAACCTTGGTGAATTTTGAACCTGGACAGAGAGAGCCAGACAAAT 5275

RESULT 11

US-09-496-694B-3

; Sequence 3, Application US/09496694B

; Patent No. 6335194

; GENERAL INFORMATION:

APPLICANT: C. Frank Bennett

APPLICANT: Elizabeth J. Ackermann

APPLICANT: Eric E. Swayze

APPLICANT: Lex M. Cowsett

FILE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION

FILE REFERENCE: ISPH-0439

CURRENT APPLICATION NUMBER: US/09/496,694B

CURRENT FILING DATE: 2000-02-02

PRIOR APPLICATION NUMBER: 09/286,407

PRIOR FILING DATE: 1999-04-05

PRIOR APPLICATION NUMBER: 09/163,162

PRIOR FILING DATE: 1998-09-29

NUMBER OF SEQ ID NOS: 249

SEQ ID NO 3

LENGTH: 14796

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

DB 291 ATGGGTGCCCGACGTTGCCCTGCTGGCAGCCCTTTCTCAAGGACACACCGGATCICI 350

QY 21 ThrPheLYeAsnTrrProPheLeuGluGlyCysAlaCysThrProGluArg 37
 |||||
 DB 351 ACATTCAGAACTGGCCCTCTTGAGGGCTGGCCTGCACCCCGGAGCG 401

RESULT 13
 US-09-833-381-1331
 ; Sequence 1331, Application US/09833381
 ; Patent No. 6672186
 ; GENERAL INFORMATION:
 ; APPLICANT: Robison, Keith E.
 ; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
 ; FILE REFERENCE: 5800-119
 ; CURRENT APPLICATION NUMBER: US/09/833,381
 ; CURRENT FILING DATE: 2001-04-11
 ; PRIOR APPLICATION NUMBER: 09/516,448
 ; PRIOR FILING DATE: 2000-02-29
 ; NUMBER OF SEQ ID NOS: 2050
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 1331
 ; LENGTH: 332
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)...(332)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-833-381-1331

Alignment Scores:	3.58e-06	Length:	332
Pred. No.:	14.00	Matches:	14
Score:	100.00%	Conservative:	0
Percent Similarity:	100.00%	Mismatches:	0
Best Local Similarity:	9.86%	Indels:	0
Query Match:	4	Gaps:	0
DB:			

US-09-690-825-34 (1-142) X US-09-833-381-1331 (1-332)

QY 68 GluProAspAspProIleGluGluHisLysLysHisser 81
 |||||
 DB 240 GAGCCAGTAGCAGCCCNATAGAGGAACATAAAAAAGCATTCG 281

RESULT 14
 US-09-672-717-199
 ; Sequence 199, Application US/09672717
 ; Patent No. 6673917
 ; GENERAL INFORMATION:
 ; APPLICANT: Korneluk, Robert G.
 ; APPLICANT: Lacasse, Eric
 ; APPLICANT: Baird, Stephen
 ; APPLICANT: Holcik, Martin
 ; APPLICANT: Young, Sean
 ; TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses
 ; FILE REFERENCE: 07891/025001
 ; CURRENT APPLICATION NUMBER: US/09/672,717
 ; CURRENT FILING DATE: 2000-09-28
 ; NUMBER OF SEQ ID NOS: 231
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 199
 ; LENGTH: 30
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: based on Homo sapiens
 US-09-672-717-199

Alignment Scores:	0.0693	Length:	30
Pred. No.:	9.00	Matches:	9
Score:	100.00%	Conservative:	0
Percent Similarity:			

Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 6.34% Indels: 0
 DB: 4 Gaps: 0

US-09-690-825-34 (1-142) x US-09-672-717-199 (1-30)

QY 69 ProAspAspProIleGluHis 77

DB 3 CCAGTATGACGCCCATAGAGACAT 29

RESULT 15

US-09-496-694B-13

; Sequence 13, Application US/09496694B

; Patent No. 6335194

; GENERAL INFORMATION:

; APPLICANT: C. Frank Bennett

; APPLICANT: Elizabeth J. Ackermann

; APPLICANT: Eric E. Swayze

; APPLICANT: Lex M. Cowsett

; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION

; FILE REFERENCE: ISPH-0439

; CURRENT APPLICATION NUMBER: US/09/496.694B

; CURRENT FILING DATE: 2000-02-02

; PRIOR APPLICATION NUMBER: 09/286,407

; PRIOR FILING DATE: 1999-04-05

; PRIOR APPLICATION NUMBER: 09/163,162

; PRIOR FILING DATE: 1998-09-29

; NUMBER OF SEQ ID NOS: 249

; SEQ ID NO 13

; LENGTH: 26

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: PCR Probe

US-09-496-694B-13

Alignment Scores:

Pred. No.: 0.682 Length: 26
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservaive: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 5.63% Indels: 0
 DB: 4 Gaps: 0

US-09-690-825-34 (1-142) x US-09-496-694B-13 (1-26)

QY 62 LysGluLeuGluGlyTrpGluPro 69

DB 2 AAGGAATTGGAAGCTGGGAACC 25

RESULT 16

US-09-833-381-1330

; Sequence 1330, Application US/09833381

; Patent No. 6672186

; GENERAL INFORMATION:

; APPLICANT: Robison, Keith E.

; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs

; FILE REFERENCE: 5800-119

; CURRENT APPLICATION NUMBER: US/09/833,381

; CURRENT FILING DATE: 2001-04-11

; PRIOR APPLICATION NUMBER: 09/516,448

; PRIOR FILING DATE: 2000-02-29

; NUMBER OF SEQ ID NOS: 2050

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1330

; LENGTH: 281

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)-(281)

; OTHER INFORMATION: n = A,T,C or G

US-09-833-381-1330

Alignment Scores:
 Pred. No.: 6.19 Length: 281
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservaive: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 5.63% Indels: 0
 DB: 4 Gaps: 0

US-09-690-825-34 (1-142) x US-09-833-381-1330 (1-281)

QY 60 CysPheLysGluLeuGluGlyTrp 67

DB 258 TCCTTCAGGAGCTGGAGGCTGG 281

RESULT 17

US-09-621-976-13359

; Sequence 13359, Application US/09621976

; Patent No. 6639063

; GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, J.B.

; APPLICANT: Jobert, S.

; APPLICANT: Giordano, J.Y.

; TITLE OF INVENTION: ESTs and Encoded Human Proteins.

; FILE REFERENCE: GENSET.054PR2

; CURRENT APPLICATION NUMBER: US/09/621,976

; CURRENT FILING DATE: 2000-07-21

; NUMBER OF SEQ ID NOS: 19335

; SOFTWARE: Patent.pm

; SEQ ID NO 13359

; LENGTH: 293

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-621-976-13359

Alignment Scores:

Pred. No.: 6.44 Length: 293
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservaive: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 5.63% Indels: 0
 DB: 4 Gaps: 0

US-09-690-825-34 (1-142) x US-09-621-976-13359 (1-293)

QY 1 MetGlyAlaProThrLeuProPro 8

DB 237 ATGGAGGCCCCACACCTCCTCT 260

RESULT 18

US-09-621-976-13398

; Sequence 13398, Application US/09621976

; Patent No. 6639063

; GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, J.B.

; APPLICANT: Jobert, S.

; APPLICANT: Giordano, J.Y.

; TITLE OF INVENTION: ESTs and Encoded Human Proteins.

; FILE REFERENCE: GENSET.054PR2

; CURRENT APPLICATION NUMBER: US/09/621,976

; CURRENT FILING DATE: 2000-07-21

; NUMBER OF SEQ ID NOS: 19335

; SOFTWARE: Patent.pm

; SEQ ID NO 13398

; LENGTH: 326

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-621-976-13398

Alignment Scores:

Pred. No.: 7.1 Length: 326
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservaive: 0

```
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.63% Indels: 0
DB: 4 Gaps: 0

US-09-690-825-34 (1-142) x US-09-621-976-13398 (1-326)

Qy 1 MetGlyAlaProThrLeuProPro 8
Db 237 ATGGAGCCCCCACACTCCCTCCT 260

RESULT 19
US-09-621-976-13384
; Sequence 13384, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 13384
; LENGTH: 337
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-13384

Alignment Scores:
Pred. No.: 7.33 Length: 337
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.63% Indels: 0
DB: 4 Gaps: 0

US-09-690-825-34 (1-142) x US-09-621-976-13384 (1-337)

Qy 1 MetGlyAlaProThrLeuProPro 8
Db 237 ATGGAGCCCCCACACTCCCTCCT 260

RESULT 20
US-09-621-976-13367
; Sequence 13367, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 13367
; LENGTH: 342
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-13367

Alignment Scores:
Pred. No.: 7.43 Length: 342
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
```

```
Query Match: 5.63% Indels: 0
DB: 4 Gaps: 0

US-09-690-825-34 (1-142) x US-09-621-976-13367 (1-342)

Qy 1 MetGlyAlaProThrLeuProPro 8
Db 237 ATGGAGCCCCCACACTCCCTCCT 260

RESULT 21
US-09-621-976-13443
; Sequence 13443, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 13443
; LENGTH: 346
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-13443

Alignment Scores:
Pred. No.: 7.51 Length: 346
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.63% Indels: 0
DB: 4 Gaps: 0

US-09-690-825-34 (1-142) x US-09-621-976-13443 (1-346)

Qy 1 MetGlyAlaProThrLeuProPro 8
Db 262 ATGGAGCCCCCACACTCCCTCCT 285

RESULT 22
US-09-621-976-13375
; Sequence 13375, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 13375
; LENGTH: 349
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-13375

Alignment Scores:
Pred. No.: 7.57 Length: 349
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.63% Indels: 0
```

```
DB: 4 Gaps: 0
US-09-690-825-34 (1-142) x US-09-621-976-13375 (1-349)
QY 1 MetGlyAlaProThrLeuProPro 8
DB 262 ATGGGAGCCCCCACCACACTCCCTCCT 285

RESULT 23
US-09-621-976-13420
; Sequence 13420, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 13420
; LENGTH: 351
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 255
; OTHER INFORMATION: n=a, g, c or t
US-09-621-976-13420

Alignment Scores:
Pred. No.: 7.61 Length: 351
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.63% Indels: 0
DB: 4 Gaps: 0

US-09-690-825-34 (1-142) x US-09-621-976-13420 (1-351)
QY 1 MetGlyAlaProThrLeuProPro 8
DB 263 ATGGGAGCCCCCACCACACTCCCTCCT 286

RESULT 24
US-09-621-976-13407
; Sequence 13407, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 13407
; LENGTH: 357
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 254..256
; OTHER INFORMATION: n=a, g, c or t
US-09-621-976-13407

Alignment Scores:
Pred. No.: 7.73 Length: 357
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.63% Indels: 0
DB: 4 Gaps: 0

DB: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.63% Indels: 0
DB: 4 Gaps: 0

US-09-690-825-34 (1-142) x US-09-621-976-13407 (1-357)
QY 1 MetGlyAlaProThrLeuProPro 8
DB 263 ATGGGAGCCCCCACCACACTCCCTCCT 286

RESULT 25
US-09-621-976-13392
; Sequence 13392, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 13392
; LENGTH: 361
; TYPE: DNA
; ORGANISM: Homo sapiens
; OTHER INFORMATION: n=a, g, c or t
US-09-621-976-13392

Alignment Scores:
Pred. No.: 7.81 Length: 361
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.63% Indels: 0
DB: 4 Gaps: 0

US-09-690-825-34 (1-142) x US-09-621-976-13392 (1-361)
QY 1 MetGlyAlaProThrLeuProPro 8
DB 263 ATGGGAGCCCCCACCACACTCCCTCCT 286

RESULT 26
US-09-621-976-13428
; Sequence 13428, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 13428
; LENGTH: 365
; TYPE: DNA
; ORGANISM: Homo sapiens
; OTHER INFORMATION: n=a, g, c or t
US-09-621-976-13428

Alignment Scores:
Pred. No.: 7.89 Length: 365
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.63% Indels: 0
DB: 4 Gaps: 0
```

US-09-690-825-34 (1-142) x US-09-621-976-13428 (1-365)

QY 1 MetGlyAlaProThrLeuProPro 8
|||||
Db 262 ATGGAGGCCCCACACTCCCTCT 285

RESULT 27

US-09-496-694B-231
; Sequence 231, Application US/09496694B
; Patent No. 6335194
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Eric E. Swayze
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: ISPH-0439
; CURRENT APPLICATION NUMBER: US/09/496,694B
; CURRENT FILING DATE: 2000-02-02
; PRIOR APPLICATION NUMBER: 09/286,407
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 09/163,162
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 249
; SEQ ID NO 231
; LENGTH: 515
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 266
; NAME/KEY: CDS
; LOCATION: (301)...(384)
US-09-496-694B-231

Alignment Scores: 10.9 Length: 515
Pred. No.: 8.00 Matches: 8
Score: 100.00%
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 5.63%
DB: 4 Gaps: 0

US-09-690-825-34 (1-142) x US-09-496-694B-231 (1-515)

QY 122 LysGluPheGluThrAlaLys 129
|||||
Db 325 AAGAGTTTGAGAGACTGCAGAG 348

RESULT 28

US-08-119-125A-1
; Sequence 1, Application US/08119125A
; Patent No. 5610011
; GENERAL INFORMATION:
; APPLICANT: SMITH, Hilda Elizabeth
; APPLICANT: VECHT, Uri
; TITLE OF INVENTION: DNA sequences which code for virulence
; TITLE OF INVENTION: Characteristics of Streptococcus suis and parts thereof, polyp
; TITLE OF INVENTION: antibodies derived therefrom and the use thereof for the diagn
; TITLE OF INVENTION: Protection against infection by S. suis in mammals, including
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Centraal Diargeeneskundig Instituut
; STREET: Fdeltwertweg 15
; CITY: PH Lelystad
; STATE:
; COUNTRY: The Netherlands
; ZIP: NL-8219
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS v.6.0
; SOFTWARE: WordPerfect v. 6.0

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/119,125A
; FILING DATE: 20-SEP-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/NL92/00054
; FILING DATE: 19-MAR-1992
; APPLICATION NUMBER: NL 9100510
; FILING DATE: 21-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Handal, Anthony H.
; REGISTRATION NUMBER: 26275
; REFERENCE/DOCKET NUMBER: SMITHHE119125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203) 838-8589
; TELEFAX: (203) 838-8794
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4376 base pairs
; TYPE: Nucleic acid with corresponding amino acids
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus suis type II (pathogenic)
; FEATURE:
; OTHER INFORMATION: Extracellular protein factor (EF) gene
; FEATURE:
; NAME/KEY: promoter -35 region
; LOCATION: bp 66 to 71
; FEATURE:
; NAME/KEY: promoter -10 region
; LOCATION: bp 89 to 94
; FEATURE:
; NAME/KEY: promoter -35 region
; LOCATION: bp 153 to 158
; FEATURE:
; NAME/KEY: promoter -10 region
; LOCATION: bp 176 to 181
; FEATURE:
; NAME/KEY: ribosome binding site
; LOCATION: bp 350 to 356
; FEATURE:
; NAME/KEY: signal peptide
; LOCATION: bp 361 to 498
; FEATURE:
; NAME/KEY: mature peptide
; LOCATION: bp 499 to 2890
; FEATURE:
; NAME/KEY: dyad symmetry regions
; LOCATION: from bp 4186 to 4198 and from bp 4203 to 4215
; FEATURE:
; NAME/KEY: dyad symmetry regions
; LOCATION: from bp 4243 to 4257 and from bp 4263 to 4276
US-08-119-125A-1
Alignment Scores: 78.9 Length: 4376
Pred. No.: 8.00 Matches: 8
Score: 100.00%
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 5.63%
DB: 1 Gaps: 0
US-09-690-825-34 (1-142) x US-08-119-125A-1 (1-4376)
QY 109 AlalysAsnLysIleAlaLysGlu 116
|||||
Db 2934 GCTAAGATAAGATTGCTAAGAA 2957
RESULT 29
US-08-119-125A-2
; Sequence 2, Application US/08119125A

Patent No. 5610011
GENERAL INFORMATION:
APPLICANT: SMITH, Hilda Elizabeth
APPLICANT: VECHT, Uri
TITLE OF INVENTION: DNA Sequences which code for Virulence
TITLE OF INVENTION: Characteristics of Streptococcus suis and parts thereof, polypeptides derived therefrom and the use thereof for the diagnosis and treatment of infection by S. suis in mammals, including protection against infection by S. suis in mammals, including
TITLE OF INVENTION: antibodies derived therefrom and the use thereof for the diagnosis and treatment of infection by S. suis in mammals, including
TITLE OF INVENTION: protection against infection by S. suis in mammals, including
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Centraal Diergeneeskundig Instituut
STREET: Edelhertweg 15
CITY: PH Lelystad
STATE:
COUNTRY: The Netherlands
ZIP: NL-8219
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS v.6.0
SOFTWARE: Wordperfect v. 6.0
CURRENT APPLICATION DATA: US/08/119,125A
FILING DATE: 20-SEP-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/NL92/00054
FILING DATE: 19-MAR-1992
APPLICATION NUMBER: NL 9100510
FILING DATE: 21-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hangal, Anthony H.
REGISTRATION NUMBER: 26275
REFERENCE/DOCKET NUMBER: SMITH119125
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 838-8589
TELEFAX: (203) 838-8794
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 6744 base pairs
TYPE: Nucleic acid with corresponding amino acids
STRANDEDNESS: single stranded
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
ORGANISM: Streptococcus suis type II (pathogenic)
FEATURE:
OTHER INFORMATION: Extracellular factor related protein (EF*) gene
FEATURE:
NAME/KEY: promoter -35 region
LOCATION: bp 66 to 71
FEATURE:
NAME/KEY: promoter -10 region
LOCATION: bp 89 to 94
FEATURE:
NAME/KEY: promoter -35 region
LOCATION: bp 153 to 158
FEATURE:
NAME/KEY: promoter -10 region
LOCATION: bp 176 to 181
FEATURE:
NAME/KEY: ribosome binding site
LOCATION: bp 350 to 356
FEATURE:
NAME/KEY: signal peptide
LOCATION: bp 361 to 498
FEATURE:
NAME/KEY: start of repetitive units R1-R11
LOCATION: bp 2869, 3097, 3292, 3520, 4087, 4381, 4609, 4837,
LOCATION: 5065, 5293, 5521:
FEATURE:
NAME/KEY: start of repetitive Asn-Pro-Asn-Leu sequences
LOCATION: bp 2932, 3160, 3355, 3583, 4150, 4444, 4672, 4900,

LOCATION: 5128, 5356, 5584:
FEATURE:
NAME/KEY: dyad symmetry regions
LOCATION: from bp 6554 to 6566 and from bp 6571 to 6583
FEATURE:
NAME/KEY: dyad symmetry regions
LOCATION: from bp 6611 to 6625 and from bp 6631 to 6644
US-08-119-125A-2
Alignment Scores:
Pred. No.: 118 Length: 6744
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.63% Indels: 0
DB: 1 Gaps: 0
US-09-690-825-34 (1-142) x US-08-119-125A-2 (1-6744)
QY 109 AlalysAsnLysIleAlalysGlu 116
Db 3529 GCTAAGAACAGATTGCCAAGAA 3552
RESULT 30
US-09-163-162-2
Sequence 2, Application US/09163162
Patent No. 6077709
GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
APPLICANT: Ackermann, Elizabeth J.
APPLICANT: Swayze, Eric E.
APPLICANT: Cowsett, Lex M.
TITLE OF INVENTION: ANTISENSE MODULATION OF Survivin EXPRESSION
FILE REFERENCE: RTS-0008
CURRENT APPLICATION NUMBER: US/09/163,162
CURRENT FILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 2
LENGTH: 21
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PCR Primer
US-09-163-162-2
Alignment Scores:
Pred. No.: 6.29 Length: 21
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.93% Indels: 0
DB: 3 Gaps: 0
US-09-690-825-34 (1-142) x US-09-163-162-2 (1-21)
QY 15 LysAspHisArgIleSerThr 21
Db 1 AAGGACCACCGCATCTCTACA 21
RESULT 31
US-09-286-407-2
Sequence 2, Application US/09286407A
Patent No. 6165788
GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
APPLICANT: Ackermann, Elizabeth J.
APPLICANT: Swayze, Eric E.
APPLICANT: Cowsett, Lex M.
TITLE OF INVENTION: ANTISENSE MODULATION OF Survivin EXPRESSION
FILE REFERENCE: ISFH-0349
CURRENT APPLICATION NUMBER: US/09/286,407A
CURRENT FILING DATE: 1999-04-05
NUMBER OF SEQ ID NOS: 48

```
; SEQ ID NO 2
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-09-286-407-2

Alignment Scores:
Pred. No.: 6.29 Length: 21
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.93% Indels: 0
DB: 3 Gaps: 0

US-09-690-825-34 (1-142) x US-09-286-407-2 (1-21)

QY 15 LysAspHisArgIleSerThr 21
DB 1 AAGGACCACCGCATCTCTACA 21

RESULT 32
US-09-496-694B-4
; Sequence 4, Application US/09496694B
; Patent No. 6335194
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Eric E. Swayze
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: ISPH-0439
; CURRENT APPLICATION NUMBER: US/09/496,694B
; PRIOR FILING DATE: 2000-02-02
; PRIOR APPLICATION NUMBER: 09/286,407
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 09/163,162
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 249
; SEQ ID NO 4
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-09-496-694B-4

Alignment Scores:
Pred. No.: 6.29 Length: 21
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.93% Indels: 0
DB: 4 Gaps: 0

US-09-690-825-34 (1-142) x US-09-496-694B-4 (1-21)

QY 15 LysAspHisArgIleSerThr 21
DB 1 AAGGACCACCGCATCTCTACA 21

RESULT 33
US-09-163-162-3/c
; Sequence 3, Application US/09163162
; Patent No. 607709
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Ackermann, Elizabeth J.
; APPLICANT: Swayze, Eric E.
; APPLICANT: Cowsett, Lex M.
; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: RTS-0008
; CURRENT APPLICATION NUMBER: US/09/163,162
; CURRENT FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 3
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-09-286-407-3

Alignment Scores:
Pred. No.: 6.57 Length: 22
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.93% Indels: 0
DB: 3 Gaps: 0

US-09-690-825-34 (1-142) x US-09-286-407-3 (1-22)

QY 48 ThrGluAsnGluProAspLeu 54
DB 22 ACTGAGAACGAGCCAGACTTG 2

RESULT 34
US-09-286-407-3/c
; Sequence 3, Application US/09286407A
; Patent No. 6165788
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Ackermann, Elizabeth J.
; APPLICANT: Swayze, Eric E.
; APPLICANT: Cowsett, Lex M.
; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: ISPH-0349
; CURRENT APPLICATION NUMBER: US/09/286,407A
; CURRENT FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 48
; SEQ ID NO 3
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-09-286-407-3

Alignment Scores:
Pred. No.: 6.57 Length: 22
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.93% Indels: 0
DB: 3 Gaps: 0

US-09-690-825-34 (1-142) x US-09-286-407-3 (1-22)

QY 48 ThrGluAsnGluProAspLeu 54
DB 22 ACTGAGAACGAGCCAGACTTG 2

RESULT 35
US-09-496-694B-5/c
; Sequence 5, Application US/09496694B
; Patent No. 6335194
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Eric E. Swayze
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: ISPH-0439
; CURRENT APPLICATION NUMBER: US/09/496,694B
```

; CURRENT FILING DATE: 2000-02-02
; PRIOR APPLICATION NUMBER: 09/286,407
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 09/163,162
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 249
; SEQ ID NO 5
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-09-496-694B-5

Alignment Scores:
Pred. No.: 6.57 Length: 22
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.93% Indels: 0
DB: 4 Gaps: 0

US-09-690-825-34 (1-142) x US-09-496-694B-5 (1-22)

QY 48 ThrGluAenGluProAspleu 54
DB 22 ACTGAGACGAGCCAGACTTG 2

RESULT 36

US-09-163-162-4
; Sequence 4, Application US/09163162
; Patent No. 6077709
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Ackermann, Elizabeth J.
; APPLICANT: Swayze, Eric E.
; APPLICANT: Cowsett, Lex M.
; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: RTS-0008
; CURRENT APPLICATION NUMBER: US/09/163,162
; CURRENT FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 4
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Probe
US-09-163-162-4

Alignment Scores:
Pred. No.: 6.84 Length: 23
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.93% Indels: 0
DB: 3 Gaps: 0

US-09-690-825-34 (1-142) x US-09-163-162-4 (1-23)

QY 40 GluAlaGlyPheIleHisCys 46
DB 2 GAGCGTGGCTTCATCCACTGC 22

RESULT 37

US-09-286-407-4
; Sequence 4, Application US/09286407A
; Patent No. 6165788
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Ackermann, Elizabeth J.
; APPLICANT: Swayze, Eric E.
; APPLICANT: Cowsett, Lex M.

; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: ISPH-0349
; CURRENT APPLICATION NUMBER: US/09/286,407A
; CURRENT FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 48
; SEQ ID NO 4
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Probe
US-09-286-407-4

Alignment Scores:
Pred. No.: 6.84 Length: 23
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.93% Indels: 0
DB: 3 Gaps: 0

US-09-690-825-34 (1-142) x US-09-286-407-4 (1-23)

QY 40 GluAlaGlyPheIleHisCys 46
DB 2 GAGCGTGGCTTCATCCACTGC 22

RESULT 38

US-09-496-694B-6
; Sequence 6, Application US/09496694B
; Patent No. 6335194
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Eric E. Swayze
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: ISPH-0439
; CURRENT APPLICATION NUMBER: US/09/496,694B
; CURRENT FILING DATE: 2000-02-02
; PRIOR APPLICATION NUMBER: 09/286,407
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 09/163,162
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 249
; SEQ ID NO 6
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Probe
US-09-496-694B-6

Alignment Scores:
Pred. No.: 6.84 Length: 23
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.93% Indels: 0
DB: 4 Gaps: 0

US-09-690-825-34 (1-142) x US-09-496-694B-6 (1-23)

QY 40 GluAlaGlyPheIleHisCys 46
DB 2 GAGCGTGGCTTCATCCACTGC 22

RESULT 39

US-09-313-294A-1818
; Sequence 1818, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.

APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
FILE REFERENCE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
NUMBER OF SEQ ID NOS: 1999-05-14
SOFTWARE: PERL Program
SEQ ID NO 1818
LENGTH: 273
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6476212 700551571H1

US-09-313-294A-1818

Alignment Scores:
Pred. No.: 67.8 Length: 273
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.93% Indels: 0
DB: 4 Gaps: 0

US-09-690-825-34 (1-142) x US-09-313-294A-1818 (1-273)

Oy 104 Leuaspargluargalalys 110
Db 9 CTAGATCGGAGCGCGCAAG 29

RESULT 40

US-09-328-111-715/c
Sequence 715, Application US/09328111
Patent No. 6262333
GENERAL INFORMATION:
APPLICANT: Endege, Wilson O.
APPLICANT: Steinmann, Kathleen E.
APPLICANT: Astle, Jon H.
APPLICANT: Burgess, Christopher C.
APPLICANT: Bushnell, Steven E.
APPLICANT: Carroll III, Eddie
APPLICANT: Catino, Theodore J.
APPLICANT: Derti, Adnan
APPLICANT: Ford, Donna M.
APPLICANT: Lewis, Marcia E.
APPLICANT: Monahan, John E.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS
FILE REFERENCE: CCD-257 (US)
CURRENT APPLICATION NUMBER: US/09/328,111
CURRENT FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: US 60/088,801
EARLIER FILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 850
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 715
LENGTH: 310
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(310)
OTHER INFORMATION: n = A, T, C or G

US-09-328-111-715
Alignment Scores:
Pred. No.: 76.2 Length: 310
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.93% Indels: 0

DB: 3 Gaps: 0

US-09-690-825-34 (1-142) x US-09-328-111-715 (1-310)

Oy 14 LeuYasphHisArgIeser 20
Db 74 TTAAGATCAGAGATCTCT 54

RESULT 41

US-09-107-532A-1678
Sequence 1678, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 1678:
SEQUENCE CHARACTERISTICS:
LENGTH: 504 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...504
SEQUENCE DESCRIPTION: SEQ ID NO: 1678:

US-09-107-532A-1678
Alignment Scores:
Pred. No.: 120 Length: 504
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.93% Indels: 0
DB: 4 Gaps: 0

US-09-690-825-34 (1-142) x US-09-107-532A-1678 (1-504)

Oy 131 ValArgGalaIleGluGln 137

Db 433 GTAAGACGTGCAATTGAGCAA 453

RESULT 42

US-09-621-976-10449

; Sequence 10449, Application US/09621976

; Patent No. 6639063

; GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, J.B.

; APPLICANT: Robert S.

; APPLICANT: Giordano J.Y.

; TITLE OF INVENTION: ESTs and Encoded Human Proteins.

; FILE REFERENCE: GENSET.054P2

; CURRENT APPLICATION NUMBER: US/09/621.976

; CURRENT FILING DATE: 2000-07-21

; NUMBER OF SEQ ID NOS: 19335

; SOFTWARE: Patent.pm

; SEQ ID NO 10449

; LENGTH: 559

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-621-976-10449

Alignment Scores:

Pred. No.:	132	Length:	559
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	4.93%	Indels:	0
DB:	4	Gaps:	0

US-09-690-825-34 (1-142) x US-09-621-976-10449 (1-559)

QY 104 LeuAspArgGluArgAlaLys 110

Db 37 CTGGACAGGGAGAGGGCCAAA 57

RESULT 43

US-09-107-532A-1373

; Sequence 1373, Application US/09107532A

; Patent No. 6583275

; GENERAL INFORMATION:

; APPLICANT: Lynn A Doucette-Stamm and David Bush

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

; NUMBER OF SEQUENCES: 710

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: GENOME THERAPEUTICS CORPORATION

; STREET: 100 Beaver Street

; CITY: Waltham

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02354

; COMPUTER READABLE FORM:

; MEDIUM TYPE: CD-ROM ISO9660

; COMPUTER: PC

; OPERATING SYSTEM: <Unknown>

; SOFTWARE: ASCII

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/107,532A

; FILING DATE: 30-Jun-1998

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/085,598

; FILING DATE: 14 May 1998

; APPLICATION NUMBER: 60/051571

; FILING DATE: July 2, 1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Ariniello, Pamela Deneke

; REGISTRATION NUMBER: 40,489

; REFERENCE/DOCKET NUMBER: GTC-012

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (781)893-5007

; TELEFAX: (781)893-8277

; INFORMATION FOR SEQ ID NO: 1373:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 561 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: circular

; MOLECULE TYPE: DNA (genomic)

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; ORIGINAL SOURCE:

; ORGANISM: Enterococcus faecium

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (B) LOCATION 1...561

; SEQUENCE DESCRIPTION: SEQ ID NO: 1373:

US-09-107-532A-1373

Alignment Scores:

Pred. No.:	132	Length:	561
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	4.93%	Indels:	0
DB:	4	Gaps:	0

US-09-690-825-34 (1-142) x US-09-107-532A-1373 (1-561)

QY 127 ThrAlaLysValArgArg 133

Db 127 ACTGCAGAAAGTACGACGT 147

RESULT 44

US-09-252-991A-4396

; Sequence 4396, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 4396

; LENGTH: 588

; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-4396

Alignment Scores:

Pred. No.:	138	Length:	588
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	4.93%	Indels:	0
DB:	4	Gaps:	0

US-09-690-825-34 (1-142) x US-09-252-991A-4396 (1-588)

QY 6 LeuP-ProAlaTrpGlnPro 12

Db 30 TTGCCACCGCGCTGGCAGCCT 50

RESULT 45

US-08-642-274D-15/c

; Sequence 16, Application US/08642274D

; Patent No. 6200749

; GENERAL INFORMATION:

; APPLICANT: Shiloh, Yosef

; TITLE OF INVENTION: MUTATED FORMS OF THE ATAXIA-TELANGIECTASIA GENE AND METHOD TO

```
; TITLE OF INVENTION: SCREEN FOR A PARTIAL A-T PHENOTYPE
; FILE REFERENCE: 229000033
; CURRENT APPLICATION NUMBER: US/08/642,274D
; CURRENT FILING DATE: 1996-05-03
; NUMBER OF SEQ ID NOS: 220
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 611
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: genomic
US-08-642-274D-16

Alignment Scores:
Pred. No.: 143 Length: 611
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.93% Indels: 0
DB: 3 Gaps: 0

US-09-690-825-34 (1-142) x US-08-642-274D-16 (1-611)
QY 86 PheLeuSerVallylsGln 92
Db 222 TTCTTGTCTGTGAAGAACAA 202

RESULT 46
US-08-952-014C-16/c
; Sequence 16, Application US/08952014C
; Patent No. 6265158
; GENERAL INFORMATION:
; APPLICANT: Shiloh, Yosef
; TITLE OF INVENTION: ATAXIA-TELANGIECTASIA GENE AND ITS
; TITLE OF INVENTION: GENOMIC ORGANIZATION
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kohn & Associates
; STREET: 30500 No. 6265158thwestern Hwy., Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: U.S.
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/952,014C
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,995
; REFERENCE/DOCKET NUMBER: 2290.00028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 810-539-5050
; TELEFAX: 810-539-5055
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 611 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-952-014C-16

Alignment Scores:
Pred. No.: 143 Length: 611
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
```

```
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.93% Indels: 0
DB: 3 Gaps: 0

US-09-690-825-34 (1-142) x US-08-952-014C-16 (1-611)
QY 86 PheLeuSerVallylsGln 92
Db 222 TTCTTGTCTGTGAAGAACAA 202

RESULT 47
US-09-134-000C-912
; Sequence 912, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 912
; LENGTH: 627
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-912

Alignment Scores:
Pred. No.: 146 Length: 627
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.93% Indels: 0
DB: 4 Gaps: 0

US-09-690-825-34 (1-142) x US-09-134-000C-912 (1-627)
QY 127 ThrAlaLysLysValArgArg 133
Db 193 ACGGCCAAAAAAGTGC GCGT 213

RESULT 48
US-09-489-039A-6367/c
; Sequence 6367, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 6367
; LENGTH: 642
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-6367

Alignment Scores:
Pred. No.: 150 Length: 642
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.93% Indels: 0
DB: 4 Gaps: 0
```

US-09-690-825-34 (1-142) x US-09-489-039A-6367 (1-642)

QY 3 AlaProThrLeuProProAla 9
 Db 274 GCGCCACCCCTCCGCGTGA 254

RESULT 49

US-09-134-000C-375
 ; Sequence 375, Application US/09134000C
 ; Patent No. 6617156
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stamm et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
 ; FILE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 032796-032
 ; CURRENT APPLICATION NUMBER: US/09/134,000C
 ; CURRENT FILING DATE: 1998-08-13
 ; PRIOR APPLICATION NUMBER: US 60/055,778
 ; PRIOR FILING DATE: 1997-08-15
 ; NUMBER OF SEQ ID NOS: 6812
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 375
 ; LENGTH: 777
 ; TYPE: DNA
 ; ORGANISM: Enterococcus faecalis
 US-09-134-000C-375

Alignment Scores:
 Pred. No.: 179 Length: 777
 Score: 7.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 4.93% Indels: 0
 DB: 4 Gaps: 0

US-09-690-825-34 (1-142) x US-09-134-000C-375 (1-777)

QY 125 GluThrAlaLysVal 131
 Db 511 GAAGAACGCTAAAAAGTG 531

RESULT 50

US-09-252-991A-4263/c
 ; Sequence 4263, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 4263
 ; LENGTH: 924
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-4263

Alignment Scores:
 Pred. No.: 210 Length: 924
 Score: 7.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 4.93% Indels: 0
 DB: 4 Gaps: 0

US-09-690-825-34 (1-142) x US-09-252-991A-4263 (1-924)

QY 6 LeuProProAlaTrpGlnPro 12
 Db 915 TTGCCACCGCGCTGGCAGCCT 895

RESULT 51

US-09-252-991A-3124/c
 ; Sequence 3124, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 3124
 ; LENGTH: 939
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-3124

Alignment Scores:
 Pred. No.: 213 Length: 939
 Score: 7.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 4.93% Indels: 0
 DB: 4 Gaps: 0

US-09-690-825-34 (1-142) x US-09-252-991A-3124 (1-939)

QY 30 GlyCysAlaCysThrProGlu 36
 Db 915 GGTTCGCGATGCACGCTGAG 895

RESULT 52

US-09-475-316A-117
 ; Sequence 117, Application US/09475316A
 ; Patent No. 6210942
 ; GENERAL INFORMATION:
 ; APPLICANT: Lewis, No. 6210942man G.
 ; APPLICANT: Davin, Laurence B.
 ; APPLICANT: Dinkova-Kostova, Albena T.
 ; APPLICANT: Fujita, Masayuki
 ; APPLICANT: Gang, David R.
 ; APPLICANT: Sarxanen, Simo
 ; APPLICANT: Ford, Joshua D
 ; TITLE OF INVENTION: RECOMBINANT PINORESINOL/LARICRESINOL REDUCTASES,
 ; FILE OF INVENTION: RECOMBINANT DIRIGENT PROTEINS AND METHODS OF USE
 ; FILE REFERENCE: WSR-1-13793
 ; CURRENT APPLICATION NUMBER: US/09/475,316A
 ; CURRENT FILING DATE: 1999-12-30
 ; PRIOR APPLICATION NUMBER: 09/307,653
 ; PRIOR FILING DATE: 1999-05-07
 ; PRIOR APPLICATION NUMBER: PCT/US97/20391
 ; PRIOR FILING DATE: 1997-11-07
 ; PRIOR APPLICATION NUMBER: 60/054,380
 ; PRIOR FILING DATE: 1997-07-31
 ; PRIOR APPLICATION NUMBER: 60/030,522
 ; PRIOR FILING DATE: 1996-11-08
 ; NUMBER OF SEQ ID NOS: 122
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 117
 ; LENGTH: 942
 ; TYPE: DNA
 ; ORGANISM: Schisandra chinensis
 ; FEATURE:
 ; NAME/KEY: CDS

LOCATION: (1)..(942)
US-09-475-316A-117
Alignment Scores: 214 942
Pred. No.: 7.00
Score: 100.00%
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 4.93%
DB: 3
Gaps: 0
US-09-690-825-34 (1-142) x US-09-475-316A-117 (1-942)
QY 130 LysValArgAlaIleGlu 136
Db 424 AAGTCAGCGTGCATAGAA 444
RESULT 53
US-09-704-640-117
Sequence 117, Application US/09704640
Patent No. 6635459
GENERAL INFORMATION:
APPLICANT: Lewis, No. 6635459man G.
APPLICANT: Dinkova-Kostova, Albena T.
APPLICANT: Fujita, Masayuki
APPLICANT: Sarkanen, Simo
APPLICANT: Ford, Joshua D
TITLE OF INVENTION: RECOMBINANT PINORESINOL/LARICRESINOL REDUCTASE,
FILE REFERENCE: WSUR-1-16492
CURRENT FILING DATE: 1999-12-30
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: PCT/US97/20391
PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: 60/054,380
PRIOR FILING DATE: 1997-07-31
PRIOR APPLICATION NUMBER: 60/030,522
PRIOR FILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 122
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 117
LENGTH: 942
TYPE: DNA
ORGANISM: Schisandra chinensis
US-09-475-316A-119
Alignment Scores: 214 942
Pred. No.: 7.00
Score: 100.00%
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 4.93%
DB: 3
Gaps: 0
US-09-690-825-34 (1-142) x US-09-475-316A-119 (1-944)
QY 130 LysValArgAlaIleGlu 136
Db 424 AAGTCAGCGTGCATAGAA 444
RESULT 55
US-09-704-640-119
Sequence 119, Application US/09704640
Patent No. 6635459
GENERAL INFORMATION:
APPLICANT: Lewis, No. 6635459man G.
APPLICANT: Dinkova-Kostova, Albena T.
APPLICANT: Fujita, Masayuki
APPLICANT: Sarkanen, Simo
APPLICANT: Ford, Joshua D
TITLE OF INVENTION: RECOMBINANT PINORESINOL/LARICRESINOL REDUCTASE,
FILE REFERENCE: WSUR-1-16492
CURRENT FILING DATE: 2000-11-02
PRIOR FILING DATE: 1999-12-30
PRIOR APPLICATION NUMBER: 60/030,522
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: PCT/US97/20391
PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: 60/054,380
PRIOR FILING DATE: 1997-07-31
PRIOR APPLICATION NUMBER: 60/030,522
PRIOR FILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 122
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 119

GENERAL INFORMATION:
APPLICANT: Lewis, No. 6210942man G.
APPLICANT: Davin, Laurence B.
APPLICANT: Dinkova-Kostova, Albena T.
APPLICANT: Fujita, Masayuki
APPLICANT: Gang, David R.
APPLICANT: Sarkanen, Simo
APPLICANT: Ford, Joshua D
TITLE OF INVENTION: RECOMBINANT PINORESINOL/LARICRESINOL REDUCTASE,
FILE REFERENCE: WSUR-1-13793
CURRENT FILING DATE: 1999-12-30
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: PCT/US97/20391
PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: 60/054,380
PRIOR FILING DATE: 1997-07-31
PRIOR APPLICATION NUMBER: 60/030,522
PRIOR FILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 122
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 119
LENGTH: 944
TYPE: DNA
ORGANISM: Schisandra chinensis
US-09-475-316A-119
Alignment Scores: 214 944
Pred. No.: 7.00
Score: 100.00%
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 4.93%
DB: 3
Gaps: 0
US-09-690-825-34 (1-142) x US-09-475-316A-119 (1-944)
QY 130 LysValArgAlaIleGlu 136
Db 424 AAGTCAGCGTGCATAGAA 444
RESULT 55
US-09-704-640-119
Sequence 119, Application US/09704640
Patent No. 6635459
GENERAL INFORMATION:
APPLICANT: Lewis, No. 6635459man G.
APPLICANT: Davin, Laurence B.
APPLICANT: Dinkova-Kostova, Albena T.
APPLICANT: Fujita, Masayuki
APPLICANT: Gang, David R.
APPLICANT: Sarkanen, Simo
APPLICANT: Ford, Joshua D
TITLE OF INVENTION: RECOMBINANT PINORESINOL/LARICRESINOL REDUCTASE,
FILE REFERENCE: WSUR-1-16492
CURRENT FILING DATE: 2000-11-02
PRIOR FILING DATE: 1999-12-30
PRIOR APPLICATION NUMBER: 60/030,522
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: PCT/US97/20391
PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: 60/054,380
PRIOR FILING DATE: 1997-07-31
PRIOR APPLICATION NUMBER: 60/030,522
PRIOR FILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 122
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 119

```

; LENGTH: 944
; TYPE: DNA
; ORGANISM: Schisandra chinensis
US-09-704-640-119

Alignment Scores:
Pred. No.: 214          Length: 944
Score: 7.00           Matches: 7
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 4.93%          Indels: 0
DB: 4                  Gaps: 0

US-09-690-825-34 (1-142) x US-09-704-640-119 (1-944)

QY 130 LysValArgAlaIleGlu 136
Db 424 AAGGTCAGGCGTGAATAGAA 444

RESULT 56
US-09-489-039A-5085
; Sequence 5085 Application US/09489039A
; Patent No. 6810836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489.039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 5085
; LENGTH: 951
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-5085

Alignment Scores:
Pred. No.: 215          Length: 951
Score: 7.00           Matches: 7
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 4.93%          Indels: 0
DB: 4                  Gaps: 0

US-09-690-825-34 (1-142) x US-09-489-039A-5085 (1-951)

QY 5 ThrLeuProAlaTyrGln 11
Db 587 ACGCTACCGCAGCATGCCAA 607

RESULT 57
US-08-969-644-21/c
; Sequence 21 Application US/08969644
; Patent No. 6096519
; GENERAL INFORMATION:
; APPLICANT: Ratti, Giulio
; APPLICANT: Comanducci, Maurizio
; APPLICANT: Tecce, Mario F.
; APPLICANT: Giuliani, Marzia M.
; TITLE OF INVENTION: PCTD PLASMID ISOLATED FROM CHLAMYDIA
; TITLE OF INVENTION: TRACHOMATIS SEROTYPE D, ITS GENES AND PROTEINS ENCODED BY
; TITLE OF INVENTION: THEM; RECOMBINANT PLASMIDS FOR THE EXPRESSION OF SAID
; TITLE OF INVENTION: GENES IN HETEROLOGOUS SYSTEMS, PREPARATION OF SAID
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
; STREET: 301 N. Washington Street
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA

; ZIP: 22046-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/969,644
; FILING DATE: 13-NOV-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/467,152
; FILING DATE:
; APPLICATION NUMBER: US/07/661,820
; FILING DATE:
; APPLICATION NUMBER: IT MI 91A000314
; FILING DATE: 07-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svensson, Leonard R.
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 1267-202P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-241-1300
; TELEFAX: 703-241-2848
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 993 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORGANISM: Chlamydia trachomatis
; STRAIN: GO/86 serotype D (trachoma biovar)
; IMMEDIATE SOURCE:
; CLONE: pUC8-pCO plasmid, ATCC 6814
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..993
US-08-969-644-21

Alignment Scores:
Pred. No.: 224          Length: 993
Score: 7.00           Matches: 7
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 4.93%          Indels: 0
DB: 3                  Gaps: 0

US-09-690-825-34 (1-142) x US-08-969-644-21 (1-993)

QY 98 LeuGlyGlupheLeuLysLeu 104
Db 88 CTGGCGGATTTTAAACTT 68

RESULT 58
US-08-444-189-21/c
; Sequence 21 Application US/08444189
; Patent No. 6110705
; GENERAL INFORMATION:
; APPLICANT: Ratti, Giulio
; APPLICANT: Comanducci, Maurizio
; APPLICANT: Tecce, Mario F.
; APPLICANT: Giuliani, Marzia M.
; TITLE OF INVENTION: PCTD PLASMID ISOLATED FROM CHLAMYDIA
; TITLE OF INVENTION: TRACHOMATIS SEROTYPE D, ITS GENES AND PROTEINS ENCODED BY
; TITLE OF INVENTION: THEM; RECOMBINANT PLASMIDS FOR THE EXPRESSION OF SAID
; TITLE OF INVENTION: GENES IN HETEROLOGOUS SYSTEMS, PREPARATION OF SAID
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
; STREET: 301 N. Washington Street

```

; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22046-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,189
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/180,528
; FILING DATE:
; APPLICATION NUMBER: US/07/991,512
; FILING DATE:
; APPLICATION NUMBER: US/07/661,820
; FILING DATE:
; APPLICATION NUMBER: IT MI 91A000314
; FILING DATE: 07-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svensson, Leonard R.
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 1267-202P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-241-1300
; TELEFAX: 703-241-2848
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 993 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORGANISM: Chlamydia trachomatis
; STRAIN: GO/86 serotype D (trachoma biovar)
; IMMEDIATE SOURCE:
; CLONE: pUC8-pGO plasmid, ATCC 68314
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..993
; US-08-444-189-21

Alignment Scores:
Pred. No.: 224 Length: 993
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.93% Indels: 0
DB: 3 Gaps: 0

US-09-690-825-34 (1-142) x US-08-444-189-21 (1-993)
QY 98 LeuGlycLupheLeuLysLeu 104
Db 88 CTGGCGAATTTTAAACTT 68

RESULT 59
US-08-468-544-21/c
; Sequence 21, Application US/08468544
; Patent No. 6248563
; GENERAL INFORMATION:
; APPLICANT: Ratti, Giulio
; APPLICANT: Comanducci, Maurizio
; APPLICANT: Tecce, Mario F.
; APPLICANT: Giuliani, Marzia M.
; TITLE OF INVENTION: PCTD PLASMID ISOLATED FROM CHLAMYDIA
; TITLE OF INVENTION: TRACHOMATIS SEROTYPE D, ITS GENES AND PROTEINS ENCODED BY
; TITLE OF INVENTION: THEM; RECOMBINANT PLASMIDS FOR THE EXPRESSION OF SAID

; TITLE OF INVENTION: GENES IN HETEROLOGOUS SYSTEMS, PREPARATION OF SAID
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
; STREET: 301 N. Washington Street
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22046-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,544
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/661,820
; FILING DATE: 28-FEB-1991
; APPLICATION NUMBER: IT MI 91A000314
; FILING DATE: 07-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svensson, Leonard R.
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 1267-202P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-241-1300
; TELEFAX: 703-241-2848
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 993 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORGANISM: Chlamydia trachomatis
; STRAIN: GO/86 serotype D (trachoma biovar)
; IMMEDIATE SOURCE:
; CLONE: pUC8-pGO plasmid, ATCC 68314
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..993
; US-08-468-544-21

Alignment Scores:
Pred. No.: 224 Length: 993
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.93% Indels: 0
DB: 3 Gaps: 0

US-09-690-825-34 (1-142) x US-08-468-544-21 (1-993)
QY 98 LeuGlycLupheLeuLysLeu 104
Db 88 CTGGCGAATTTTAAACTT 68

RESULT 60
US-08-978-404B-9
; Sequence 9, Application US/08978404B
; Patent No. 5968782
; GENERAL INFORMATION:
; APPLICANT: Stevens, Richard L.
; TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
; TITLE OF INVENTION: FIBRINOGEN
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.

```
/ STREET: 600 Atlantic Avenue
/ CITY: Boston
/ STATE: MA
/ COUNTRY: U.S.A.
/ ZIP: 02210-2211
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/978,404B
/ FILING DATE: 25-NOV-97
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/032,354
/ FILING DATE: 04-DEC-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Plumer, Elizabeth R.
/ REGISTRATION NUMBER: 36,637
/ REFERENCE/DOCKET NUMBER: B0801/7090
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617-720-3500
/ TELEFAX: 617-720-2441
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 9:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1095 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-978-404B-9

Alignment Scores:
Pred. No.: 246 Length: 1095
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.93% Indels: 0
DB: 2 Gaps: 0

US-09-690-825-34 (1-142) x US-08-978-404B-9 (1-1095)

QY 3 AlaProThLeuProAla 9
Db 646 CCCCCCACCCTACCACTGCA 666

RESULT 61
US-09-475-316A-61
; Sequence 61, Application US/09475316A
; Patent No. 6210942
; GENERAL INFORMATION:
; APPLICANT: Lewis, No. 6210942man G.
; APPLICANT: Davin, Laurence B.
; APPLICANT: Dinkova-Kostova, Albena T.
; APPLICANT: Fujita, Masayuki
; APPLICANT: Gang, David R.
; APPLICANT: Sarkanen, Simo
; APPLICANT: Ford, Joshua D
; TITLE OF INVENTION: RECOMBINANT PINORESINOL/LARICRESINOL REDUCTASES,
; TITLE OF INVENTION: RECOMBINANT DIRIGENT PROTEINS AND METHODS OF USE
; FILE REFERENCE: WSUR-1-13793
; CURRENT APPLICATION NUMBER: US/09/475,316A
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: 09/307,653
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: PCT/US97/20391
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: 60/054,380
; PRIOR FILING DATE: 1997-07-31
; PRIOR APPLICATION NUMBER: 60/030,522
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 61
; LENGTH: 1190
; TYPE: DNA
; ORGANISM: Thuja plicata
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13)..(951)
; US-09-704-640-61

Alignment Scores:
Pred. No.: 265 Length: 1190
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.93% Indels: 0
DB: 4 Gaps: 0

US-09-690-825-34 (1-142) x US-09-704-640-61 (1-1190)

QY 130 LysValArgAlaIleGlu 136
Db 430 AAGGTTGGCGTGCCATTGAA 450
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/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 61
/ LENGTH: 1190
/ TYPE: DNA
/ ORGANISM: Thuja plicata
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (13)..(951)
/ US-09-475-316A-61

Alignment Scores:
Pred. No.: 265 Length: 1190
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.93% Indels: 0
DB: 3 Gaps: 0

US-09-690-825-34 (1-142) x US-09-475-316A-61 (1-1190)

QY 130 LysValArgAlaIleGlu 136
Db 430 AAGGTTGGCGTGCCATTGAA 450

RESULT 62
US-09-704-640-61
; Sequence 61, Application US/09704640
; Patent No. 6635459
; GENERAL INFORMATION:
; APPLICANT: Lewis, No. 6635459man G.
; APPLICANT: Davin, Laurence B.
; APPLICANT: Dinkova-Kostova, Albena T.
; APPLICANT: Fujita, Masayuki
; APPLICANT: Gang, David R.
; APPLICANT: Sarkanen, Simo
; APPLICANT: Ford, Joshua D
; TITLE OF INVENTION: RECOMBINANT PINORESINOL/LARICRESINOL REDUCTASE,
; TITLE OF INVENTION: RECOMBINANT DIRIGENT PROTEIN AND METHODS OF USE
; FILE REFERENCE: WSUR-1-16492
; CURRENT APPLICATION NUMBER: US/09/704,640
; CURRENT FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: 09/475,316
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: 09/307,653
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: PCT/US97/20391
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: 60/054,380
; PRIOR FILING DATE: 1997-07-31
; PRIOR APPLICATION NUMBER: 60/030,522
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 61
; LENGTH: 1190
; TYPE: DNA
; ORGANISM: Thuja plicata
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13)..(951)
; US-09-704-640-61

Alignment Scores:
Pred. No.: 265 Length: 1190
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.93% Indels: 0
DB: 4 Gaps: 0

US-09-690-825-34 (1-142) x US-09-704-640-61 (1-1190)

QY 130 LysValArgAlaIleGlu 136
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Db 430 RAGGTCGGCGTGCATTGAA 450
RESULT 63
US-09-328-352-3331/c
; Sequence 3331, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Berton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/328,352
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 3331
; LENGTH: 1194
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-3331
Alignment Scores:
Pred. No.: 266 Length: 1194
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.93% Indels: 0
DB: 4 Gaps: 0
US-09-690-825-34 (1-142) x US-09-328-352-3331 (1-1194)
QY 109 AlaLysAsnLysIleAlaLys 115
Db 473 GCTAAAAACAATAAGCAAAA 453
RESULT 64
US-09-252-991A-8373/c
; Sequence 8373, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 8373
; LENGTH: 1230
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-8373
Alignment Scores:
Pred. No.: 273 Length: 1230
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.93% Indels: 0
DB: 4 Gaps: 0
US-09-690-825-34 (1-142) x US-09-252-991A-8373 (1-1230)
QY 8 ProAlaTrpGlnProPheLeu 14
Db 99 CCGGCGTGGCAGCGTTCCTC 79
RESULT 65
US-09-252-991A-8504

; Sequence 8504, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 8504
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-8504
Alignment Scores:
Pred. No.: 279 Length: 1257
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.93% Indels: 0
DB: 4 Gaps: 0
US-09-690-825-34 (1-142) x US-09-252-991A-8504 (1-1257)
QY 8 ProAlaTrpGlnProPheLeu 14
Db 1216 CCGGCGTGGCAGCGTTCCTC 1236
RESULT 66
US-09-475-316A-69
; Sequence 69, Application US/09475316A
; Patent No. 6210942
; GENERAL INFORMATION:
; APPLICANT: Lewis, No. 6210942man G.
; APPLICANT: Dinkova-kostova, Albena T.
; APPLICANT: Fujita, Masayuki
; APPLICANT: Gang, David R.
; APPLICANT: Sarkanen, Simo
; APPLICANT: Ford, Joshua D
; TITLE OF INVENTION: RECOMBINANT PINORESINOL/LARICRESINOL REDUCTASES,
; FILE REFERENCE: WSUR-1-13793
; CURRENT APPLICATION NUMBER: US/09/475,316A
; PRIOR FILING DATE: 1999-12-30
; CURRENT APPLICATION NUMBER: 09/307,653
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: PCT/US97/20391
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: 60/054,380
; PRIOR FILING DATE: 1997-07-31
; PRIOR APPLICATION NUMBER: 60/030,522
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 69
; LENGTH: 1282
; TYPE: DNA
; ORGANISM: Tsuga heterophylla
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(922)
US-09-475-316A-69
Alignment Scores:
Pred. No.: 284 Length: 1282
Score: 7.00 Matches: 7

Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 4.93% Indels: 0
 DB: 3 Gaps: 0

US-09-690-825-34 (1-142) x US-09-475-316A-69 (1-1282)

QY 130 LysValArgAlaIleGlu 136
 |||||
 DB 404 AAGGTCGCGCGCCATTGAA 424

RESULT 67

US-09-704-640-69
 ; Sequence 69, Application US/09704640
 ; Patent No. 6635459

; GENERAL INFORMATION:

; APPLICANT: Lewis, No. 6635459man G.
 ; APPLICANT: Davin, Laurence B.
 ; APPLICANT: Dinkova-Kostova, Albena T.
 ; APPLICANT: Fujita, Masayuki
 ; APPLICANT: Gang, David R.
 ; APPLICANT: Sarkanen, Simo
 ; APPLICANT: Ford, Joshua D

; TITLE OF INVENTION: RECOMBINANT PINOESINOL/LARICRESINOL REDUCTASE,
 ; TITLE OF INVENTION: RECOMBINANT DIRIGENT PROTEIN AND METHODS OF USE

; FILE REFERENCE: WSUR-1-16492

; CURRENT APPLICATION NUMBER: US/09/704,640

; PRIOR FILING DATE: 2000-11-02

; PRIOR APPLICATION NUMBER: 09/475,316

; PRIOR FILING DATE: 1999-12-30

; PRIOR APPLICATION NUMBER: 09/307,653

; PRIOR FILING DATE: 1999-05-07

; PRIOR APPLICATION NUMBER: PCT/US97/20391

; PRIOR FILING DATE: 1997-11-07

; PRIOR APPLICATION NUMBER: 60/054,380

; PRIOR FILING DATE: 1997-07-31

; PRIOR APPLICATION NUMBER: 60/030,522

; PRIOR FILING DATE: 1996-11-08

; NUMBER OF SEQ ID NOS: 122

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 69

; LENGTH: 1282

; TYPE: DNA

; ORGANISM: Tsuga heterophylla

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (2)..(922)

US-09-704-640-69

Alignment Scores:

Pred. No.: 284 Length: 1282

Score: 7.00 Matches: 7

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 4.93% Indels: 0

DB: 4 Gaps: 0

US-09-690-825-34 (1-142) x US-09-704-640-69 (1-1282)

QY 130 LysValArgAlaIleGlu 136
 |||||
 DB 404 AAGGTCGCGCGCCATTGAA 424

RESULT 68

US-09-475-316A-65

; Sequence 65, Application US/09475316A

; Patent No. 6210942

; GENERAL INFORMATION:

; APPLICANT: Lewis, No. 6210942man G.

; APPLICANT: Davin, Laurence B.

; APPLICANT: Dinkova-Kostova, Albena T.

; APPLICANT: Fujita, Masayuki

; APPLICANT: Gang, David R.

; APPLICANT: Sarkanen, Simo
 ; APPLICANT: Ford, Joshua D
 ; TITLE OF INVENTION: RECOMBINANT PINOESINOL/LARICRESINOL REDUCTASE,
 ; TITLE OF INVENTION: RECOMBINANT DIRIGENT PROTEINS AND METHODS OF USE

; FILE REFERENCE: WSUR-1-13793

; CURRENT APPLICATION NUMBER: US/09/475,316A

; CURRENT FILING DATE: 1999-12-30

; PRIOR APPLICATION NUMBER: 09/307,653

; PRIOR FILING DATE: 1999-05-07

; PRIOR APPLICATION NUMBER: PCT/US97/20391

; PRIOR FILING DATE: 1997-11-07

; PRIOR APPLICATION NUMBER: 60/054,380

; PRIOR FILING DATE: 1997-07-31

; PRIOR APPLICATION NUMBER: 60/030,522

; PRIOR FILING DATE: 1996-11-08

; NUMBER OF SEQ ID NOS: 122

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 65

; LENGTH: 1308

; TYPE: DNA

; ORGANISM: Thuja plicata

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (164)..(1105)

US-09-475-316A-65

Alignment Scores:

Pred. No.: 289 Length: 1308

Score: 7.00 Matches: 7

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 4.93% Indels: 0

DB: 3 Gaps: 0

US-09-690-825-34 (1-142) x US-09-475-316A-65 (1-1308)

QY 130 LysValArgAlaIleGlu 136
 |||||

DB 581 AAAGTAGACGTGCGCATTTGAA 601

RESULT 69

US-09-704-640-65

; Sequence 65, Application US/09704640

; Patent No. 6635459

; GENERAL INFORMATION:

; APPLICANT: Lewis, No. 6635459man G.

; APPLICANT: Davin, Laurence B.

; APPLICANT: Dinkova-Kostova, Albena T.

; APPLICANT: Fujita, Masayuki

; APPLICANT: Gang, David R.

; APPLICANT: Sarkanen, Simo

; APPLICANT: Ford, Joshua D

; TITLE OF INVENTION: RECOMBINANT PINOESINOL/LARICRESINOL REDUCTASE,

; TITLE OF INVENTION: RECOMBINANT DIRIGENT PROTEIN AND METHODS OF USE

; FILE REFERENCE: WSUR-1-16492

; CURRENT APPLICATION NUMBER: US/09/704,640

; CURRENT FILING DATE: 2000-11-02

; PRIOR APPLICATION NUMBER: 09/475,316

; PRIOR FILING DATE: 1999-12-30

; PRIOR APPLICATION NUMBER: 09/307,653

; PRIOR FILING DATE: 1999-05-07

; PRIOR APPLICATION NUMBER: PCT/US97/20391

; PRIOR FILING DATE: 1997-11-07

; PRIOR APPLICATION NUMBER: 60/054,380

; PRIOR FILING DATE: 1997-07-31

; PRIOR APPLICATION NUMBER: 60/030,522

; PRIOR FILING DATE: 1996-11-08

; NUMBER OF SEQ ID NOS: 122

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 65

; LENGTH: 1308

; TYPE: DNA

; ORGANISM: Thuja plicata

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (164)..(1105)
US-09-704-640-65

Alignment Scores:
Pred. No.: 289 Length: 1308
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.93% Indels: 0
DB: 4 Gaps: 0

US-09-690-825-34 (1-142) x US-09-704-640-65 (1-1308)
QY 130 LysValArgAlaIleGlu 136
DB 581 AAGTTAGACGGCCATTGAA 601

RESULT 70
US-09-475-316A-71
; Sequence 71, Application US/09475316A
; Patent No. 6210942
; GENERAL INFORMATION:
; APPLICANT: Lewis, No. 6210942man G.
; APPLICANT: Davis, Laurence B.
; APPLICANT: Dinkova-Kostova, Albena T.
; APPLICANT: Fujita, Masayuki
; APPLICANT: Gang, David R.
; APPLICANT: Sarkanen, Simo
; APPLICANT: Ford, Joshua D
; TITLE OF INVENTION: RECOMBINANT PINOSESINOL/LARICRESINOL REDUCTASES,
; FILE REFERENCE: WSUR-1-13793
; CURRENT FILING DATE: 1999-12-30
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: PCT/US97/20391
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: 60/054,380
; PRIOR FILING DATE: 1997-07-31
; PRIOR APPLICATION NUMBER: 60/030,522
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 71
; LENGTH: 1328
; TYPE: DNA
; ORGANISM: Tsuga heterophylla
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (20)..(946)
US-09-704-640-71

Alignment Scores:
Pred. No.: 294 Length: 1328
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.93% Indels: 0
DB: 4 Gaps: 0

US-09-690-825-34 (1-142) x US-09-704-640-71 (1-1328)
QY 130 LysValArgAlaIleGlu 136
DB 428 AAGTTGCGCGCCATTGAA 448

RESULT 72
US-09-205-258-212
; Sequence 212, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT FILING DATE: 1998-12-04
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: PCT/US98/11422
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,885
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,375
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,881
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,880
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,896
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,020
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,876

; FEATURE:
; NAME/KEY: CDS
; LOCATION: (20)..(946)
US-09-475-316A-71

Alignment Scores:
Pred. No.: 294 Length: 1338
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.93% Indels: 0
DB: 3 Gaps: 0

US-09-690-825-34 (1-142) x US-09-475-316A-71 (1-1328)
QY 130 LysValArgAlaIleGlu 136
DB 428 AAGTTGCGCGCCATTGAA 448

RESULT 71
US-09-704-640-71
; Sequence 71, Application US/09704640
; Patent No. 6635459
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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 212
; LENGTH: 1551
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE

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; LOCATION: (420)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1017)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1408)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1423)
; OTHER INFORMATION: n equals a,t,g, or c
; OTHER INFORMATION: n equals a,t,g, or c
US-09-205-258-212

Alignment Scores:
Pred. No.: 339 Length: 1551
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.93% Indels: 0
DB: 4 Gaps: 0

US-09-690-825-34 (1-142) x US-09-205-258-212 (1-1551)

Qy 13 PheLeuLysAspHisArgile 19
Db 177 TTTTGAAGATCATAGGATA 197

RESULT 73
US-09-648-004-9
; Sequence 9, Application US/09648004
; Patent No. 6498242
; GENERAL INFORMATION:
; APPLICANT: CHEN QIONG
; APPLICANT: THOMAS, STUART
; APPLICANT: NAGARAJAN, VASANTHA
; TITLE OF INVENTION: BIOLOGICAL METHOD FOR THE PRODUCTION OF ADIPIC ACID AND
; TITLE OF INVENTION: INTERMEDIATES
; FILE REFERENCE: CL-1341-A
; CURRENT APPLICATION NUMBER: US/09/648,004
; CURRENT FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/252,553
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 9
; LENGTH: 1644
; TYPE: DNA
; ORGANISM: Acinetobacter sp.
US-09-648-004-9

Alignment Scores:
Pred. No.: 358 Length: 1644
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.93% Indels: 0
DB: 4 Gaps: 0

US-09-690-825-34 (1-142) x US-09-648-004-9 (1-1644)

Qy 129 LysLysValArgAlaile 135
Db 1226 AAGAAGGTCCTCGAGCTATA 1246

RESULT 74
US-09-107-532A-2080
; Sequence 2080, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush

```

CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/208,036
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/887,382
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1779 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: Bacillus caldotenax
STRAIN: YT-G(DSM406)
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-208-036-16

Alignment Scores: 385 Length: 1779
Pred. No.: 7.00 Matches: 7
Score:

Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 4.93% Indels: 0
 DB: 1 Gaps: 0

US-09-690-825-34 (1-142) x US-08-208-036-16 (1-1779)

Qy 5 ThrLeuProAlaTrpGln 11

Db 876 ACATTACGCCAGCTTGGCAA 896

Search completed: August 16, 2004, 03:24:53
 Job time : 112 secs